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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No. EPI-067191

First Inventor or Application Identifier Jonathan W. Nyce

Title LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE...

Express Mail Label No. EJ 664079305 US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO:

Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

1. ☒ * Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)
2. ☒ Specification [Total Pages
(preferred arrangement set forth below)
 - Descriptive title of the invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the invention
 - Brief Summary of the invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
3. ☐ Drawing(s) (35 U.S.C. 113) [Total Sheets
4. Oath or Declaration [Total Pages
 - a. ☐ Newly executed (original or copy)
 - b. ☐ Copy from a prior application (37 C.F.R. § 1.63(d))
(for continuation/divisional with Box 16 completed)
 - i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

5. ☐ Microfiche Computer Program (Appendix)
6. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 - a. ☒ Computer Readable Copy
 - b. ☒ Paper Copy (identical to computer copy)
 - c. ☒ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

7. ☒ Assignment Papers (cover sheet & document(s))
8. ☐ 37 C.F.R. § 3.73(b) Statement (when there is an assignee) ☒ Power of Attorney (2)
9. ☐ English Translation Document (if applicable)
10. ☒ Information Disclosure Statement (IDS)/PTO-1449 ☒ Copies of IDS Citations
11. ☐ Preliminary Amendment
12. ☒ Return Receipt Postcard (MPEP 503)
(Should be specifically itemized)
13. ☐ * Small Entity Statement filed in prior application, (PTO/SB/09-12) Status still proper and desired
14. ☐ Certified Copy of Priority Document(s) (if foreign priority is claimed)
15. ☒ Other: checks, cover letter

* NOTE FOR ITEMS 1 & 13: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

16. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in a preliminary amendment.

☒ Continuation ☐ Divisional ☐ Continuation-in-part (CIP)

of prior application No: 60,127,958

Prior application information: Examiner

Group / Art Unit:

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 4b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

17. CORRESPONDENCE ADDRESS

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Name	Viviana Amzel, Ph.D.				
	ARTER & HADDEN, LLP				
Address	725 South Figueroa Street				
	Suite No. 3400				
City	Los Angeles,	State	CA	Zip Code	90017
Country	USA	Telephone	(213) 430-3520	Fax	(213) 617-9255

Name (Print/Type)	Viviana Amzel, Ph.D.	Registration No. (Attorney/Agent)	30,930
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

SEQ. BOX

For: **LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONTRICION, LUNCH INFLAMMATION, ALLERGY(IES) & SURFACTANT DEPLETION**

Commissioner for Patents, Washington D C 20231, on April 4, 2000, by Jenny R. Wilson

Jenny R. Wilson

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY
STATUS (37 CFR 1.9(f) AND 1.27 (d)) - NONPROFIT ORGANIZATION**

Docket No.
P66 42161

Serial No.
To Be Assigned

Filing Date
Herewith

Patent No.

Issue Date

Applicant/ Jonathan W. Nyce and W. James Metzger
Patentee:

Invention:

Low Adenosine Anti-Sense Oligonucleotide, Compositions, Kit & Method for Treatment of Airway Disorders
Associated with Bronchoconstriction, Lung Inflammation, Allergy(ies) & Surfactant Depletion

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION: East Carolina University
ADDRESS OF ORGANIZATION: 103 Spilman Building
Greenville, North Carolina 27858

TYPE OF NONPROFIT ORGANIZATION:

- ☐ University or other Institute of Higher Education
- ☒ Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3))
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Name of State: Citation of Statute:
- ☐ Would Qualify as Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3)) if Located in The United States of America
- ☐ Would Qualify as Nonprofit Scientific or Educational under Statute of State of The United States of America if Located in The United States of America
Name of State: Citation of Statute:

I hereby declare that the above-identified nonprofit organization qualifies as a nonprofit organization as defined in 37 C.F.R. 1.9(e) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in:

- ☐ the specification to be filed herewith.
- ☒ the application identified above.
- ☐ the patent identified above.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the above-identified nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed on the next page and no rights to the invention are held by any person, other than the inventor, who could not qualify as an independent inventor under 37 CFR 1.9(c) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern or organization to which I have assigned, granted, conveyed, or licensed or am under an obligation under contract or law to assign, grant, convey, or license any rights in the invention is listed below:

- ☒ no such person, concern or organization exists.
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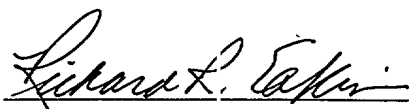
Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Richard R. Eakin
 TITLE IN ORGANIZATION: Chancellor
 ADDRESS OF PERSON SIGNING: East Carolina University
103 Spilman Building
Greenville, North Carolina 27858

SIGNATURE:



DATE:

4/21/99

**LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT
& METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED
WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,
ALLERGY(IES) & SURFACTANT DEPLETION**

5

BACKGROUND OF THE INVENTION

Field of the Invention

This patent relates to a composition comprising oligonucleotides (oligos) that are anti-sense to adenosine receptors, and contain low amounts of or no adenosine (A). These agents are suitable for the treatment, among others, of pulmonary diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, allergic rhinitis, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

15 **Background of the Invention**

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the depletion reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A₁ receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A₁ receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor antagonist is available for clinical use attests to the general toxicity of these agents. Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding

an appropriate route of administration to deliver them to their site of action. Many in vivo experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature. Although anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as pharmacological agents in human disease, finding practical and effective applications for these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature. The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being an inherent difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%. Anti-sense oligonucleotides have been used in therapy by many, including the present inventor, who in his previous work successfully treated various diseases and conditions by direct administration of these agents to the lung. In many instances, other workers have had to face the difficulties associated with the delivery of DNA molecules to a desired target. Thus, the route of administration may be of extreme importance for treating generalized diseases and conditions as well as those which are localized. In contrast, up to the present time, the delivery of anti-sense agents to the lung has been relatively undeveloped. As described by the present inventor in more detail below, the lung is an excellent target for the direct administration of anti-sense oligonucleotides and provides a non-invasive and a tissue-specific route.

Clearly, there exist presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of adenosine mediated ailments afflicting the pulmonary and respiratory ailments affecting the lung airways, including respiratory problems, bronchoconstriction, inflammation, allergy(ies), depletion or hyposecretion of surfactant, etc., which is highly effective and sufficiently selective to avoid detrimental side effects produced by other therapies. In addition, there is a definite need for making available a delivery method that will require low amounts of therapeutic agents and will be effective for the rapid and targeted access of tissue genes or mRNAs and the reversal of untoward effects afflicting a subject.

SUMMARY OF THE INVENTION

The present invention generally relates to a pharmaceutical or veterinary composition, comprising an anti-sense oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies), and/or surfactant depletion and/or hyposecretion, when administered to a mammal, the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and a pharmaceutically or veterinarily acceptable carrier or diluent. The targets are typically molecules associated with airway disease, cancer, etc., such as transcription factors, stimulating and activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding proteins, and malignancy associated proteins, among others. Examples are oligo(s) targeted to adenosine receptor(s) and it(they) are typically

present in the composition in an amount effective to reduce adenosine mediated effect(s), such as airway obstruction, inflammation, allergy(ies), and surfactant depletion, among others. The adenosine receptor is preferably selected from the group consisting of the adenosine A₁, A_{2b}, and A₃ receptors, and in some instances even adenosine A_{2a} receptors. The oligo of the invention may be applied to the preparation of a medicament for (a) reducing adenosine-mediated bronchoconstriction, impeded respiration, inflammation, allergy(ies), depletion production of surfactant, and other detrimental pulmonary effects in a subject in need of treatment, and/or for (b) treating specific diseases and conditions such as asthma, cystic fibrosis, allergic rhinitis, COPD, etc. For the first time this invention provides the targeted administration of one or more oligonucleotides directly into the respiratory system. The oligos may be directed to any target and are intended for fast delivery through the mucosal tissue of the lungs for hybridization to a desired target polynucleotide, e. g. mRNA, to prevent gene transcription and translation, such that protein expression will be reduced, hampered, or completely stopped. Thus, this invention also provides a more general method for administering oligonucleotides that are anti-sense to targeted genes and mRNAs associated with any type of diseases, by direct administration into the respiratory system, e. g. by inhalation, by introduction of a solution or aerosol into the respiratory airways, and/or directly into the lung.

The present oligos, moreover, are suitable for reducing effects mediated by a variety of target proteins and genes, for example adenosine-mediated effects, including pulmonary, respiratory, and other associated effects, e. g. bronchoconstriction, inflammation, immune mediated reactions, allergy(ies) and other airway problems, which may be caused by different conditions, including cancer. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), bronchitis, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agents are also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present agent is effectively administered prophylactically and therapeutically in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects. The oligo(s) may be administered by any means known to a subject, e. g. to the lungs of the subject, more generally through any and all systemic and topical routes. This oligonucleotide(s) (oligo(s)) employed are anti-sense to a target DNA or RNA, e. g. an adenosine receptor DNA or RNA, and preferably consist essentially of up to about 15% adenosine (A), and more preferably contain no adenosine. The oligos are provided in the form of specific compositions and formulations, with a carrier or diluent, and optionally with other therapeutic agents and additives which are used for administration by specific routes, e.g. into the respiratory system, topically, transdermally, parenterally, by implantation, and the like. The oligo is also provided as a capsule or cartridge, and in the form of a kit. The oligos of the invention may be produced by selection of specific targeted segments of the gene or mRNA encoding the adenosine receptor as described below. In one preferred embodiment, the selection is made to obtain oligos that consisting essentially of less than about 15% adenosine (A). This may be done by selecting the target as done above, which includes genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxta-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, an alternative, e. g. a universal base(s) or other base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than about 15%, and down to no adenosine. Similarly, alternative and/or universal bases may be substituted for adenosine, e. g. specific

adenosine A1, A2b and A3 receptor antagonists or A2a receptor agonists, theophylline, enprophylline, and many other adenosine receptor antagonists known in the art as well as agonists with significantly reduced agonist activity with respect to adenosine, e. g. less than 0.5%, less than 0.3%, and the like.

5 The invention will now be described in general in conceptual and experimental terms, with reference to specific examples. Other objects, advantages and features of the present invention will become apparent to those skilled in the art from the description that follows.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

10 This invention arose from a desire by the inventor to improve on prior art treatments for pulmonary and other diseases, which technology is generally fraught with detrimental side effects and by the need of administering high doses of therapeutical agents. The present invention arises from the inventor's own discovery that adenosine receptor targeted anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation and/or allergy(ies), constrict bronchial tissue, obstruct the lung airways, depletion surfactant secretion, or otherwise impede normal breathing. In general, many diseases and conditions are associated with or cause inflammation, constrict bronchial tissue or the lung airways, depletion secretion of surfactant, augment allergy(ies), or otherwise impede normal breathing. This treatment is selective for specific targets associated with or mediating these symptoms, and the agents are administered in up to 1000-fold lower doses than those seen in the art. The inventor, in addition, wanted to provide a treatment which would improve the outcome and life style of patients undergoing other procedures or being administered other therapies, including antibody therapy, chemotherapy, radiation, phototherapy, and surgery e.g. cancer surgery, and that could be effectively administered preventatively, prophylactically or therapeutically. He reasoned that he could further improve on this discovery by selecting oligos of reduced adenosine content, or reducing the adenosine content of otherwise targeted anti-sense oligos corresponding to endogenous polynucleotide sequences. The present invention is premised on the discovery by the inventor that 15 oligonucleotides are metabolized in vivo to their mononucleotides. Adenosine (A)-containing oligonucleotides break down and release adenosine which, in turn, activates adenosine receptors, thereby causing bronchoconstriction, inflammation, surfactant depletion, allergy(ies), and the like. He, thus, conceived of employing low adenosine-free adenosine oligos to avoid these side effects upon their administration. He succeeded in this endeavor and is providing in this patent novel and improved compositions, formulations and methods which afford greatly improved results when compared with previously known treatments for preventing and alleviating bronchoconstriction, allergy(ies), inflammation, breathing difficulties, surfactant depletion and blockage of airways, as well as for other conditions which affect the lung directly or indirectly. In different embodiments, one or more nucleic acids of the invention may be formulated alone, and/or with one or more surfactant components and/or with a carrier, and/or with other therapeutic agents and/or formulation agents known in the art. The compositions of this invention, thus, may be incorporated into a variety of formulations for systemic and topical administration. Moreover, the inventor also provides a broad method for delivery of anti-sense oligonucleotides (oligos) through the respiratory system, as a fast means of starting treatment to address acute attacks of asthma and other diseases and conditions that have a rapid onset. In addition, the present agents have long halflives and may be administered at very low doses. This makes them ideal for once a week type therapies. In the past, anti-sense oligonucleotides received considerable theoretical consideration as being potentially useful as pharmacologic agents for the treatment of human disease. Wagner, R., Nature 372: 333-335 (1994). However, it has been difficult to actually apply these molecules to alleviating and curing human diseases. One important consideration in the pharmacologic application of these molecules has been the failure of various routes of administration to deliver the compounds to its target while avoiding invading the circulation and, therefore, other untargeted tissues which, thus, produces a plethora of side effects. Most in vivo experiments utilizing anti-sense oligonucleotides involved a direct application of the oligo to limited regions of the brain. See, Wahlestedt, C., Trends in Pharmacol. Sci. 15: 42-46 (1994); Lai, et al., Neuroreport 5: 1049-1052 (1994); Standifer, K., et al., Neuron 12: 805-810

(1994); Akabayashi, A., et al., Brain Res. 21: 55-61 (1994). Others applied them into the spinal fluid. See, e.g. Tseng, L., et al., European J. Pharmacol. 258: R1-3 (1994); Raffa, R., et al., European J. Pharmacol. 258: R5-7 (1994); Gillardon, F., et al., European J. Neurosci. 6: 880-884 (1994). Such applications, clearly, have no practical clinical utility due to their invasive nature. Thus, the systemic administration of anti-sense oligonucleotides poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues. The systemic administration of anti-sense oligonucleotides also poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues.

The respiratory system, and in particular the lung, as the ultimate port of entry into the organism, however, is an excellent route of administration for anti-sense oligonucleotides. This is so not only for the treatment of lung disease, but also when utilizing the lung as a means for delivery, particularly because of its non-invasive and tissue-specific nature. Thus, local delivery of antisense oligonucleotides directly to the target tissue enables the therapeutic use of these compounds. Fomivirsen (ISIS 2302) is an example of a local drug delivery into the eye to treat cytomegalovirus (CMV) retinitis, for which a new drug application has been filed by ISIS. The administration of a drug through the lung offers the further advantage that inhalation is non-invasive whereas direct injection in to the vitreous of the eye is invasive. The composition and formulations of this invention are highly efficacious for preventing and treating diseases and conditions associated with bronchoconstriction, difficult breathing, impeded and obstructed lung airways, allergy(ies), inflammation and surfactant depletion, among others. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of Supraventricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The invention will be described with respect to the adenosine receptors as targets, but is similarly applicable to any other target with respect to the pulmonary administration of anti-sense oligos. The examples provided below show a complete inhibition of such adenosine receptor associated symptoms in a rabbit model for human bronchoconstriction, allergy(ies) and inflammation as well as the elimination of the ability of the adenosine receptor agonist par excellence, adenosine, to cause bronchoconstriction in hyper-responsive monkeys, which are animal models for human hyper-responsiveness to adenosine receptor agonists. The pharmaceutical composition and formulations of the invention, therefore, are suitable for preventing and alleviating the symptoms associated with stimulation of adenosine receptors, such as the adenosine A₁ receptors. The compositions and formulations of this invention, thus, are also suitable for prevent the untoward side effects of adenosine-mediated hyperresponsiveness in certain individuals, which are generally seen in diseases affecting respiratory activity.

The method of the present invention may be used to treat airway diseases and conditions in a subject of any kind and for any reason, with the intention that the adenosine content of anti-sense compounds be minimized, reduced or eliminated so as to prevent its liberation upon anti-sense degradation. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the compositions and formulations of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, allergic rhinitis, impeded respiration, Acute Respiratory Distress Syndrome (ARDS), renal damage and failure associated with ischemia as well as the administration of certain drugs, side effects associated with adenosine administration e.g. in Supraventricular Tachycardia (SVT) and in adenosine stress tests, infantile Respiratory Distress Syndrome (infantile RDS), ARDS, pain,

cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, metastatic cancer such as hepatic metastases, lung, breast and prostate metastases, among others. The present compositions and formulations are suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present compositions and formulations may also be administered effectively as a substitute for therapies that have significant negative side effects. The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. For consistency's sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids). Nucleotide sequences are presented herein by single strand only, in the 5' to 3' direction, from left to right. In addition, nucleotide and amino acids are represented herein in the manner recommended by the IUPAC-IUB Biochemical Nomenclature Commission, or (for amino acids) by three letter code, in accordance with 37 CFR 1.822 and established usage. See, e.g., PatentIn User Manual, 99-102 (Nov. 1990) (U.S. Patent and Trademark Office, Office of the Assistant Commissioner for Patents, Washington, D.C. 20231); U.S. Patent No. 4,871,670 to Hudson et al. at col. 3, lines 20-43. The present method utilizes anti-sense agents to inhibit or down-regulate gene expression of target genes, including those listed in Tables 1 and 2 below. This is generally attained by hybridization of the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide or anti-sense oligo" is generally a short sequence of synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein. The terms "desAdenosine" (desA) and "des-thymidine" (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des A or des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another lacking its undesirable activity, such as acting as an agonist or having a triggering effect at the adenosine A receptor(s). In the present context, the substitution is generally accomplished by substitution of A with a "universal or alternative base", presently known in the art or to be ascertained at a later time. As used herein, the terms "prevent", "preventing", "treat" or "treating" refer to a preventative, prophylactic, maintenance, or therapeutic treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms associated with adenosine receptor stimulation. The term "down-regulate" refers to inducing a decrease in production, secretion or availability and, thus, a decrease in concentration, of intracellular target product, be it a receptor e. g. adenosine A₁, A_{2b}, A₃, bradykinin 2B, GATA-3, or other receptors, or an increase in concentration of the adenosine A_{2a} receptor. The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to

design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with an alternative or a universal base, or an adenosine analog incapable of significantly, or having substantially reduced ability for, activating or antagonizing adenosine A₁, A_{2b} or A₃ receptors or which may act as an agonist at the adenosine A_{2a} receptor. Any number of adenosines present may be substituted by an alternative and/or universal base, such as heteroaromatic bases, which binds to a thymidine base but has less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors. Based on his prior experience in the field, the inventor reasoned that in addition to "downregulating" specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of a mRNA molecule which encodes a protein associated with impeded breathing, allergy(ies), lung inflammation, depletion of lung surfactant or lowering of lung surfactant, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject's lung. In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, α -methoxy ethyl and similar modifications, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See, Milligan et al.; Cohen, J. S. D., supra. In another preferred embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See Tidd, D. M. and Warenus, H.M., *Be. J. Cancer* 60: 343-350 (1989); Shaw, J.P. et al., *Nucleic Acids Res.* 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention, as do α' modifications, such as α' methoxy ethyl, and the like. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See, Milligan, et al., supra. In addition, a plurality of substitutions to the carbohydrate ring are also known to improve stability of nucleic acids. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, supra. Preferred backbone analogue residues include phosphoramidate, phosphorothioate, methylphosphonate, phosphotriester, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal, triformacetal, thioether, carbamate, boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, C₅-substituted nucleotides, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), methoxymethyl (MOM), and methoxyethyl(MOE), and methyleneoxy(methylimino) (MOMI) residues, and combinations thereof. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, supra. Where appropriate, the agent of this

invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable salts is administered. A single agent of this invention has the capacity to attenuate the expression of a target mRNA and/or various agents to enhance or attenuate the activity of a pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mononucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, i.e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i.e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As. The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region. The flanking regions of the exons may also be targeted as well as the spliced segments in the precursor mRNAs. The mRNA sequences of the adenosine receptors and of many other targets are derived from the DNA base sequence of the gene expressing either receptors, e.g. the adenosine receptors, the enzymes, factors, or other targets associated with airway disease. For example, the sequence of the genomic human A₁ adenosine receptor is known and is disclosed in U.S. Patent No. 5,320,963 to Stiles, G., et al. The A₃ adenosine receptor has been cloned, sequenced and expressed in rat (see, Zhou, F., et al., P.N.A.S. (USA) 89: 7432 (1992)) and human (see, Jacobson, M. A., et al., U.K. Patent Application No. 9304582.1 (1993)). The sequence of the adenosine A_{2b} receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., Genomics (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the remaining exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques. The sequences for the adenosine A_{2a} bradykinin, and other genes as well as methods for preparation of oligonucleotides are also known as those of many other target genes and mRNAs for which this invention is suitable. Thus, anti-sense oligonucleotides that downregulate the production of target sequences associated with airway disease, including the adenosine A₁, A_{2a}, A_{2b}, A₃, bradykinin, GATA-3, COX-2, and many other receptors, may be produced in accordance with standard techniques. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress

syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer.

The adenosine receptors discussed above are mere examples of the high power of the inventor's technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is one associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 and Table 2 below, among others. The anti-sense agent(s) of the invention have a low A content to prevent its liberation upon in vivo degradation of the agent(s). For example, if the system is the pulmonary or respiratory system, a large number of genes is involved in different functions, including those listed in Table 1 below.

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1 β (IL-1 β)
Interleukin-1 β Receptor (IL-1 β R)	Eotaxin
Tryptase	Major Basic Protein
β 2-adrenergic Receptor Kinase	Endothelin Receptor A
Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesion Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule (VCAM)
Substance P	Endothelial Leukocyte Adhesion Molecule Endothelin ETA
Rantes	(ELAM-1)
Receptor	GM-CSF, Endothelin-1
Cyclooxygenase-2 (COX-2)	Neutrophil Chemotactic Factor
Monocyte Activating Factor	Defensin 1,2,3
Neutrophil Elastase	Platelet Activating Factor
Muscarinic Acetylcholine Receptors	5-lipoxygenase
Tumor Necrosis Factor α	Substance P
Phosphodiesterase IV	Histamine Receptor
Substance P Receptor	CCR-1 CC Chemokine Receptor
Chymase	Interleukin-4 (IL-4)
Interleukin-2 (IL-2)	Interleukin-5 (IL-5)
Interleukin-12 (IL-12)	Interleukin-7 (IL-7)
Interleukin-6 (IL-6)	Interleukin-12 Receptor (IL-12R)
Interleukin-8 (IL-8)	Interleukin-1 (IL-1)
Interleukin-7 Receptor (IL-7R)	Interleukin-14
Interleukin-14 Receptor (IL-14R)	CCR-3 CC Chemokine Receptor
CCR-2 CC Chemokine Receptor	CCR-5 CC Chemokine Receptor
CCR-4 CC Chemokine Receptor	GATA-3 Transcription Factor
Prostanoid Receptor	MAP Kinase
Neutrophil Adherence Receptor	Interleukin-15 Receptor (IL-15R)
Interleukin-15 (IL-15)	

	Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
	NFAT Transcription Factors	STAT 4
	MIP-1 α	MCP-2
	MCP-3	MCP-4
5	Cyclophilin (A, B, ϵ etc.)	Phospholipase A2
	Basic Fibroblast Growth Factor	Metalloproteinase
	CSBP/p38 MAP Kinase	Tryptase Receptor
	PDG2	Interleukin-3 (IL-3)
	Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
10	FK506-Binding Protein	α 4 β 1 Selectin
	Fibronectin	α 4 β 7 Selectin

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

	cMad CAM-1	LFA-1 (CD11a/CD18)
	PECAM-1	LFA-1 Selectin
15	C3bi	PSGL-1
	E-Selectin	P-Selectin
	CD-34	L-Selectin
	p150,95	Mac-1 (CD11b/CD18)
	Fucosyl transferase	VLA-4
20	STAT-1	STAT-2
	CD-18/CD11a	CD11b/CD18
	ICAM2 and ICAM3	C5a
	CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
	LTB-4	AP-1 Transcription Factor
25	Protein kinase C	Cysteinyl Leukotriene Receptor
	Tachykinin Receptors (tach R)	I6B Kinase 1 & 2
	Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
	STAT 6	c-mas
	NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
30	Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
	Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
	Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
	Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
	Medullasin	Interleukin-16 Receptor (IL-16R)
35	Adenosine A ₁ Receptor (A ₁ R)	Tryptase-I
	Adenosine A _{2b} Receptor (A _{2b} R)	Adenosine A ₃ Receptor (A ₃ R)
	β Tryptase	STAT-3
	Adenosine A _{2a} Receptor (A _{2a} R)	IgE Receptor β Subunit (IgE R β)
	Fc-epsilon receptor CD23 antigen	IgE Receptor α Subunit (IgE R α)
40	IgE Receptor Fc Epsilon Receptor (IgERFc ξ R)	Substance P Receptor
	Histidine decarboxylase	Tryptase-1
	Prostaglandin D Synthase	Eosinophil Cationic Protein
	Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
	Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
45	Neutrophil Oxidase Factor	Cathepsin G
	Macrophage Inflammatory Protein-1-Alpha/Rantes Receptor	Interleukin-8 Receptor α Subunit (IL-8 R α)
		Endothelin Receptor ET-B

These genes, and others, are involved in the normal functioning of respiration as well as in diseases associated with respiratory pathologies, including cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, chronic bronchitis, respiratory distress syndrome (ARDS), allergic rhinitis, lung cancer and lung metastatic cancers and other airway diseases, including those with inflammatory response.

Anti-sense oligos to the target receptors, e. g. the adenosine A₁, A_{2a}, A_{2b}, and A₃ receptors, CCR3 (chemokine receptors), bradykinin 2B, CAM (vascular cell adhesion molecule), and eosinophil receptors,

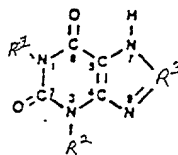
among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents may be utilized by the present method alone or in conjunction with anti-sense oligos targeted to other genes to validate pathway and/or networks in which they are involved. For better results, the oligos are preferably administered directly into the respiratory system, e.g., by inhalation or other means, of the experimental animal, so that they may reach the lungs without widespread systemic dissemination. This permits the use of low agent doses as compared with those administered systemically or by other generalized routes and, consequently, reduces the number and degree of undesirable side effects resulting from the agent's widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. Anti-sense oligonucleotides to the A₁, A_{2b}, A₃, bradykinin B2, GATA-3, CAM (vascular cell adhesion molecule), eosinophil receptors, and COX-2 receptors, among others, have been shown to be effective in the down-regulation of the respective receptor proteins in the cell. One novel feature of this treatment, as compared to traditional treatments for adenosine-mediated bronchoconstriction, is that administration is direct to the lungs, or in situ to other tissues, organs or systems of the body. Additionally, a receptor protein itself is reduced in amount, rather than merely interacting with a drug, and toxicity is reduced. Other proteins that may be targeted with anti-sense agents for the treatment of lung conditions include, but are not limited to: CCR3 (chemokine) receptors, human A₂, adenosine receptor, human A_{2b} adenosine receptor, human IgE receptor β , human Fc-epsilon receptor CD23 antigen, human histidine decarboxylase, human beta tryptase, human tryptase-I, human prostaglandin D synthase, human cyclooxygenase-2, human eosinophil cationic protein, human eosinophil derived neurotoxin, human eosinophil peroxidase, human intercellular adhesion molecule-1 (ICAM-1), human vascular cell adhesion molecule-1 (VCAM-1), human endothelial leukocyte adhesion molecule-1 (ELAM 1), human P selectin, human endothelial monocyte activating factor, human IL-3, human IL-4, human IL-5, human IL-6, human IL-8, human monocyte-derived neutrophil chemotactic factor, human neutrophil elastase, human neutrophil oxidase factor, human cathepsin G, human defensin 1, human defensin 3, human macrophage inflammatory protein-1-alpha, human muscarinic acetylcholine receptor HM3, human fibronectin, human GM-CSF, human tumor necrosis factor α , human leukotriene C4 synthase, human major basic protein, and human endothelin 1. Although not intended to be exclusive, a more extensive list of genes is provided below. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent's widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. In these latter targets, and in target genes in general, it is particularly imperative to eliminate or reduce the adenosine content of the corresponding anti-sense oligonucleotide to prevent their breakdown products from liberating adenosine.

As used herein, the term "treat" or "treating" asthma refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of the lung disease. The term "downregulate" refers to inducing a decrease in production, secretion or availability (and thus a

decrease in concentration) of the targeted intracellular protein. The present invention is concerned primarily with the treatment of human subjects. However, the agents and methods disclosed here may also be employed for veterinary purposes, such as is the case in the treatment of other mammals, such as cattle, horses, wild animals, zoo animals, and domestic animals, e. g. dogs and cats. Targeted proteins are preferably mammalian and more preferably of the same species as the subject being treated. In general, "anti-sense" refers to the use of small, synthetic oligonucleotides, resembling single-stranded DNA, to inhibit gene expression by inhibiting the function of the target messenger RNA (mRNA). Milligan, J. F. et al., *J. Med. Chem.* 35(14), 1923-1937 (1993). In the present invention, inhibition of gene expression of the A₁ or A₃ adenosine receptor is desired. Gene expression is inhibited through hybridization to coding (sense) sequences in a specific messenger RNA (mRNA) target by hydrogen bonding according to Watson-Crick base pairing rules. The mechanism of anti-sense inhibition is that the exogenously applied oligonucleotides decrease the mRNA and protein levels of the target gene or cause changes in the growth characteristics or shapes of the cells. Id. See, also Helene, C. and Toulme, J., *Biochim. Biophys. Acta* 1049, 99-125 (1990); Cohen, J. S. D., Ed., *Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression*; CRC Press: Boca Raton, FL (1987). As used herein, "anti-sense oligonucleotide" is defined as a short sequence of synthetic nucleotide that (1) hybridizes to any coding sequence in an mRNA which codes for the targeted protein, according to hybridization conditions described below, and (2) upon hybridization causes a decrease in gene expression of the A₁ or A₃ adenosine receptor. The receptors discussed above are mere examples of the high power of the present technology. In fact, a large number of genes may be targeted in a similar manner by practicing the present methods, to significantly down-regulate or obliterate protein expression and observe any changes wrought to one or more functions within a system, e.g. the respiratory system and other lung disease associated targets. By means of example, in the respiratory system, the targets may be associated with difficulties of breathing, bronchoconstriction, inflammation, allergic rhinitis, chronic bronchitis, surfactant depletion, and others associated with diseases and conditions such as chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, inhalation burns, Acute Respiratory Distress Syndrome (ARDS), cystic fibrosis, pulmonary fibrosis, radiation pneumonitis, tonsillitis, emphysema, dental pain, oral inflammation, joint pain, esophagitis, cancers afflicting the respiratory system either directly such as lung cancer, esophageal cancer, and the like, or indirectly by means of metastases, among others. These functions are of great interest because of their association with respiratory dysfunction, as is the case in asthma, allergies, allergic rhinitis, pulmonary bronchoconstriction and hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis (CF), Acute Respiratory Distress Syndrome (ARDS) as well as infantile and pregnancy-related RDS, cancer, etc., which either directly or by metastasis afflict the lung, the present anti-sense oligonucleotides may be directed to a list of target mRNAs, which includes the targets listed in Table 1 above, among others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C and/or having a specific type and/or extent of activity, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a thymidine (T) nucleic acid content of up to and including about 15%, preferably, about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no thymidine. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%, preferably about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no adenosine. When the selected fragment comprises at least one thymidine base, an adenosine base may be substituted in the corresponding anti-sense nucleotide fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 10%, preferably less than about 1%, and more preferably less than about 0.3% of the adenosine base agonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors, and heteroaromatic bases which have no activity at the adenosine

A_{2a} receptor, when validating in the respiratory system. Other adenosine activities in other systems may be determined in other systems, as appropriate. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynyl aryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkyloxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO₂aryl, among others. Similar modifications in the sugar are also embodiments of this invention. Reduced adenosine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA serves to prevent the breakdown of the oligos into products that free adenosine into the system, e.g. the lung, brain, heart, kidney, etc., tissue environment and, thereby, to prevent any unwanted effects due to it. By means of example, the NF6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or desthymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above, in Table 2 below, and others associated with functions of the brain, cardiovascular and renal systems, and many others. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B transcription factor, typically about 10 to 30 sequences may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenosine content may suffice to render the anti-sense oligonucleotides less active or even inactive against the target. In accordance with this invention, these so called "non-fully desA" sequences may preferably have a content of adenosine of less than about 15%, about 12%, about 10%, about 7%, about 5%, and about 2% adenosine. Most preferred is no adenosine content (0%). In some instances, however, a higher content of adenosine is acceptable and the oligonucleotides still fail to show detrimental "adenosine activity". A particular important embodiment is that where the adenosine nucleotide is "fixed" or replaced by a "Universal or alternative" base that may base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T.

A universal or alternative base is defined in this patent as any compound, more commonly an

adenosine analogue, which has substantial capacity to hybridize to thymidine, while at the same time having reduced, or substantially lacking, ability to bind adenosine receptors or other molecules through which adenosine may exert an undesirable side effect in the experimental animal or in a cell system. Alternatively, adenosine analogs which completely fail to activate, or have significantly reduce ability for activating, adenosine receptors, such as the adenosine A₁, A_{2b} and/or A₃ receptors, most preferably A₁ receptors, and those that may even act as agonists of the adenosine A_{2a} receptor, may be used. One example of a universal base is α -deoxyribofuranosyl-(5-nitroindole), and an artisan will know how to select others. This "fixing" step generates further novel sequences, different from those anti-sense to the ones found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. Other examples of universal or alternative bases are 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3 - nitropyrrole - 2' - deoxynucleoside, 5 - nitro-indole, 2 - deoxyribosyl - (5 - nitroindole), 2-deoxyribofuranosyl - (5-nitroindole), 2' - deoxyinosine, 2' -deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4, 5 - c] oxazine - 7 - one and 2 - amino - 6 -methoxy aminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3 - nitropyrrole 2' - deoxynucleoside 2 - deoxyribofuranosyl - (5 - nitroindole), 2' - deoxyinosine and 2' - deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H - 3, 4 - dihydropyrimido [4,5 - c] [1, 2] oxazin - 7 - one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2 - amino - 6 - methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art or will become available are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl. Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem.260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992); Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon, M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (10): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding being incorporated herein by reference. When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% "desA" anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be "fixed" by replacement with a "Universal" or "replacement" base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A. Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

Table 2: Cancer Targets

Transforming Oncogenes	Therapy Targets
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl 2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase
Angiogenesis factors	Adhesion Molecules
Oncogenes	Folate Pathway Enzymes
DNA repair genes	(One Carbon Pool)
	Telomerase
	HMG CoA Reductase
	Farnesyl Transferase
	Glucose-6-Phosphate Transferase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like. The present technology is particularly useful in the treatment of cancer ailments given that traditional cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desired pathway or target. This approach provides a significant advantage over standard treatments of cancer because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells that, for instance, express all three targets while normal cells that may express only one or two of the targets will be significantly less affected or even spared. A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions. Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1 α , MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophilins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1, CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well. In another embodiment, at least one of the mRNAs to which the oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohipophyseal receptors, adenohipophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated. The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A₁ receptor, adenosine A₂B receptor, adenosine A₃ receptor, endothelin receptor A, endothelin receptor B, IgE high affinity receptor, muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1 β receptor (IL-1 β R), interleukin-1 receptor (IL-1R), interleukin-1 β receptor (IL-

1 β R), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, parasympathomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohipophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein. The encoded enzymes for development of the oligos of the invention include synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and , polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase, β 2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipoxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil elastase, phospholipase A₂, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition, however, is suitable as a target for this invention. Suitable encoded factors for application of this invention are, among others, NF κ B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor α (TNF α), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned. Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein. Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1 β (IL-1 β), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11), CCR-5 CC chemokine, and Rantes. Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation. Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are α 4 β 1 selectin, α 4 β 7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcl-2. Others, however, are also suitable for use with this invention.

The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence's total number of nucleotides. These fragments

may be selected from any portion of the longer oligo, for example, from the middle, 5'- end, 3'- end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenosines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal or alternative base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A₁ and/or A₃ receptors. In fact, such replacement nucleotide acts as a "spacer". Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60.

Human Receptor-related Antisense Polynucleotide

5'-GGCGGCCTGG AAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C TGCTTTTCT TTTCTGGGCC
TCTGTGGTCT GTTFTTTTCT GGCCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCCCBTGB
TGGGCBTGCC GTCGTCTTG CCCTCCTTTG GCTGCCGTGC CCGCTCCCCG GCCTCCTGGC GGGTGGCCGT
TGGGCCCGTG TTCCCTGGG GCCTGGGGCT CCCTTCTCTC GCCCTTCTTG CTGGGCCTCT GCTGCTGCTG
GTGCTGTGGC CCCGTACA CCGAGGAGCC CATGATGGG ATGCCACAGA CGACAGGCGT BCBCCBGGB
GCCCCBTGBTG GGCFTGCCBC BGBCBBCBGG C GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC
CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC
CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG
CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG
CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC ACA
GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT
CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT
TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC
CC TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT GCC
TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT
GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG
TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG
AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB
TGG CGG TCC TGC TTG GBT TCT CCC GB GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA
GTA GAG TAG GGC ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC
TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT
TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT
TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT
TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GCC TGT
GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG
G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG
BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA
TTGA CCT TCC AAG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB
TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC
TGC GCT CCT GCG CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC

CTC CTG GTC GCG (TT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG
 GGC TGC GTG CGC (TT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC
 GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG
 CTG GGG GGT GCT (CC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC
 5 CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA
 GAC AGG GCA GGG (GA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC
 GCA GGA CAG AGG IGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC
 BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT
 CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG
 10 GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC
 TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG
 CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG
 GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT
 TCC CTG TGC CCC T T CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA
 15 GGA CAG AGC CAG (CA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC
 GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G CTCAGTGGCC
 CCAAAAGGA TGA (TAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT GTCTGTCTGTG
 TCTTTCTTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCTGT GTCTTTCTTT
 TGCTCTTGGT GTG(TCTTGGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTG GTGTCTTTCC TTTGCTCTTG
 20 GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC
 TCGGCCCCCG GCCGCGCTCG GCTCCTCTCC CTCTGGCCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC
 GGCCTGTGCC TGC(CGCGGC GCTGGCCCTT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC
 GCGCCGGGGC CTG(TCCGCT CTGCGGGGCG TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG
 GCTGGGCGGC CGG(CCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC
 25 GGGGGTTTCT GGCGTGGGG GTCTTGCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC
 GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTGTG TTTTCCCTG GCGTCCCTGT
 GCCCCTCTCC TCTCTTCTCT CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGTCTC TTGGTTTGGG
 GCTTTTTTTC TCTTCTCTCT TTTTCGTGCG TGGGCCCTCC GCACGCCTCT TGCCACCTCC TGCGCAGGGC
 AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG
 30 CATGCTTCTT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCCGCTC TTGCCBCCTC
 CTGCGCBGGG CBG(CGCTTG GGGCCBGC GCCTCCCGGC GCGGCCBGC BGGCBGCCBG CBGCGCGCBG
 CCGBCGGCCB GCBTGTCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGBCBGG C GCTGCCCGGC
 GGGGTGTGCG CTTGCGGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC
 TTGTCCTCT TCCTCTTCTT CCTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCT CGGGGTCCCG
 35 GGGCTTCTGG CCTT(GCCGT TCATGGTGGC TAGGTGGGGC GTTCTGGTG GCTBGGTGGG GC GGG GTG GGT
 BGG CCG TGT CTG G3GGT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT
 TCT CCT TCG GGC C(T CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT
 TGGCG CTG GCG GGG GGG CCT C(TGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG
 TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG
 40 CCGGG GTG GGT AGG CCG TGT CTG GGGGT GGC CAT GTT GGT TGC CCGG CCC GCG GCT GCA GGG G
 ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTAGATC ATCAAAATCC CACATCTGTG
 GATCTGTAAT ATTTACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB
 CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBTGB BBTBTBGBTC BTBTTTCCB CCBTCTGTG
 GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG
 45 TGGCTCGGTG CTTCTGCCCC TGTGTGTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC
 CTCTTCTCT TTGT(CGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTCC GCCCTGTGCG GCGGGAAGCC
 TCTCTCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGGCG GTCCGCACAG
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	GAGCCATCTC	CATCTGAAG	GAACCTCAAAG	ACTCAAGTGG	GAACGACTGG	CACTGCCACC	ACCAGAAAGC
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	GCTCAACCAA	TAACTATTGC	ACAACCACCT	GTCCCTGCCT	CAGTTCCTC	TTCTGTAACA	TGAAGTCGTT
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	TCATTACGCA	GACGTAACATG	GGATATGTTT	ACTATAAGGA	AAAGACACTG	AGGTCTAGA	TGATCCTATC
	ACAACCTGAG	AGTAGTTTTT	ACTCCATTTA	CAGGTGAGGT	CATTGTGGTT	CAAGGACGTT	AAGTAACTTC
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	CCCACCCTCC	CTCCCATCT	GTATCCTCCA	ATCATCTTCA	GTGCTTTGCT	GATAGAAGGT	ACGGAAATAC
	GATGCCACAG	ACTCTCCAGG	AAGACAGAAA	CTAGGCAGAT	GGGCTGGCCA	TGGTCTCCAA	GCCGACTGG
	AATCTCCAGG	TCTCGAATGA	TATCATTTTT	CTCTTTTAAT	AAATTAACTC	ACCCACCACA	CGGCTTTGAG
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25	CGGAAGCTTC	AAGGAGGTCA	AGGGTCCAAC	ACTTGAGATT	GTTAGTGCTG	TTGGTGGATA	CTGCAGAATA
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	GGGCTGCCCT	TCTGGGCCAT	CACCATCTCC	AACAACCTCG	ACTGGCTCTT	TGGGGAGACG	CTCTGCCGCG
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	CATGCTCCTG	AATCTCGTGG	GCTTCTGCT	GCCCTGAGT	GTCATCACCT	TCTGCACGAT	GCAGATCATG
	CAGGTGCTGC	GGAACAACGA	GATGCAGAAG	TTCAAGGAGA	TCCAGACGGA	GAGGAGGGCC	ACGGTGCTAG
40	TCTTGTTTGT	GCTGCTGCTA	TTCATCATCT	GCTGGCTGCC	CTTCCAGATC	AGCACCTTCC	TGGATACGCT
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	AGTCTTGGA	GGTGTAACAG	GGAGTGTGCC	AGAAAGGGGG	CTGCAGGTCA	GAACCCATTC	AGATGGAGAA
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	AAAACACCGG	AGACTAATTC	CTGCCCTGCC	CAATTTTCGA	GGGAGCATGG	CTGTGAGGAT	GGGGTGAAC
	CACGCACAGC	CAAGGACTCC	AAAATCACAA	CAGCATTACT	GTTCTTATTT	GCTGCCACAC	CTGAGCCAGC
	CTGCTCCTTC	CCAGGAGTGG	AGGAGGCCCTG	GGGGAGGGGAG	AGGAGTGACT	GAGCTTCCCT	CCCGTGTGTT
50	CTCCGTCCCT	GCCCCAGCAA	GACAACCTAG	ATCTCCAGGA	GAACCTGCCAT	CCACGTTTGG	TGCAATGGCT
	GAGTGCACAA	GTGAGTTGTT	GCCCTGGGTT	TCTTTAATCT	ATCAGCTAGA	ACTTTGAAGG	ACAATTTCTT
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	TCACTGATGG	ACAAGGAGGT	CTGTGCCAAA	GAAGAATCAA	TAAGCACATA	TGAGCACTTC	TGTATATCAG
	TATTGAGCAC	TGTAGGCA	ATGTTCTCTC	CCTGGAAGAT	ATCAATGTTT	CTGTCTGTTT	GTGAGGACTC
	CGTGCCCAACC	ACGGCCTCTT	TCAGCGCCGA	CATGCTCAAT	GTCACCTTGC	AAGGGCCAC	TCTTAACGGG
	ACCTTTGCCC	AGAGCAAATG	CCCCCAAGTG	GAGTGCGTGG	GCTGGCTCAA	CACCATCCAG	CCCCCTTCC

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Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.8	2.1	9	16
Income	15.5	3.2	10	25
Health status	1.8	0.6	1	3
Life satisfaction	4.2	1.5	1	7
Depression	1.5	0.8	1	3
Stress	2.5	1.2	1	5
Resilience	3.5	1.0	1	5
Optimism	4.5	1.2	1	7
Gratitude	5.5	1.5	1	9
Forgiveness	6.5	1.8	1	10
Empathy	7.5	2.0	1	11
Compassion	8.5	2.2	1	12
Kindness	9.5	2.5	1	13
Generosity	10.5	2.8	1	15
Patience	11.5	3.0	1	16
Humility	12.5	3.2	1	17
Modesty	13.5	3.5	1	18
Shame	14.5	3.8	1	19
Guilt	15.5	4.0	1	20
Envy	16.5	4.2	1	21
Jealousy	17.5	4.5	1	22
Anger	18.5	4.8	1	23
Dislike	19.5	5.0	1	24
Disrespect	20.5	5.2	1	25
Disapproval	21.5	5.5	1	26
Disagreement	22.5	5.8	1	27
Dislike	23.5	6.0	1	28
Disrespect	24.5	6.2	1	29
Disapproval	25.5	6.5	1	30
Disagreement	26.5	6.8	1	31
Dislike	27.5	7.0	1	32
Disrespect	28.5	7.2	1	33
Disapproval	29.5	7.5	1	34
Disagreement	30.5	7.8	1	35
Dislike	31.5	8.0	1	36
Disrespect	32.5	8.2	1	37
Disapproval	33.5	8.5	1	38
Disagreement	34.5	8.8	1	39
Dislike	35.5	9.0	1	40
Disrespect	36.5	9.2	1	41
Disapproval	37.5	9.5	1	42
Disagreement	38.5	9.8	1	43
Dislike	39.5	10.0	1	44
Disrespect	40.5	10.2	1	45
Disapproval	41.5	10.5	1	46
Disagreement	42.5	10.8	1	47
Dislike	43.5	11.0	1	48
Disrespect	44.5	11.2	1	49
Disapproval	45.5	11.5	1	50
Disagreement	46.5	11.8	1	51
Dislike	47.5	12.0	1	52
Disrespect	48.5	12.2	1	53
Disapproval	49.5	12.5	1	54
Disagreement	50.5	12.8	1	55
Dislike	51.5	13.0	1	56
Disrespect	52.5	13.2	1	57
Disapproval	53.5	13.5	1	58
Disagreement	54.5	13.8	1	59
Dislike	55.5	14.0	1	60
Disrespect	56.5	14.2	1	61
Disapproval	57.5	14.5	1	62
Disagreement	58.5	14.8	1	63
Dislike	59.5	15.0	1	64
Disrespect	60.5	15.2	1	65
Disapproval	61.5	15.5	1	66
Disagreement	62.5	15.8	1	67
Dislike	63.5	16.0	1	68
Disrespect	64.5	16.2	1	69
Disapproval	65.5	16.5	1	70
Disagreement	66.5	16.8	1	71
Dislike	67.5	17.0	1	72
Disrespect	68.5	17.2	1	73
Disapproval	69.5	17.5	1	74
Disagreement	70.5	17.8	1	75
Dislike	71.5	18.0	1	76
Disrespect	72.5	18.2	1	77
Disapproval	73.5	18.5	1	78
Disagreement	74.5	18.8	1	79
Dislike	75.5	19.0	1	



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	ACACCATCCC	TGCCACCAT	AGTAAGAAGT	CCAGCCCACG	TCCAGGAGAA	GAGGAAGCAG	ATTCTCTCTT
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50	GTGAAGACCA	CGCTACTCC	CTCACTCAAC	CTCTTGCTAC	TTCCACCTC	TCCTGTCCAA	CATCTAGTGT
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	CAACAGCCAT	GAAATAAGAA	ATGCAAAAGCG	ATTACAGGATG	AGAGCAATAC	CCTACTCCAA	AGAAGGCAAC
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	TGGAGTTTAC	CAC TGATAAT	AAGGGTGCAA	AATGTAAATT	ACTAATGTTT	ATTGAGCCTA	GTGCAGTGCG
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	CTGGAGCGCG	GGCATGACAGA	AAACAGCCTG	AGCTCCACCT	CGGCTTCTCC	TTGTCTGGC	TGGTTGTCT
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	CAC TTTCTTT	CAGCCTCGAC	ATGCTCAATG	TCACCTTGCA	AGGGCCCACT	CTTAACGGGA	CCTTTGCCCA
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	ATG						



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[illegible]

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[illegible]

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40 Human Enzyme-related Antisense Polynucleotide

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[illegible]

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	CCGGGGCCTC	ATGGCCACCC	CTGCCAAGCT	GAACCGTCAG	GATGCCATGT	TAGTGGATGA	GCTCCGGGAG
	CGGCTGTTTC	GGCAAGTGAG	GAGGATTGGG	CTGGACCTGG	CAGCTCTCAA	CATGCAACGA	AGCCGGGACC
	ACGGCCTTCC	AGGTGAGGGG	GCTGTCCACC	TCTTCTCCCA	GCTTTGCTCG	GGCCAGGCTG	CTCAAGGGGT
50	TCTGGGAAGA	CCCTGTGACC	CGACTGCCTG	GTAGGTTCTG	GTGGCAGAAA	CGAGGTGTTT	TCACCAAAAG
	ACAGCGCAAG	GCCCTGAGCA	GAATTTCCCT	GTCTCGAATT	ATATGTGACA	ATACCGGTAT	CACCACGGTT
	TCAAGGGACA	TCTTAGAGC	CAACATCTAC	CCTCGGGGCT	TTGTGAACCT	CAGCCGTATC	CCCAGGTTGA
	ACCTATCAGC	CTGGTAGAGG	ACATGAGGCT	TCTGCAGGTA	AGGGGAGGGC	ACCTCCAGCA	CCCTGGGCTG
	GTTAAGCCCT	ACATCT					

General Information	
Project Name	Project Alpha
Project Manager	John Doe
Project Number	12345
Project Status	In Progress
Project Start Date	2023-01-01
Project End Date	2023-12-31
Project Budget	\$1,000,000
Project Location	New York, NY
Project Description	Development of a new software application for data analysis.
Project Objectives	1. Develop a user-friendly interface. 2. Implement advanced data processing algorithms. 3. Ensure high security and data integrity.
Project Risks	1. Delay in resource allocation. 2. Changes in requirements. 3. Integration issues with existing systems.
Project Deliverables	1. Requirements document. 2. Design specifications. 3. Development code. 4. Testing reports. 5. Deployment plan.
Project Stakeholders	1. Project Manager (John Doe) 2. Project Sponsor (Jane Smith) 3. Project Team (Alice, Bob, Charlie) 4. Project Customers (XYZ Corp.) 5. Project Vendors (ABC Inc.)
Project Communication	1. Weekly status meetings. 2. Monthly progress reports. 3. Quarterly steering committee meetings. 4. Ad-hoc communication as needed.
Project Documentation	1. Project Charter. 2. Project Management Plan. 3. Project Communications Plan. 4. Project Risk Management Plan. 5. Project Quality Management Plan.
Project Approval	1. Approved by Project Sponsor (Jane Smith) on 2023-01-01. 2. Approved by Project Steering Committee on 2023-01-15.

CCCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT
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[illegible]



Human Factor Related Anti-sense Oligonucleotide

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT
CTG BGC TGT GGC GGC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT
C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB
5 BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC
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Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	Male	10.5	0	1
Marital Status	Married	15.2	0	1
Education	High School	12.8	0	1
Occupation	Unemployed	18.5	0	1
Income	\$15,000	12.5	0	1
Health Status	Good	10.8	0	1
Smoking Status	Non-smoker	12.2	0	1
Alcohol Consumption	Low	11.5	0	1
Exercise Frequency	Low	10.5	0	1
Stress Level	Low	11.2	0	1
Sleep Quality	Good	10.8	0	1
Depression Score	Low	10.5	0	1
Life Satisfaction	High	11.5	0	1
Family Size	2	1.5	0	5
Home Ownership	Owned	12.5	0	1
Vehicle Ownership	Owned	13.2	0	1
Insurance Coverage	Health	14.5	0	1
Religious Belief	Christian	15.8	0	1
Political Affiliation	Democrat	16.2	0	1
Volunteer Work	Yes	11.8	0	1
Charitable Donations	Low	10.5	0	1
Community Involvement	Low	10.2	0	1
Neighborhood Safety	Good	11.5	0	1
Local Government Satisfaction	High	12.2	0	1
Environmental Concern	High	13.5	0	1
Climate Change Belief	Yes	14.2	0	1
Renewable Energy Support	Yes	15.5	0	1
Waste Recycling Participation	Yes	16.8	0	1
Local Business Support	Yes	17.2	0	1
Public Transportation Use	Low	10.5	0	1
Carpooling Frequency	Low	10.2	0	1
Bike Commuting Frequency	Low	10.5	0	1
Public Space Usage	Low	10.8	0	1
Local Festival Participation	Low	11.2	0	1
Community Meeting Attendance	Low	11.5	0	1
Local News Reading Frequency	Low	11.8	0	1
Local Radio Listening Frequency	Low	12.2	0	1
Local TV Watching Frequency	Low	12.5	0	1
Local Newspaper Subscription	Low	12.8	0	1
Local Radio Subscription	Low	13.2	0	1
Local TV Subscription	Low	13.5	0	1
Local Newspaper Circulation	Low	13.8	0	1
Local Radio Circulation	Low	14.2	0	1
Local TV Circulation	Low	14.5	0	1
Local Newspaper Readership	Low	14.8	0	1
Local Radio Readership	Low	15.2	0	1
Local TV Readership	Low	15.5	0	1
Local Newspaper Advertising	Low	15.8	0	1
Local Radio Advertising	Low	16.2	0	1
Local TV Advertising	Low	16.5	0	1
Local Newspaper Circulation Growth	Low	16.8	0	1
Local Radio Circulation Growth	Low	17.2	0	1
Local TV Circulation Growth	Low	17.5	0	1
Local Newspaper Advertising Growth	Low	17.8	0	1
Local Radio Advertising Growth	Low	18.2	0	1
Local TV Advertising Growth	Low	18.5	0	1
Local Newspaper Circulation Decline	Low	18.8	0	1
Local Radio Circulation Decline	Low	19.2	0	1
Local TV Circulation Decline	Low	19.5	0	1
Local Newspaper Advertising Decline	Low	19.8	0	1
Local Radio Advertising Decline	Low	20.2	0	1
Local TV Advertising Decline	Low	20.5	0	1
Local Newspaper Circulation Stability	Low	20.8	0	1
Local Radio Circulation Stability	Low	21.2	0	1
Local TV Circulation Stability	Low	21.5	0	1
Local Newspaper Advertising Stability	Low	21.8	0	1
Local Radio Advertising Stability	Low	22.2	0	1
Local TV Advertising Stability	Low	22.5	0	1
Local Newspaper Circulation Increase	Low	22.8	0	1
Local Radio Circulation Increase	Low	23.2	0	1
Local TV Circulation Increase	Low	23.5	0	1
Local Newspaper Advertising Increase	Low	23.8	0	1
Local Radio Advertising Increase	Low	24.2	0	1
Local TV Advertising Increase	Low	24.5	0	1
Local Newspaper Circulation Decrease	Low	24.8	0	1
Local Radio Circulation Decrease	Low	25.2	0	1
Local TV Circulation Decrease	Low	25.5	0	1
Local Newspaper Advertising Decrease	Low	25.8	0	1
Local Radio Advertising Decrease	Low	26.2	0	1
Local TV Advertising Decrease	Low	26.5	0	1
Local Newspaper Circulation No Change	Low	26.8	0	1
Local Radio Circulation No Change	Low	27.2	0	1
Local TV Circulation No Change	Low	27.5	0	1
Local Newspaper Advertising No				

[illegible][illegible]

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	GTGCCCAGGA	TGGC GCTCTG	TCCATTGCCT	GGGGCCGCCA	ATTGCTACTC	TGGGTACGG	AGGAAGGACA
	GGGTCTGAG	AGAC ACCAGA	GACCTCACAC	AGCCCTGAAA	ACATGGGGCT	CCTTCATAAG	TGTTTCCCAT
	CACCAACAGG	GAGACCACGT	GGAGGCCTTG	CAGCCCCACT	CGGTGCTTCT	CCACCAAATC	CCAAGGGCAG
	TGACGCTGAC	GTCTGTGGAA	AGCAGAGAAA	GCCCTGGCTC	CCAAAGCCCT	GAAGTCCCTG	TGGAGCTGAC
10	ATTCCCTGAG	TGACGCTGTG	AATGGAAGGA	ACTCAAGTGC	GGGTGGTAGG	CCACCTCCTG	GCCCAGGCCT
	GGGTGAACCT	TGACGGGACA	CATGTAGTCA	CAATCCCATC	CTCCCATTCT	CCTTCTCAGA	GGAAGGAAGT
	GGGCATCCAT	CTGCCTCATC	TCTCTCCCGT	GGGGAAGATG	GGGAGTTTCA	GGGGAACTTT	CACATAAATT
	TCACCAGCTC	AGATCTCCTG	TGAGGATGGG	GCCCACCATG	CTCCCGGTGC	TGCCAGAGGC	CCTGAGCCCC
	TCCCAGGGTC	CCTGCGTTTG	AGCCAGCCCT	GTATCATCCC	CAGGAGCTGA	ATGTCAGAGC	AATGGATAGA
15	ATTAGATGGA	AAGAGCTCTC	AATTTGACCT	GAGACTGTCC	CCAGATACTC	AGGAAAAACA	GGACGTGCGC
	CAGAGTGGGC	AGCAGGTGAG	TGGCAGGTTA	TAGGTCTCTG	GTTTGAGITT	GTTCTCACGT	GAGACAGACC
	CAGCCCCTCA	CTCCATTCA	ACACTGGGTT	TAAATGGTG	CAAGATAGGA	GCAATTTTCT	GGTCCCAAGA
	GCAGGAGGAA	GGGATTTTCT	GGGGTTTCTT	GAGTCCAGAT	TTGCATAAGA	TCTCTGAGT	GTGCATTGTT
	CTTTGAGGAC	CATTCTCTGA	CTCACCAGT	AAGTGGCTGA	ATTCTAACCT	CTGTAATGAG	CATTGCACCC
20	AATACCAGTT	CTGAACCTCA	CCTGGTGACC	AGGGACCAGG	ACCTTTATAA	GGTGGAAGGC	TTGATGTCCT
	CCCCAGACTC	AGCTCTGGT	GAAGCTCCCA	GCCATCAGCC	ATGAGGGTCT	TGTATCTCCT	CTTCTCGTTC
	CTCTTCATAT	TCCTGATGCC	TCTTCCAGGT	GAGATGGGCC	AGGGAAATAG	GAGGGTTGGC	CAAATGGAAG
	AATGGCGTAG	AAGTCTCTCTG	TCTCTCTCA	TTCCCTCCA	CCTATCTCTC	CCTCATCCCT	CTCTCTCCTT
	CCTCTCTCTG	TGTGTCCTCT	CCATCCTTTT	CTCCTGCTTC	TCTCTCTCT	TCCCTCTCTC	TCTTTTCTCT
25	GTCTTTCTTT	TTCTCTCTCT	CCTAGAGCAT	GTCTTTCTTT	CTTTCTCTTT	CCTTTCTTCT	ACCCACACTT
	TTAGACTGAA	TGCCCTATTT	AATTGAACAA	AGCATGGCTT	CCTTCAATAG	AAAAGGAGTT	TGAGAACCCA
	ATGGACACCT	CATCTGTTCT	TCTAAGCCAA	TATGAAGGAG	CCGAGTAGCT	TGTAATATATC	ATCTCTTCAC
	TGCTTTCCAT	GCTACAACTG	CTGAGACTAT	GGTTGAAACC	TGTTAGGTGA	CTTTTAAAT	AAAAGGCAGA
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	GGAGGCGGGC	AGGTGGGGAG	GGAGGGACGG	AAGGAGGGAG	GGAGGGAGGG	AGGGAGGGAG	GGAGGGATAA
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40	GTGTGTGTTA	AAATGGAGGT	ATGGTGGCTT	TGATATTATC	TTCTTGTTGT	GGAGCTGAAT	TCACAAGAGA
	TCGTTGCTGA	GCTCTACCA	GACCCACCT	GGAGGCCCCA	GTCACCTAGG	AGAGACTCAGG	GTCTTTCACA
	ATCAGGTTCT	ACAAAAATAA	ACATCCCCC	AACCACAGCA	GTGCCAGTTT	CCATGTCAGA	AACCTAGATC
	CAAAATGACTG	ACTCTCGTCT	CATTATCATG	ATGGAAGAGC	CCAGGCTTGA	GAAAGAAGCC	CGCTGCGGAT
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45	GCTCTTTTGT	TGTGTTTTTT	CCCTGTTAGG	TGTTTTTGGT	GGTATAGGCG	ATCCTGTTAC	CTGCCTTAAG
	AGTGGAGCCA	TATCTCATCC	AGTCTTTTGC	CCTAGAAGGT	ATAAACAAAT	TGGCACCTGT	GGTCTCCCTG
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	TCCCTTCTTC	TGGCTAAGGT	TTCTTATGCA	ATTATCTGAGTGGT	AAAAAGATTCT	TATATCTGCT	GTTTGATGAA
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	AATGAAGCCT	CTATTTACCT	TGGTTGGCGG	AACACATTTA	AGGGACTCTG	TATTGATACC	AGGCTTCAAA
	CTTTGGGAAG	TGTAATGGCC	AACTTAAACA	CATCCACAGG	AGAATGAAGA	GGTTTGGGAA	GGGACCAGAA
	ACCAGGCATT	GAGGACAATG	AGAAGAGTTT				

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 5 AAGCATTGCT TCCTTCAATA GAAAAGGAGT TTGAGAACCC AATGGACAAC TCACTCGTTC TTCTAAGCCA
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	TTCCCTTGCA	TGGGACGAA	GCTTGGCTCC	AAAGCATCCA	GGTGAGAGAG	GCAGGCATGC	AGAGCTGCTA
	AGTCTAGAGG	GAAGGACGGG	AGAGAGGTTT	CAGAGTTGGG	TCTCAGCAGT	CTATGTCAC	GAGGTGGCTT
	CACCTAGAAT	CTCAGGCAT	TGATTTTCTC	ATCTAGAAAT	TGAACAGAGA	GCCAAATAAA	CCTGAGAAAC
	TTTATTTCTC	CAAAAGCTTG	ATTCCAAGAA	ACATCTGTGA	AATTCACTAA	GTTTAAGATA	TGAAGAGACA
15	GACTAGTTAT	TTCTGGATCT	AAACAAGTAG	ACTTAGTTGT	AAAGAGAACA	TTTTACTCTA	TCTACAGAAG
	AGCTTTTAAA	AACAGCAGCC	AAGCCTGAGG	GTAAGTTCAG	GTGTGTGTGT	GATGGGGCAG	GAATGCAAAA
	ATGAGAGCAA	AGCAGAATGA	GTCTCAAATT	CTGTGTGACA	AGCACTGCTC	TGCGTGTTTA	TTCTATCGA
	CTGAGGTTGT	TCTGCTACC	GGCTGCAATG	CAGCCAGCAT	CACCTGTCAG	CTAGCATGTG	ACTTCCCCGA
	GATTTCTTTT	CTTACCCAT	GCTAACTCCA	TACTCAATTT	CTCATGCTCT	CCCTGTCCCA	GGCTCAAGGA
20	AAAACATGGA	CTGTATTGTC	AGAAATCCAG	CGTGCAATGC	AGGAGAACGT	CGTATGGAA	CCTGCATCTA
	CCAGGGAAGA	CTCTGGGCAT	TCTGCTGCTG	AGCTTGCAGA	AAAAGAAAAA	TGAGCTCAAA	ATTTGCTTTG
	AGAGCTACAG	GGATTGCTA	TTACTCTGT	ACCTTCTGCT	CAATTTCCCT	TCCTCATCTC	AAATAAATGC
	CTGTATACAA	GATTTCTGTG	TTTCCACCTC	TTTAATGTGT	GATATGTGTC	TGTGTCAAGA	CACTTGGGAT
	ACACGTACCA	AAACGCAAAA	TCAAAATTTT	GAACAATATA	CCTACCTTGC	TATAGAAGAC	CTGGGACAGA
25	GGACTGCTGT	CTGCTCTCT	TGGTCACCCT	GCCTAGCTAG	AGGATCTGTG	ACCCAGCCA	TGAGGACCCT
	CGCCATCCTT	GCTGCCATTC	TCCTGGTGCG	CCTGCAGGCC	CAGGCTGAGC	CACTCCAGGC	AAGAGCTGAT
	GAGGTGTCTG	CAGCCCCGA	GCAGATTGCA	CGGACATCC	CAGAAGTGGT	TGTTTCCCTT	GCATGGGACG
	AAAGCTTGGC	TCCAAAGCAT	CCAGGCTCAA	GGAAAAACAT	GGACTGCTAT	TGCAGATAC	CAGCGTGCAT
	TGCAGGAGAA	CGTCTGCTATG	GAACCTGCAT	CTACCAGGGA	AGACTCTGGG	CATTCTGCTG	CTGAGCTTGC
30	AGAAAAAGAA	AAATGAGCTC	AAAATTTGCT	TTGAGAGCTA	CAGGGAATTG	CTATTACTCC	TGTACCTTCT
	GCTCAATTTT	CTTTGATCAAA	TTTACCTATT	ATGCATTTGA	TATATAAATA	AGTATATAAA	TGCACACACA
	GACACAGCAA	TGATGGTGAA	CAGTCTTCAT	ACAATTATAT	GGATGAATCT	CATAAAATGC	TGAGTTAAAG
	AAATCAGAGC	AAAAGAACATA	TACTGAAAGA	TTCTCTCTAT	ATACAAAAGT	CAAAAATAGG	TGGACCAATT
	CATGGTGGTG	TTAGAAATCA	GAAGAGAGGC	TACCTTTGTG	GGGAGGGGAC	AGTTTAATGC	CCAGAAAGCG
35	TAAATAAGGA	ATCTCTGGG	GAGTGGTAAT	GATCTGGATG	CTGGCTACAG	GATGTGTTGG	TTGTAATAAT
	GCATTTTTTT	ATACTAGCT	TTTTCCATGT	GTATATTATA	CTTCAAAGAA	GTTCAGTTAA	TATTTCTCTA
	TGTCATGTGA	GAGTAGCTCA	GTTAGCCCCA	GCAAGCCTCT	GGCTTAATCT	TGTTTTACCT	TAAGCCATCA
	GTCATTTACA	AGTAGGAAAA	TTACAGGGGA	AAGTTAGAGT	ATAAAATCCA	GAATGAAGGT	TTACTGGGTA
	AGAGTCTCTC	CATTTTCCAA	AGCCCGTTTA	TTCTTGATT	CCAGTTCTTA	AGAAGTCTCA	GCATTGTGTC
40	TTTTTCATGT	ATCTTACAAG	AAGACAGCAT	GTGCTTCTAA	CACCTGATAC	ATTGTATCTA	CCAGCACTTG
	GTAACAGCAA	AAGAACCACA	TTTTTCTTGT	AGGAGAAATT	TGGTGCCCTAT	TTCTTACCAG	GCACCAATAA
	TGGGGACGAA	TAGTGGGAT	TAAAGATACA	GTAGAAAGTA	TTTAAAACTT	GCCAGGGGGC	AATAGTCTGA
	AAATAAGTAA	ATTGTGTCTA	TAGAATGGAA	GTACAGGCT	CTTTCTTTT	TCCCACAAG	ATCTGCTCCT
	TGAGCCCCTA	GAGACTTTTC	TGTCTGTAC	TGTTTCTTCA	TTCTCATCT	GCAGAGCCAG	CCCTGAGAAG
45	TGCAGACCAA	AGCAGGGGAA	GGCTCTGCAA	AGATGTACAA	ATGGAAGTCA	CCTTAATAAC	CTCTGACTGC
	TGCGCATAAT	ACAATTCAC	CAAAAGAGGG	GTAAACAAT	GGAACAGAAT	ACAGAGGCCA	GAAATAATG
	TGAACACTGA	CAACCATCTG	ATCTTTGACA	AAATCCACAA	AAACAAGCAA	TGGAGAAAGG	ACTCCCTATT
	CCATAATGGT	GCTGGGATAA	CTGTCTAGCT	ATATACAGAA	GATTGAACCT	GGGCCCCCTC	CTTACATCAT
	ATACAAAAAA	TAAATCAAGA	TGGAGTAAAG	ACTTAAATCT	AAAACCAAC	ACTATAAAAA	CCCTGGAAGA
50	TAGCCTGGGA	AATACCATTC	TGGACATAAG	ACCTGGCAAA	GACTTCTATG	CAGACACCA	AAAGCAATAG
	CAACAAAAAC	CAAAATTGACT	AATGAAACTA	ATGAAACTCT	TTAGTTGTAC	AACAGATAGT	TTATCTGTAC
	AACAAAAATA	ACTATCAACA	GAGTAAACAA	CCTACAGAAT	GGAAAAATTT	TTTGCAAACT	ATGCATCTGA
	CAAAGGTCTA	ATAACAGAA	TCTATAAGGA	ATTTAAACAA	ATTTACAAGC	AAAAAAATGA	CCTCATTAAT
	AAGTGGGCAA	AGGACATGAA	CAGATGCTTT	TCAAAATAAG	ACATTACAC	ATCCAACAAC	CATATGAAAA
55	GATGTTTAAC	ATCACTAATC	ATTAGAGGAA	TACAAATCAA	AAGCATAATA	AGATACCATC	TAATACCAAT
	AGGAATGACT	ACTATTAATA	AGTCAGACAA	TAACAGATGC	TGGTGAAGGT	TGTGGAGAAA	AGGGAATGTT
	TATGCACTGT	TAGTGGGAAT	GTAACACTAGT	TCAGCCATTG	TGGAAGAGAG	TGTGGTGATT	CCTCAAAGAA
	TGTAAAACCG	AACAGCTTT	ATCAACAGCA	ATCCCATTA	TGGATATACA	CCAAAAGGAA	CATGAATTTG
	TTTACCGTAA	AGGCGCATGC	ATGCATATGT	TCATTACAGC	ACTATTTACG	ATAGCAAAGA	C



5	TTAGAGTAAT	TAACATTTAT	TAAGCAAAGA	GCCAAGTACC	TTACACACAT	GATGTTTAAT	CTCACAAATGA
	TCTTTAATCT	CATAACAACC	GTCCATTGTA	TGTACATATG	TGGAAATTGA	GCCTTGGAGA	GATTAAATGC
	ATGGGGCATG	CCA'TTTGACT	AGAAACTGGA	AGCATCAGGA	TTTAAACTCA	GTTCTGAATG	GTTTGTAGG
	CTTTGTTTTT	TCCACATTAT	AGCATGGCCT	GCCATGAAGA	ACAGGTCCTT	TCTGGTGTTC	GTCTTGTTTG
	GTTTAAGTGA	AGCAAAATATT	TATTTAAATA	TTCAGATAT	GCTGT'AAAAT	TTTTACTCAA	AAATTGTAGT
10	ACAGTATGGA	TCT'CTGAAG	CCAAATAACT	CTTATTCAAT	GCTTAGTTGA	GAAATTTTAT	GGAGTAGTTC
	TCAATTTTTA	TGT'GTTCGA	CTGCAAAGGT	AAGTCTTATG	GAAAGATTCA	CTGTAATTTT	TTTTCTCAT
	TTGGACATCA	GCT'TTCTTT	TTCTCAGAG	CCGCTGAAAG	ATAATTTTTA	AAAAAAAAC	CTTGTTTTTA
	TATCAAGTGG	GGA'CATTTT	TCCAAATGAA	AACCGTGTAT	TCA'TTTTATA	TGATAAAATC	AATGTTATTA
	TTTTTAAAAT	TTTGATTTAA	AAATCATTAA	AAATAAATTT	TCAGATATTA	CCTGAAATTC	TACCATCCAG
15	AGATAATAGT	GCT'AAAGAT	TTGATATATA	GACACACACA	CATATATACA	TATATATCAT	CCTAAACTTT
	TTTGATATAA	TGT'ATATAA	GTTTTTAATA	AAA'ACTAGGA	GATTAATGCC	CTTTGAATGA	AAATAAATAC
	AATGTGTATG	CTT'AAACATC	TTGCCTTTAC	TTTATAACAT	TTATCACAGC	AGTCATGAGA	TAATGATTTA
	CATGGTCATT	GTT'AGTAAGC	TAATAGCTAA	GTGCATGAAC	TCTGGAGCTA	GCCTCCCTGG	ATTTTAATCC
	CAGATCTGTC	ACTGACCAGC	TGAGCAATAC	TAGGTAAATT	GCTCTTGTTT	CTTAGTTTCT	TCATCTGTAA
20	AATAGAGATA	AAAAATAATAT	CCACCTCAT	GGATTGGTGT	GAGCATTAAA	TGAGCATACG	TATGTAGGCC
	ACTTAACAAC	AATGCCTTCA	CATACTGAAC	ACAAATATAC	GAGCTGTGTT	CTTATTTGGC	TCATGTTTTT
	CCTACCACTA	AGC'GCATGC	ATGCAAGGAC	CATGTTGGTT	TTGTTCCACA	TTGCATCCCC	AACCTGGTAT
	ACAGTGTGCA	TTC'ATAGATT	GTTGACTATT	ATTACTAGTG	GCATTTAACA	AATATCTGTT	AAATGAGTGA
	AGAAATACCC	ATT'ACTGCA	AGTGTGTCTA	ATATTGATGG	CATAATGGGG	GAAACTCAA	CTCTGGAGTC
25	AAACAGGTTT	TAA'ACCTTA	TTCCCTCATC	CTCAGTTATT	GACGTTTTTT	TTTTGGCAGG	TGTGTGTGTG
	GGACAACCTA	TTG'AC'TTTT	CTGAATTTCC	AGCTTCGCAT	ATATAAAAATA	GAGATAGTGA	TTCA'TTCTTG
	CAATGTATGG	ATT'GAGACA	ATTGTGTAAG	TTTATCAATA	AATAGTAGCT	ATTTTTGTAT	AAGTATTACA
	TATAATATCC	AGGC'CACTGC	TTTGCATAAC	CCAAAAGGGG	CACCATTTCAT	GCAGAAATACA	ACATAAATGG
	TGTCCCTGGA	GCAGTGCAGT	ATAGGAACCC	TGAGGGGACC	TACAGTATAC	TTTATAGTTC	ATAGATTACA
30	AATTATCCCT	TTATCAGAGT	CTCTCAAGGT	TGGATGTATT	TGAGGTCCAT	AAGAGCAATT	TAGGATTAAC
	AGTAGCTGCA	GAA'ACCATCT	GCAGTGATAT	TCTCATTTTA	AATCCGCGGG	AAAGAAGACA	GCTATAAACT
	TGGGACCTGG	GTT'AAAGCAT	TTTAAATGCC	AAGTTCACCA	TTTTCTAAAA	CACAACAAAT	ACCCAGTGAG
	AGAGGGAGAA	GGGAAGTAAA	TGCCTCTGAA	TAAGCAAGTT	AATGTCAGTA	GTTGTA'CTGT	ATGCATATTG
	ATGAAACAATA	GAGGAACCAA	TGTCCAATCA	GATGAGCAGG	ATATTTGGCA	ATAACAAGTT	GCCTTTGAGG
35	AAAAATGATT	TTCT'GGCAA	GTTCTTTATC	AGCATACAA	AGCTAAAAGC	TACGCTTATC	ATCACTTATA
	CTAGCATACC	CTG'TGTGCA	AATGCTGTCT	GTGTTTGCAT	CTGCTATTGT	TGATGCCTGG	TGCATGAATC
	AGGACTCCAG	CCC'ACAAGTT	TTCCCAGAAC	TTTCTTATGG	CCATCATCTT	TAAGTGTCTG	GTGAACAGTC
	ATAGTTTGGT	ACAC'AAAAGG	GTCAACCTGG	GGGATGGCTA	GGGTTTGACT	CAGTCGTTAC	ATTTCAATAG
	AGCAGGAAGG	GGAAATGGTG	GCCTGTAACC	TCAGGGAATT	TTGCCAGTTG	GTCCACCCCA	CTCTCTCTCT
40	CCTGCTCTGA	GGAA'GTGGCA	CAGCCTAGAA	CAGCACCACA	GGTGAGAGAA	ATGCAAACCC	TAACCAGAGA
	AGCAGACTCT	TTGC'CATGAT	TAATAGTTCA	GGACCACCAC	CAGCTTTTAT	TAAAATTTT	AATAACACTC
	AAGTATTGGC	AGAA'AGAAAT	AATCTTGGGT	TAACTATAAC	TAGAATATTG	ACTCTTCCTC	TGTGGAAGAA
	TCAGCCAATC	ACA'TTGT'TT	ACATCAGTTT	CCCTGAAGAA	GAAAAATACA	CTGATGTTGC	AGCAAGACAA
	ATTTAAGCTA	GATG'ATAAATA	ACTTCCTTTA	GCCTGTAATG	CTAGGCTAAT	TACATATTGG	AACTATTTTT
45	TCAGGGAAGA	ATTG'TGTAGG	GTTTCAGGGA	AGAATTCTGA	AGAAAATATA	GAGCTGAAAT	GATCTTGCAG
	CTCACTGAAA	CTG'AGGGTT	TAGATCCACA	CTGATACTCG	TTCTATTATC	ACTGTAATGA	AGGCTGATGG
	AATAAGTAAA	AATG'TTTTGT	ATTAGTATGT	TTTTACACTT	ATTTGCAAGG	CATAAATAGG	TTAGGTTTTG
	ATCTTAATTT	AATT'CTAACA	TGTATTGTGC	ACAAGCTGTG	AGCAGTTTTC	AGGAGTTAGG	TATCTGGCCA
	TGACTGATTT	TTCA'GGAGTT	AATCATCTGG	TAGAAGGGTC	ATACACAATA	GGAAGATGTG	TGTGACAGGT
50	TGTGATCATT	ACTATAATCA	CACAGATAGC	TGTAGAATTT	TAGGCTGGCA	GGGTGGCTCA	GGCCTGTAAT
	CCCAGCACTT	TGGGAGGCCA	AGGCAGGCGG	ATCAAGAGGT	CAGGAGATGG	AGACCATCCT	CGCTAACACG
	GTGAAACCCC	GTC'GTACTA	AAAATACAAA	AAAAAAAAAA	AGCCAGGCGT	GGTGGTGGGC	GCCTGTAGTC
	CCAGCTACTT	GGGAGGCTGA	GGCAGGAGAA	TGGCGTGAAC	CCGGGAGGTG	GAGCTTGCAG	TGAGCCGAGA
	TCGCATCACT	GCAATCCAAC	CTGGGCGACA	GAGGGAGACT	CAGTCTCAAA	AAAAAAAAAA	AAAAAAAAAGTC
55	ATGTTAGATC	CAG'AGGGTA	GCAACTGGGG	CTGGGCTGTC	AGTCAACTCA	GTCAACTCAG	TCAACTCTGC
	TCCCCACAG	GAGA'TGCCAG	TGATGCATTT	TCATGGCCAA	CATTGTCAGT	CAGCATCATT	GAATTACTCT
	TGATTATAGA	GAC'ACAGCTG	CAACAGATTC	CCCATTAAT	ATGATGTTTC	TTGCAATGTT	TGGAAGGTAC
	TCCTTTTTAG	TAACGGAAAT	CCCTCTTCT	GGCTTGCTGA	AAGTTT'TTTC	TTTCCATTTT	AAAAATCGTG
	AATTCTTTT	TGCAATATTG	AGGTGGTTAT				

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5	CTTTTTCCTCA	CTTCTTATG	GTTTATCTT	TCAATTTTTC	TCTAACTCT	TAAGTTGGGT	GTTTAATTTT
	TAGCTTGCTT	TGCTTTTTTA	GGATAAGCAT	TAAAACCTACA	AATTTTCCTT	GTTATTCTTT	TGCTGCACCC
	CAAATGTGTG	ATAATTCTAT	TGTCTAATTT	CTATTCAATT	AGAATACTTT	AAAGTTTCTT	TTTGGTTTTT
	AAAAACTAAC	TTT TAAATT	GACAAATAAA	AATTGTGTAT	ATTTATTGTG	CACAGCATAT	GGCTTTGAAA
	TATATGTAC	TTG TGAATG	GCTAAATTTA	GCTTATTAAT	GTATGCATTA	TCTCACATAC	TTATCATTTT
10	TTGTGGTGAG	AGCTATGTGA	CTTTTGAAC	TATGAGTTAT	TTAAATATTT	TTAAATTAT	AAGCATATTG
	GGATTTAAG	TAA TTTAC	TTTTATTATT	AACCTATAAC	AAGTAGAACA	GTTAACCTGT	ATGATTCTAC
	ATCATTGAAA	TTTATTGACA	TTTGCTTCAT	AGTCTATTAT	ATGGTCTACT	TTTGTCTCATG	TTACATTCTGT
	AGTAGAATTG	GCTAATAGTT	GAGTAAAGTA	CACATATGTC	TATGAAATCA	AGTGTAAATCC	AGAGAAAAAG
	AGAAATTTAC	TGAATATATT	GTTCTAGGTG	CTATTATATG	TTGTCATGTT	TAATCCTCAC	CACAATTGTA
15	TGAGGCAGCC	ATAATTAATT	CCACTTTACA	CATGAGGAGC	CTGAGGGTTA	AAAAAAAAGC	TAGCTCTAC
	ATTTGTAAAG	AATGAAGCAA	AGATACAAAT	GAAGGCCAC	ATATCCTATA	ACTAGATATT	TAAGCATTTT
	AATCAAGCT	TTAAAACTGC	TAAATAAAAT	GTGCTCCAAT	TTCTATATTG	ACAGACATAC	CTTCCTAATG
	AGCTGGGGTT	CGAATTTAGA	AATCTTTTAT	GCTTCAGAGT	CCACACTGAA	ATGTGGAGGC	ACATAGTGAG
	TTGGTCCCCA	GCT TCACTG	CACCCACCTT	CTCTTTACTA	AATCACCTTT	CACATACATG	TATGAAACCC
20	CCAGCCTCCA	AGTCCAAACC	CTAAACAAAA	TGGGACACCC	TTGTGCATAC	ACAGAGACAC	AGCCCATCCT
	CAGGAAAAACC	TGG TAAAGTC	CATACAAGTT	CTGGAAGCAA	GCTTGGGACG	GTTTCAGTAG	TGTGGTCTAT
	AAGGGAGGCC	TCA TGAAGACA	GGTTTTCTTA	ATTCTGTGAA	CTTCTCCAC	AGTAGAAAGG	GTGCTGGAGG
	AGGGTCAGAG	TGA TGAAGTTC	TAAAGCATGG	GTCCTGAGTA	GGGGCCACTC	TTGCCCAAGT	CTAAGAAGGG
	TACTAGAATA	GCACACTACT	ACTAGATACT	AGAACCCAGA	TACAAGCACA	GGTCTTCTGA	AATTAATAAT
25	AATAATAACT	ATTACCATTA	TTATACCAGT	AGCTGTCAAT	TATTTAGTGC	TTATTATTTG	CCAGTCACTG
	TTCTAAATTC	TTTACATGTA	TTATACAAT	GCCATATAAC	TGCCATATGA	GGGATGTACT	CTCATTGTCA
	CCATTTTACC	GATC AGAAAA	CTGGCATAAA	ACGTTTAAAT	AACTTGTCCA	AGTTACAGAG	CTTAGTGAAG
	CCACAATGTT	GCTCAATTTG	CTCTCAAACT	TCAAAGGGAT	GGGAAGGACA	CCTAAGTCAT	AGAGTCTTTA
	AGAATCAGAG	CTAGAAGGAA	TCTTAGATGT	TATCTAGTCA	GCCTCCTCCC	ATTACAGTCC	AAGAGAAGAT
30	GGCCCTGAGT	TACTGTGAGC	TATTTTGTGA	TGTGAATTGC	AAGTGAATAT	ACATTCTACT	GAAGATAAAA
	GATATTTAAA	GATATCGCTG	GATATAGGAA	CAGTGGTTTT	AAATCTCTAG	GCTTTAACTT	TTCTCAGAAC
	AAGAAATCCT	TTT TGGTTT	AATCTATATG	CACATCTGTA	TTTTTCTCAA	TTATCGGGTA	GTAAATATA
	ACTTTTCTTC	TGTAATATTT	TTTAACTTTA	ATGAGTGTTC	CTCATAATAG	AAAAGTTTGG	AAACCATTGC
	TATGGGTATA	TACTTTCTAA	AGGGATAGTA	ATTTCTCTAG	AATATTCTAT	TAATGCTCCA	GAAGTAATTA
35	GCACAATGTG	GCAAGTCTGT	GCATCATCAA	CTATACATTC	TGCTGTTTTA	CTCCAAATCC	ACATGAAACT
	GATTATACAG	TCA T AGGCGA	GCCAGTGGA	GAGGCATTTT	TGGAGACTTC	CTGGTACATT	GAGACAGGGT
	CGGCCAGTCT	GCG T AGGGT	CTTGGTCAAA	ACTGCATTTT	TGAAACTAAA	CTCAGATTGC	TTTCTTTTAA
	GGGGTCAGAA	CTG ATTCAAA	TCTACATTTT	TAAAAGCCTT	AGATGTGGGG	CTTTTCCTAT	TCCCAGTCTC
	CGCTATTGGT	CTTTGTGAAT	CCACAGGCCAA	TTTGCCACAA	TCCTTGACTC	TCTCTTATAT	TAAGAATTAA
40	ACAGCTAAGT	TCA TGCAGAG	GAAATATAAC	AAAGGAGGGA	CTTTCCTACA	AGATCTTTGA	AAAATGGAAC
	ATTTGCATAA	GTCATATTTA	GCCGAAGCTG	TTGTTTTATA	TTTTCTTTTC	TGAATACTTT	GTTACACCTC
	CTCCCAGCCA	ACCCCCCCC	TCCCTGACCC	CAACTGTACA	GAGACAAAAG	CCTTCACAAT	GGTTTACACT
	TGAACCTTCC	TGGCTCCACC	CTCATCTACC	CGCTGAATA	ATTACATTCA	CTGACTGGTC	TCCCCTGCTT
	CCGTTTATCT	CCAC TCCTAA	ACCCTCTGAC	ACCTTAATCT	TCCCAGAATA	CCATTGTGAT	CCTGTTCCAC
45	TCTTGCTCAA	GTTT TCCCAG	AAACTAGAGT	ACAAACTTTA	TAAGCTTTAG	AGTTGAAAGC	CACTCTATCT
	CTTTTTCATC	CCCAGGTCTC	TGCCAAGGCA	GTATAACCTG	TCCAACATCT	CTAACTTCAA	TACCTTTGTC
	TTAGATACTA	GAC TCTCCTC	CTGGTTTCTA	ATTAAACCTG	ATCTAGGATC	TAATTTTGCC	TCTGAATTCT
	GTTGCCCTTT	GCCAAGTGAT	CTCTTCCTCC	TCTGAGCCCG	AGCATCTCTG	AGCTTGCACA	CTTAGCATAG
	CCATAGCACA	CACAGCCTTA	GCTTGCAGTT	CAGGGTGTTT	ACCTTCCTCC	CCCTTCAGAA	TGCTGGATCC
50	CCAGGGATAG	GAA TCTGCCC	CTTAGTGTC	CATAGCCCTT	GGTAGTATGT	CTGCGACTCG	TACATTTTCA
	GCAAATGTTT	AAT TGGTTAA	TTGAAGACAA	CTGTCCCATG	CCTTAAGCCT	CTCTTTTTGC	TAAACATGCC
	TGTGTCCTTT	GTCATTGAAC	AACTATTTTG	ATCTATTTTC	TTCTTGACAT	AGGGGTCAGT	TCCGAGGATG
	CTGAAATCAA	GAGACATAGC	TTATTCTCTC	AAAATTGCTT	TCAAGAGTGA	TTTTGTTGTG	AATTGAGAAC
	TGGCTGCCTA	CTTTTGGA	ACCCACTTCA	GCAAGAGTGT	TTGAAACCAA	ATCTATTCTA	AGTAATTTTT
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	ATTCAAGTAA	TCT TTAGACA	CTGTCTAGCT	ATATGAACCT	AGACAAACTA	ATATCTCTGA	GCTTCAAGTT
	CTTAAAAATTT	AAA T GAGGA	CAATACCATC	TATGGCCGGG	GATTAATATGC	TATGAGGAAT	GTAACACAGA
	TGTCAGGTAC	CATC TCTCTA	AAATCCAGAT	AAAATGAATT	AAAAAATCTG	CGCCGAAACC	CTCTCTAAGA
	GTT						

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Cognitive Function	
Measure	Score
Trail Making Test (TMT) - Part A	15.2
TMT - Part B	18.5
Stroop Color Word Test	22.1
Digit Span (Wechsler D-4)	12.8
Block Design (Wechsler D-4)	14.5
Verbal Comprehension (Wechsler D-4)	11.3
Perceptual Reasoning (Wechsler D-4)	13.7
Full-Scale IQ (Wechsler D-4)	100.5
MoCA (Montreal Cognitive Assessment)	24.8
MMSE (Mini-Mental State Exam)	28.5
MMSE-2 (Mini-Mental State Exam - 2)	29.1
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
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MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
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MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
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MMSE-2 - Memory	4.5
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MMSE-2 - Attention	4.8
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MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
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MMSE-2 - Attention	4.8
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MMSE-2 - Language	4.0
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MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
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MMSE-2 - Attention	4.8
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MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
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MMSE-2 - Attention	4.8
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MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.2
MMSE-2 - Attention	4.8
MMSE-2 - Memory	4.5
MMSE-2 - Language	4.0
MMSE-2 - Total	18.5
MMSE-2 - Orientation	5.



5	CTACAATCT	TCTGCTAGT	CATACTCCTA	TTACCATTC	TCAACTACTT	GTAATGCC	TGCCCTTTT
	TACAGTGCTG	ATTATACTT	TTCTCCAAA	CCATCATAAC	TGATATCTCC	TGGTTTTACC	TCAAACCGCC
	ACCTTAAGT	CTCTTTAAA	GTGGATAGAA	GATCTTCAGT	GACAAGGTAC	ACTCCAATAC	TTTACCCTA
	ATAAAGCCCT	ATTCTTTACT	TTTATATTCA	CTCTTATTCT	TGTTCCCAT	CTTATGCCAC	TCTCTACCTC
	TCCCCAGCTA	TCTCCACCAC	ACTATCAATC	TCACTCACTC	TCTCCTAGCC	ATTTCTAATC	CTTCTTTAAC
10	AAACAATTGC	TGGCTTTTAC	ATTTCTCTTT	CCTCCAAAAT	CACCCAGTCC	TCAATTTACT	CAGTGCTAAA
	AAAGGGGACT	CTGATATTT	TAAATGAAG	AGTGTGTTT	TTACCTAAAT	CAATCTGGCC	TGGTATATGA
	CAACATAAAA	AAAATCTCAAG	GATAGAGCCA	AAAACCTTGC	CAACCAAGCA	AGTAATTATG	CTGAACCCCT
	TTGGGCACTC	TAAATTAGATG	TCTTGGGTTT	TCCCATTCT	TAATCCTTTA	ATACCTGTTT	TTCTCTTTCT
	CTTATGCAGA	CCTTGTGTCT	TCCATTTAGT	TTCTCAATTC	ATACAAAACC	GTATCCAGGC	CATCACCAAT
15	CATTCTATAC	GACAAATGTT	TTAAGGGAGG	AGACCACCCC	TCATATTGTC	TTATGCCCAA	TTTCTGCCTC
	CAAAGAAAAG	AGTAAAAATG	AAAAGGCAGA	AATGAAATCC	ACAGGCAGAC	AGCTGATGTC	CACACCCTGG
	GCCTGGTGGT	TAAGATCAAC	CCCTGACCTA	ATCAGTTATG	TTATCTATAG	ATTACAGACA	TTGTATGGAA
	AAGCACTGTG	AAAATCCCTG	TCTTGTCTG	TTCTCTAAT	TACCACTACA	CGCAGCCCTT	AGTCATGTAC
	CCCTGCTTGG	CTCCCTCTGC	TTGCTCAATC	AGTCATGACC	CTCTCAGCGA	GACCCCTTA	GAGTTGTAAG
20	CCCTTAAGAG	GAAATGGAAT	TGTTCACTCG	GAGAGCTCGG	TTTTTGAGAC	ATGAGTCTTG	CCAATGCTCC
	CAGCTGAATA	AAGCTCTTCC	TTCTTTAACT	CAGTGTCTGA	GGGGTTTTGT	CTGTGTCTTG	TCCTGCTACA
	GTTTCATCTA	ACAATCCCAT	AATATCACCC	CTTACCACAA	AATCTTCTTT	CAGCTTAATC	TCTCCCACTC
	TAGGTTCTCA	CGCCACCCCT	AATCCTGCTC	GAAGCAGCCC	TGAGAAACAT	CGCCCGTTAT	CTCTCCACAC
	CACCCCCAAA	AATTTTCACT	GCCCCAACAC	TTTACCACTA	TTTCGTTTTA	TTTTTCTTAT	TAATATAAGA
25	AGATAGAAAT	GTCAGGCCCT	TGAGCCCCAAG	CCTGCACGTA	TACATCCACA	TGGCCTGAAG	CAAGTGAAGA
	ATCAGAAAAG	AAGTGAATAAT	GGCTGGTTCC	TGCCTTAACT	GATGATATTC	CACCATTGTG	ATTTGTTTCT
	GCGCCACCTT	GACTGAGGGA	TAAACCTTGT	GAAATCTCTT	CCCCTGGCTC	AGAAGCTCCC	CCACTAGCCA
	CCTTGTGACC	CCCACCCCTA	CCCACAAGTG	AAAAACCCCC	TTTGACTGTA	ATTTTCCACT	ACCCACGCCAA
	ATCCTATAAA	ACAGCCCCAC	CCCATCTCCC	TTTGCTGACT	CTATTTTTGG	ACTCAGCCCA	CCTGCACCCA
30	GGTGATTCAA	AAGCTTCATT	GCTCACACAA	AGCCTGTTTG	GTGGTCTCTT	CACACCGACA	CGCGTGATAA
	TTATTATATT	ACTTTTAACT	AAAACCTTT	CAGAGTCTCG	CAGGGAAGGC	TGTATATATC	TCATAAAATG
	TTGGGGCCCA	CTGCATCAGA	CAAGGCCACA	AAGGCCAAAAG	GGAAGTAAAG	ATCTCATTAT	TTCTCCTAAT
	AATTTCCCTG	TCTTTGTCTA	TAAATGGTGG	GTAGGCTGTT	ATGGTGATGG	CAGATTTTCT	TTCCATAAAA
	TGTCCATAAT	AGGACATTTG	AACAGAAAGG	AAAAATCAAA	TTGCTGAAGT	TGAAAGAGGG	CAATGCAAGG
35	AACCTTTGGAG	AAAGCAACTGT	ACAGAGAAGT	CAACTGGCAG	ATGGGAGGAA	GTTTAAAGGG	AAAAATATAG
	ATGTCTAAAG	AATATCATTTA	TTCATTTTCC	ACAGTGCAAT	TTGGACAAGA	AGCCTCTTTC	TTGCTCTTTT
	CTATTCTCAT	TAAATCATTAT	GAGCTCAAGC	AATCCTTCTG	CCTCAGCTTC	CCGACTAGCT	AGGACTACAG
	GTATGTGCTA	CTATGCCCAG	CTAATTTTTT	AAAAATTAGA	TTTTAATTTG	GTGAACATTT	TCTGTAGGAA
	ACTACAATAA	TACATGCCCAG	GCACATTGAT	CTTGGGTGAA	CAAATCAGAA	GGAATGAATA	ATTCTGTGTT
40	CCTGGGACTC	TGACAAATTTT	ATGAACTTGG	TACTCTGAGT	AAAGCATAGG	AGGAGTTATT	TCATAAAATG
	TGGAGACACA	TCATGTGACA	AAGATAATGG	GATCCCCATT	TCATAAATAA	ATCTGAAGTT	CAGAGAGAGT
	AACAACCTGG	CAGGGTACACA	TCACGGAGAC	AGAGGCAGGG	TCTCCCACTG	TGCTCTGAC	TCCTGTCTCC
	AGGCCCTTCC	TCTCTCCGCA	AGCAGAAAGT	CAGGGGGCAG	AGCTGACCTT	GTGCAGTGAA	AATCTGAGGG
	CTGAGTTTCT	ATTGGAACAC	AAGTGAAAGA	CTTCTGGCT	TCTAATCTCA	GGATAAGGAC	TCAGAGCTCC
45	ATCTGTTCCA	GCCTTAGGAT	AAGAACCAGA	ATCTTACACC	ATGAAAGCAT	GAAAGGTAAG	ATTTGAGTGA
	GGAAAAAATA	AAAAAAAGTC	TGTGTTTCAG	ATTCAAGTTCA	CAAAGCAGTT	TCATACTTAA	GGTACCATCA
	CAATAACCCT	GTGCGGTAAG	CAAGGCCAAAT	TTCATTCTTG	TTTTATGGGC	ATAGGAAGTA	AGTCTCAGGG
	AGGTTAAGAC	CAAGGTTTCT	GGAGAATTTT	ATATTATGAA	TCTTGATTTA	TGGGATTACT	ATTATGTAAT
	TCCTAAGATC	ATAATAGGAAT	CCTAGAGCTT	GAATATAGAA	CTTTATTTTT	AAATCTATAT	ACATCATAAT
50	TCCAAGGAGT	AGTGTCCTATT	TGGGTTCTCT	GGCCCTGATG	TGTTAGTGGA	ATAAACATTT	TTGTGAGGGT
	TGCCATGTGT	GTCTGTGCAC	GTGTGCACTG	TACACCTCCA	GGGGATGTAC	CCTAAACCAC	ATGAATGTGA
	TTTGACATC	CAACATTTAC	AGTGTACTAT	AGGGAGAATC	TTTTGCAACA	GCTTTTGCTA	TAATACAGAA
	TCTGAGATGT	CTTTGAGAAA	GAAAAGTGTA	ATCATTACCA	AAAAATTATT	CTCATAATGT	GTGCAAAATTT
	GTATGAAATC	TATATTGGCC	ATGGGACAAG	GAGGTATTTT	CAGCTAGCTT	CTGAAAGGGC	TCTATTCTCT
55	CATAAGAATT	CAGCTGTTGA	CATTAGGTGA	TATCTGCCCA	GGTCATCAGA	TGCCATAGAG	AAAGAGGGTT
	TGCTGAAACT	TATATCAGCA	GTGCACGTGA	TGCTCTTTCT	GATTTATTTG	AACATTCATT	TATTGAGTGT
	CAAGTAATGC	ACTATGATACT	CCAGGGATCT	GACACAAAAT	CTGCCCTGAA	GGAGCATGTA	ATTCACCTGG
	GGAGAAAAACA	AAAATATATGA	TAATTTCAAA	ATAACAAAAT	AGGCAAACTA	GTTAACACTT	AAAAAGCAGG
	CTTTATTCAA	ATGCAAAATTT	GCATGTTACA	GGGTAACCTT	TCAGTAAGAA	GCCAGGAAGA	GGAGCTCATC
60	ATGGGTTGGA	TTACTAAAGG	ACTAGTTATA	AAAGAAGTGG	TGGGGTTGAG	GGAGGCCTGA	GATGAAATTT
	AAAGAATATG	TAGATCTCTAG	GTAAGTGGAT	AAAAGGTCTG	GGGGCAGGGG	AAAGGAGAGC	ATTTCTATTGT
	GAATCAAGGA	ATTCTCCAC	CTGTTTAAAC	TCTTCCATAT	GACATCAAAG	AGATGTCACT	TGCAGCTAGC
	ATTTCAGTGA	TGTTTCTTTA	CTAATAATAT	CGTGATAAAA	GAAACATTGA	CTATAAGAAA	TAGGAATGGG
	TCTCATAAAA	GGAACACAGA	AAACCCCCAA	ACTAAAAAAC	AGCGCAGGCT	ATTTCTCTCT	TCTCTCTTTT
	TGCTTGCCAC	TCATAGATG	CTAGGTGTGG	AAGTCAGCCA	ACTGAAAAAG	AGAGGTGGCT	GAAGAAGGTT
	GGGAGGCTGA	AGCCAGTTAA	ATAGGATGGT	CCAATTCACA	GACGGCAGGG	CTACAGTGCA	AATAGGACTC

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	5.5	10	25
Health status	1.5	1.0	1	3
Stress level	2.5	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
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Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
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Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
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Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5	1	5
Income satisfaction	3.0	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.0	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.0	1.5	1	5
Overall satisfaction	3.5	1.5	1	5
Healthcare satisfaction	3.0	1.5	1	5
Education satisfaction	3.5	1.5</		

5	CTTTAGTGAT	ATCC CAAAAG	ACCTCAAGAT	AAAGCCCAT	TCACATGGCT	TATACATTAG	TTTATGATCT
	GGCTTCTGGT	GCC`CATT	TCCCCACTTT	TTCCTTTGCA	TTCTAAGCAA	TGGCCCATAC	TAAGTTTGTG
	ATTGGTAGGA	TGG`TGCCCA	AACCAGCATC	CAATCCCTTC	AGAAATCATC	TCACCTCATT	TCTAGCATTT
	TAAAGGAAGC	TCA`TTGTCC	AGCTGGGTAC	TGAATATGTC	ACCAAAGTCC	TCCTTTCATA	GTTTATTTTA
	CTTAAACTCT	CCTTCCTAAA	ATTCCAGAGC	AAGTCACTAA	ACCCTAGATA	CTGAGAAATA	TTTTTCCATC
10	TTCATTTCTG	CCAC GTGGGC	CATCAACTTT	CACATGTCTG	CATCTCCTCC	CACTGTGCTA	TTTCTCCAGT
	AGAAGAAATT	TGAGCTTCAA	GACCAAACTG	AAAAATACTT	GCCTCCTTGG	GGAAGCTGTA	GGTAGAATTC
	ATGCTCCCTA	TCTT`TCCAC	ATTCTGAAG	GACAATGCCT	GTTAGAGCAA	TTGAATGCAA	ATAGTCAATT
	GAATAAGCAT	TTA`TCATTT	CTCAATAAGT	GCTTGTTCAA	TTGAATATTT	CTTAAATAAT	ATATTTAAGA
	ACAAGAAGAA	CAC`ACCACAA	TGTTTTTAAC	CCTCAGAAAA	AATTCTGAGG	TAATCAGAAA	AATCTCCCTT
15	TACATAAACT	GCCCTTTTCT	AATAGGGATT	ACTTGTTCTG	TCATTCATT	ATTCAGCTCC	ACTAGCACC
	AAAAGCACAG	CTC`GAAAGG	AAGCTAGTAG	ATTTATCACC	TTATCTGGTC	ATTTGGATGA	GGACCCAGG
	TAAATAAACT	ACT`TGGGGT	TAATGTGTCT	AGCTAGAGCA	GGAAGTAACT	TAAGGAAGTA	GAGAATGAAT
	CAGCAGATGT	GGAACTCTCT	CGCCACTAAT	AAAACCTACC	TTCTCTTGGA	TTTCTTGCC	GAAAATAGAA
	AATAGAGAA	AGG`ATTAGC	AAAAATTAGA	CAATTTAAAG	TTTTTCAAGT	AAGGGAGAAG	GAAGACTCCC
20	ACTCTCAAAA	CTG`TCTTTG	AAGTATATTA	GGTATTTGTT	AGGTGGACCC	TATCTGTGTC	AAAGGAGATT
	TGAGGAACTG	GCTT`AATAAA	CAGTGGTAGA	CACATAATACA	GAACAGACAT	TTTGATGCAG	ATGCCTCTG
	AGGTTCCATT	CCATT`CTCCG	TGCTACTCAA	GAAGACAGAA	25441	TTGCTAAATT	GCCTGGTGGC
	ATGTCCATT	AAGT`GTTTAT	CCCTTCCCAA	TCTGCCATCT	CATCCTACCT	GCAGATTCTT	CCCTTGAGGG
	ACAGCTGCTA	ATA`CTGTA	ACTATGTGCC	ATTACAGCTC	ACAGCATCAT	CTCTATGAGA	ATCCACAAGA
25	GAATTTCACT	TTGC`TCTTGT	TGGTAGGAAT	TGTGCAGCCT	CATCTGAGTA	ACTAATGTGT	TTTTATCTTA
	CAAACACAAG	GAA`TATCACA	TGGTCTCTCT	TTGACTGGCT	GTAAGGAAAC	TCAGAGCTT	ATCTGAGACC
	CTCTCTCACT	AAGT`ATATA	AACTTTGTGA	CATACATTTT	TGTGCCATAA	CTCAACCTT	GGTTCCAAAT
	GATTTTTGTA	CCCI`AAGTTT	AAATTTGGCT	TTCTTTTTTT	TTTTTTTGTA	CTCAATAAAA	CATCAAGCTC
	ATTTATTATT	GCGA`AGAGCG	AAACAACAAA	GCTTCCACAG	CGTGGAAGGG	GACCCGAGTG	GGTTGCCCAA
30	ATTGGCTTCT	TTTT`CTTACT	TTTTAATTAA	TTTTAATTTG	CTATACTGAA	CACATTTTGT	ACTGTTCTCA
	CATTCTTTTT	GAAA`AAAGCA	GAATATAAAT	AAGTAGATAA	CTTAAAAAAA	ACTCTTTGAG	CAGAAAGAAT
	CATTTGGGAG	GCA`TATATT	TCAGTGGCTG	TAAAGTGGCA	TTCTAGAATC	ATCCTACCCA	GGTGAAAGCC
	CTATTTTGCC	ACCI`GAGTGT	TAGTGTGTAT	TTGAACAGCT	ACTTTCTTTT	CTAAACTACA	ATTTCTTCAT
	CTGTTAAAGA	GGC`ATAATA	TGTATCATC	CTCATTTGGT	TGATAAAATA	AAATATTTC	AAGTATTTAG
35	TTCAGGTCTC	AGCA`CTGAGA	CAGTGTGCA	TTACTGTTTT	AATCCTTTAA	AGTATTTAAG	ACTACTATTT
	GAAATCTTTT	CTTC`AAAAAT	TCAGCCTGCT	GATGACCAAG	TGCATCTGAG	CAGGGGGAAT	CAAACTGAA
	TTAATTTTCA	ATT`CTGGTTA	GCTTCACATA	AATATTTTTT	TTAGGGATGA	TGAACCTAAC	AGCAATAGAT
	GAGTAAGAAT	CTG`TCTCTAC	TGAGAGAGTT	TCATTTTGAA	GAAAAAGGAA	CTAAGGGGGC	ATGTGTTTCA
	TTTCATGCCC	TGGT`CTAACC	CTGTGTGTTG	GTTCTGTGTG	GAAATTCTTC	CAACCGAGGA	AAAAACCACT
40	TCACAAATCT	GAA`GACCACT	GATTTTAGAA	GATGTATCTG	GACTGGAGTC	TAATCTCTGA	CTCTGGGTCC
	TGCTGATATG	GTAI`TTTTGA	GATTTGGCCT	AAAACATCAT	TGCCCTGGTT	TCCTTATTTA	CCAAACAGGG
	CCAAATGGTAG	TGAC`TAATCA	GAAAATGATA	ATGCCTGGTG	CACAAAATGT	GTCTAGATGA	GCCCATGAC
	AAGACACAT	GTTT`CTGGAA	CTGTTCTTTA	TTCCTTTCT	AAAAGAAAGG	AGGGAAAGTC	TCCATACTAA
	GACTACTAGG	GCAC`GGGACA	AAGTGCTAGA	GTCAGAAGAT	TCATCTGAGG	ACAGAAGAAT	AGGGGTGAAG
45	GCTCTAGTCA	CTTC`ATTGGC	TACCATGCTC	TAAATAGTTA	CCTGTGCCCT	TTTTCTAACT	ATTAGAACCC
	AAAAAGCCTA	TAA`ATTCTCT	CTCTCTCTCT	CTCTCTCTCT	GTGTATATAT	ATACATATAC	ACACACACAT
	AGACACACAC	ACAC`ACCTAA	ACACACACAT	AGAGATTAT	GACTTTTTAC	TTTTATCCTT	GTAAATGCCA
	TTAACTATAT	TTTG`CTTAG	ATTTAGCCTG	GGAATGTAGC	CATTATTTCT	ACCATTGCCT	CCATAGGAAA
	AATACTCTTC	ATGT`TTTAA	GGACCAACT	ACAACATAAA	TCTTTGGAAA	GCAGAAATCA	TTGTAAGTTG
50	GTGAAAAATG	AAG`ATGTTGT	TTATAAAATG	AAGACTTTTT	TTTTTTTTTT	TTTTGAGACA	GGGCCTCACT
	CTGTTGTGGA	GTGC`AGTGGT	GCTGTCATGG	CTTACTGCAG	CCTTGACCTC	CTGGGTTCAA	GTGATCTCTC
	CACCTCAGTC	TCC`IGGGTAG	CTGGGACTAC	ATGTGCATGC	TACCATGCCT	GACTAATTTT	TTGTATTTTT
	GTAGAGATGT	GGT`TCGCCA	TGTTGCCCCAG	GCTGGTCTTG	AACCTCGTGG	CTCAAGTAAT	CCTCCTGCCT
	CAGCCTCCAA	AAGT`GCTGGG	ATTAGAGGTG	ACAGCCAAGG	TGCCTGGCCC	ACAGATGAAG	ACTATTTAAT
55	GTTATCTTAA	AGA`TACCTA	AGCTTCCTAC	CAAGCCAGTG	ATCTTTTG	GCTTCTGTTT	TCTTTGTTGG
	CATAACTGTA	ACTA`GCTTAA	CTGCCCCTTA	TCTGTTCTCT	GTTTGCCCCA	CACCTGATTC	CACAGCAGTT
	TCAAGGTTAT	CGGT`TTGAGA	TCTGTGACAG	AAATGACTCC	AAGTAAAAAA	ATTTAAAAAC	AACCCCTCTA
	ATTTTTTTTAC	CCTT`GCTTAT	AAAACAGCCT	TAGCCAGCTA	ACCCCTCACT	ACATGCAAAAT	GAGTTTGATT
	CTATTCTTTT	GATT`CTACAA	ACACTTATTA	AA			



	CAATTAGGGA	CTGATAAATA	ATATTTTTGT	AATTGCCAGT	GTAATGGAC	AGGGGGCAAC	CTTTACATAC
	CATATTCAGT	GAACAGAATA	CGTACTAACT	AATTTGATGG	AAGGAAAATT	AAAATGACAA	TCAACTGAGC
	CCACAGAAAG	GCAACACAGA	GCAGTTGGTT	AGCAATTGTT	TCGAGATCAT	CCCTGAACCT	GAAACAGGTA
5	TATCTTTTTT	TTTTTTTTT	TTGAGACAGA	GTCTCACTCT	GTCACCAGGC	TGGAGTGCAA	TGGTGCGGTC
	TCAGTCTCACT	GCAACCTCCG	CCTCCCGGGT	TCAAGTGATT	CTTCTGTCTC	AGCCTCCCGA	GTAGCTGGGA
	TTACAGGTGC	CCGACACCAC	GCCTGGCTAA	TTTTTGTAAT	TTTAGTAGAG	ACAGGGTTTC	ACCATTGTGG
	CCAGGCTGGT	CTTC AACTGC	TGAGCTCATG	ATCCGCCCGC	CTCGGCCCTC	CAAAAGTGCTG	GGATTACAGG
	CATGAGCCAC	CACA CTTGGC	CAAAAACAGGT	ATATCTTAAA	AGCTGCCCAA	TGTCCATGAA	TGTTACAGCC
	TTGAATGGTT	CTTC CAGGTG	AGTTTGGCCA	AATGTGGCAC	CATACACCCA	AGGCCTGCTG	CAGGCTAGTG
10	GGTTGCTCAC	ACTTTAAAGC	TGAGACACAC	TCATGCCTTA	AGGTAAAGGG	AGTGATAATC	TGGGCAGCAG
	ATGTTAACTT	CTCA AGGCAG	TCCTCCTCT	CTTTCTCTCT	CCAGTGACGG	ATGGTTGGAA	AGCATATAT
	GTGCATTTGG	TTACAGCTGT	GGCCTTGGTG	AATAGATACT	TGGGAGAATA	CATGGGAATT	TCTCCCAGGG
	TTAATGCAAT	GCCCATGTGT	TGGGAACCCAG	GTGACTCTTG	AAGAGGTCAG	GTATTTGGGA	GCAGTGCCTT
15	GAACACCTTAG	TGGA CATTAG	ACCCACTTCC	TAGTGGAAAT	GTAGCATTTA	AATCCAAGGC	ATGTAGGCTC
	TTAGAGGACA	GAGATAGTGT	GTCATTTTTT	CAGAATTAAT	TAAGAGCAGG	CCAGGCGTGG	TGGCTCACAC
	CTGTAATCCA	AGCCCTTTGG	GAGGCCAAGG	CAGGCAGATC	ACGAGGTCAG	GAGATCGAGA	CCACTCTGGC
	TAACACAGTG	AAACCCCGTG	TCTACTAAAA	ATACAAAAAA	TTAGCTGGGC	ATGGTGGCAC	GCTCCTGTAG
	TCCCAGCTAC	TTGGGAGGCT	GAGGTGGGAG	AATAGCTTGA	ACCCAGAAGG	CGGAGGTTGC	AGTGAGCTGA
20	AATTGCACCA	CTGC ACTCTA	GCCTGGTGAC	AGAGTGAGGC	TCTGTCTCAA	AAAAAAAAAA	GTATTAAGA
	ATTACATAAG	AGCA AAGAAC	CATTAGAATA	TCTCACTTAG	TTGTTATCAG	CCTAGCAAGC	TGCCTTGAAG
	GTAATAGACA	TTTTTAAAA	TTTATCAGAT	GAAAAGCGAA	AATCAGCCAA	CCTGTTTTAA	TGAAGGTGTG
	TCTTGGGCTG	ATTACATGT	CTCCAGGGAC	TGATGGCTCT	AGAATGTAAA	GCTTGGCATC	CTGCTTGTGT
	TGAATCTATC	ACATTAATT	TCTGTGGGT	TTCTTTTTT	TTTCTTTTC	ACTTTAAAGT	TGTGTCTTTT
25	TCATGTGAAG	TTAACTCAC	ATACCTTTTT	TTAATCTCCT	TGCCAGCCAA	ATGATAAATG	CCAACCCAGA
	GAATGCAGTA	ACCATGACTG	CCACTGGAAT	GAAGAGGGGG	TTATAATCAC	CCTCCTTAAT	CATTGAGAAA
	CTTTTGTTCA	ATTCGAAAG	AGAAATCAGT	AAGGCACATA	GCATGAGACC	ACCAGCATT	TTTCCTTAGT
	CTATCTCATG	ATAITTGACT	TTTTTCCTCC	TTACATCTCC	CAGTAGTAGC	CCATTTGATG	CCATTTGACA
	GATGAGGAAA	CTGGCATGGG	AAGGCCCTG	ATGAGTCTAC	AGCATAGGCA	AAGACTGGAC	CAGCCTTGCT
30	AGTCTAATGC	CTACAGAATC	TCAATGCCA	GATTTGTGGT	TCATAGAGTT	CCTGAAAATG	CACATAAAAA
	TGTTGGCAAG	AATGTCATC	GTGTATTTA	GCTCCATGGA	CTTGTCAAT	GACTGGAAT	CTGAAACACA
	GAGAAAGAGCT	AAAAGCCTAA	TACAACCTCA	GGAAAAATAA	AAGCCAATGA	TCTGAACCTG	ATAATTACCC
	AGTCAAAGGA	AATCATTAAT	GCTTTTACTT	TAAAGCAGTT	GTGCAAAAAA	AAGCACTTGA	TTTTTACATG
	CCAAGGACCT	GCACTAATTT	CTTTCCAATG	CAGTAGTTAC	CACCTCCCTC	TACTTCTTTC	ACGAATAAGT
35	AAAAGGGCAT	GTTTAGAGAT	ACTCTTGTA	GTGTAACATA	AGTTCATTTG	GGAGCCTCTA	TTTGAANAATA
	CTGGTATAAA	AAAATACTCG	TCTCTGATA	CTAACATTTG	AAGGAATCTA	CTTTTTTACA	TATTGGCAGA
	GGGTCTGATT	CTATCCTTAG	TTCTTCCCCT	TACTTTGATG	AACCTTTTCA	AGGTGATTTG	ATCCCCACAC
	CCAAATATAT	GATTAGAGAG	AGGCTCAAGT	TCCCAGGAGC	TCCAGACAGA	AGGTACCTGT	TGGCTTGATG
	AAGATGAGGA	GGAAATGAAC	ACTAGCTAGG	CCTTAAAGGG	AAATGTCTCT	GATAGGCCCTA	ATACACAGTC
40	CTCTGCTAAA	GGCTTCCCTG	CCTCTCTCTG	CTCATCCACT	CTACTCCCTG	GCCCTGGGCA	CGCAGCACAC
	AGAGATCAGC	ATTCTGACA	GCTTCTGTAG	ATCCTACCAT	TTAAAGACTT	TTGTCATCCA	TGCAGATAGT
	CTCAGGAGCA	GACACAGGTA	GCTATTCTTT	CACATGCTAG	CTTAACATGC	ATTTGCTTTA	GCACCTATTG
	CCAGGCACTG	TGTCAGGTGG	AGGGTATACA	AAGATGAACA	AGACATGATT	CTTCTCATAT	ACAGATAGAT
	TTTGAGGGCA	TTACCTTAGT	GATGATTCAG	GAGTATCCAT	TATTTGGGGA	AGTAGGTGGT	CATTAGTGAC
45	CTTTTACAGG	CATTTC AATG	GGCTAACAGA	GATGTTAGAT	TGTAGTGGA	TAGAAGAATG	GGTAAAAAGT
	AAATCAGTGA	GTTAGATT	TAGGAGTTAA	GATGGCAAGA	GGTGAGAACA	AAAAAAGGAA	ATGATTGTCA
	TTAAAGGAGG	ATGA AAGACC	AGCCAAAGAT	TTTACAGTGA	GTTAAGCATA	CAATTTTATT	TCTAGGCCAC
	ATATTCTTAG	CAAAACAACA	TGTAAATGTT	TATGTATGTC	TTTCTCATA	TCTGCTCATC	CATCAGCTCC
	ATCGTTAAGA	TTTCAGTTTT	CCAGGACAAA	CTTACTCACT	TTGACATATT	GGACTAGGAT	TTGACCAGAT
50	TCCAGATGAT	TCACAAATGG	TTTTCTTCTT	CCCAATTAAC	TCAGTTCCTT	CTGAGCAGAT	GAAGGTACAT
	GCAGAGGTAA	AGCTGAAGCT	GGCCAGGGGA	TGGCTACAGT	TCATGATCCC	CAAATCTGGT	GCTGATAGAG
	GCTCACTACTG	AATCACTTCA	ATGAAAAACA	AAAAAAAAAA	AAAGACAAAA	CAGTATTTCT	GAGTAGAGAC
	CCTCCCTTGA	GCAAGGATT	TTTAGCCAAA	GCTGCCTGAC	TACATTACTT	GTGATATTGC	TTCCAGGCTT
	TATTTTCTTG	AGAAATGATG	TGGGTGGTGA	ATGAGAGATG	AAGGCAAGGA	AGCATTGAAA	GCTGTGGGGA

[illegible]

[illegible]

Cognitive Function	
Trail Making Test (TMT)	10.0
Digit Span (DS)	12.0
Block Design (BD)	15.0
Verbal Fluency (VF)	18.0
Stroop Test (ST)	20.0
Symbol Digit Modalities Test (SDMT)	22.0
Trail Making Test (TMT)	25.0
Digit Span (DS)	28.0
Block Design (BD)	30.0
Verbal Fluency (VF)	32.0
Stroop Test (ST)	35.0
Symbol Digit Modalities Test (SDMT)	38.0
Trail Making Test (TMT)	40.0
Digit Span (DS)	42.0
Block Design (BD)	45.0
Verbal Fluency (VF)	48.0
Stroop Test (ST)	50.0
Symbol Digit Modalities Test (SDMT)	52.0
Trail Making Test (TMT)	55.0
Digit Span (DS)	58.0
Block Design (BD)	60.0
Verbal Fluency (VF)	62.0
Stroop Test (ST)	65.0
Symbol Digit Modalities Test (SDMT)	68.0
Trail Making Test (TMT)	70.0
Digit Span (DS)	72.0
Block Design (BD)	75.0
Verbal Fluency (VF)	78.0
Stroop Test (ST)	80.0
Symbol Digit Modalities Test (SDMT)	82.0
Trail Making Test (TMT)	85.0
Digit Span (DS)	88.0
Block Design (BD)	90.0
Verbal Fluency (VF)	92.0
Stroop Test (ST)	95.0
Symbol Digit Modalities Test (SDMT)	98.0
Trail Making Test (TMT)	100.0

5	CTAATAACAA	GTTCTGAAAT	TAAGGCAGCA	ATTAATAGCC	TACCAACTAA	AAAAAGCCCA	GGACCAGATG
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	AACTCTCAAT	AAACTAGGTA	TTGATGGAAC	GTATCTCAAA	ATAAATAAGAG	CTATTTATGA	CAAAACCCACA
	GCCAATAGCA	TACTGAATGG	GCAAAAACCTG	AAAGCGTTCC	CTTTAAAAAC	TGGCACAAGA	CAAGTATGCC
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	AAATCCCATT	GTCTCAGCCC	AAAATCTCCT	TAAACTGATC	AGCAACTTCA	GCAAAGTCTC	AGGTTACAAA
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	ACCTGACTTC	AAACTATACT	ACAAGGCTAT	AGTAACCAAA	ACAGCATGGT	GCTGGTACAA	AAACAGATAT
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	GAGGATTTTA	AAGAGCACCA	TGAATTTTAC	AGAAGAATGA	TCTTTTCACT	TCCTATTGAG	CTGGGTGCTT
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[illegible]

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1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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 30 CTTGTTTTAA AGTT.CACAAG TATTGTGTGA ATTGCAGGCA ACCCCTTGAC TCCCTGATTG CCTGGTCTTC
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5 GAATCTGGAC AAGCTTGAC CAGACATGAC AGAATAGAAA TTTCTTTTCC TATTTATCTC TTTGAATAAA
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 GGGCAGGGGA GTGCTTTCAG GATGAACTG TCACAATAGG GTGTGCACTC CCATGAGAAT CTAACACCGC

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Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10.1	0	20
Marital Status	Married	15.3	0	30
Education	High School	12.4	0	25
Income	\$25,000	18.7	0	50
Health Status	Good	10.2	0	20
Exercise Frequency	Weekly	11.5	0	25
Stress Level	Low	8.9	0	20
Sleep Quality	Good	12.1	0	25
Dietary Habits	Healthy	13.6	0	30
Work Satisfaction	High	14.2	0	30
Life Satisfaction	High	15.8	0	35
Family Size	2.1	1.3	0	5
Home Ownership	Owned	16.4	0	35
Commute Time	30 min	15.2	0	60
Neighborhood Safety	Safe	17.1	0	40
Access to Parks	Yes	18.3	0	45
Public Transportation	Good	19.5	0	50
Local Economy	Strong	20.2	0	55
Community Involvement	Active	21.1	0	60
Local Government	Responsive	22.3	0	65
Local Schools	Good	23.5	0	70
Local Healthcare	Good	24.2	0	75
Local Environment	Clean	25.1	0	80
Local Culture	Diverse	26.4	0	85
Local History	Rich	27.2	0	90
Local Future	Bright	28.1	0	95
Local Values	Strong	29.3	0	100
Local Identity	Clear	30.5	0	100
Local Pride	High	31.2	0	100
Local Love	Deep	32.1	0	100
Local Belonging	Strong	33.4	0	100
Local Connection	Deep	34.2	0	100
Local Commitment	High	35.1	0	100
Local Dedication	High	36.3	0	100
Local Devotion	High	37.2	0	100
Local Loyalty	High	38.1	0	100
Local Faithfulness	High	39.2	0	100
Local Integrity	High	40.1	0	100
Local Honesty	High	41.3	0	100
Local Sincerity	High	42.2	0	100
Local Candor	High	43.1	0	100
Local Frankness	High	44.2	0	100
Local Directness	High	45.1	0	100
Local Openness	High	46.3	0	100
Local Transparency	High	47.2	0	100
Local Accountability	High	48.1	0	100
Local Responsibility	High	49.2	0	100
Local Obligation	High	50.1	0	100
Local Duty	High	51.3	0	100
Local Obedience	High	52.2	0	100
Local Compliance	High	53.1	0	100
Local Cooperation	High	54.2	0	100
Local Collaboration	High	55.1	0	100
Local Partnership	High	56.3	0	100
Local Alliance	High	57.2	0	100
Local Coalition	High	58.1	0	100
Local Consortium	High	59.2	0	100
Local Joint Venture	High	60.1	0	100
Local Venture Capital	High	61.3	0	100
Local Investment	High	62.2	0	100
Local Funding	High	63.1	0	100
Local Capital	High	64.2	0	100
Local Assets	High	65.1	0	100
Local Resources	High	66.3	0	100
Local Wealth	High	67.2	0	100
Local Prosperity	High	68.1	0	100
Local Affluence	High	69.2	0	100
Local Richness	High	70.1	0	100
Local Opulence	High	71.3	0	100
Local Lavishness	High	72.2	0	100
Local Extravagance	High	73.1	0	100
Local Extravaganza	High	74.2	0	100
Local Extravagance	High	75.1	0	100
Local Extravagance	High	76.3	0	100
Local Extravagance	High	77.2	0	100
Local Extravagance	High	78.1	0	100
Local Extravagance	High	79.2	0	100
Local Extravagance	High	80.1	0	100
Local Extravagance	High	81.3	0	100
Local Extravagance	High	82.2	0	100
Local Extravagance	High	83.1	0	100
Local Extravagance	High	84.2	0	100

[illegible][illegible]



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5	TGTTTTGT	TGTTTGT	GGGGGACAGG	GTCTTGCTTT	GTCACCAAAA	CTGGAGTGTA	GTGGTGCGAA
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	TGAGACCGCA	GGTGCGTGCT	ACCATGCGTG	GCTAATTTTC	TATTTATATA	TTATTTTTT	GGTAGACATG
	AGGTCTTGTC	ATGTTTCCCA	GGTGGTCTTT	AACTCCTGGG	CTCAGACAGT	CCTCCCGCCT	CAGCCACCCA
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Sensitivity analysis	
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1.1.3	0.00
1.1.4	0.00
1.1.5	0.00
1.1.6	0.00
1.1.7	0.00
1.1.8	0.00
1.1.9	0.00
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1.1.88	0.00
1.1.89	0.00
1.1.90	0.00
1.1.91	0.00
1.1.92	0.00
1.1.93	0.00
1.1.94	0.00
1.1.95	0.00
1.1.96	0.00
1.1.97	0.00
1.1.98	0.00
1.1.99	0.00
1.1.100	0.00

5	TGTGTAATCT	GGGTGTTAC	ACCTAGTTTC	AGACCTTCTC	CAGGCTCTTT	TCAAGGAGGC	CTATTCCTTT
	CAAAAGCAGT	TAAIGGAACT	GCTGGACATG	GTTTGCATGG	ACCCTTTAGT	AGATGACAAT	GATGATATTT
	TGAATATGGT	AATAGGTGAG	TGAAGAAAAC	TTTCTGCTTA	GTATATGGTG	ACTATAAAATC	ATGTATCAAT
	TAAAATTGTC	TCTAATGATT	CATGTTATTT	TCTTACTAAT	TATGCATTAA	AATTGATTTA	AATCTTACCA
	AATAAAATTTT	TAATCTTGAA	ATTTGGAATT	TGTAAAAATTT	ATTTTGGGTA	CCTTAACCTA	GATTTGCGTA
10	TTTAGTTACT	GTAATTTCTC	CACAATGATT	AACTTATATA	ACTTTATAAT	CTCTGAGGTT	GTCCATATTC
	AGAGACAATA	ACTTTCACAT	TTTTTTAAAC	ATAACTGATA	TTGAGATGCA	GTTTATATTT	CTCTCCAGAA
	TACATACATA	TACGTGCATA	TGTGTATGTA	AATATGTCTA	TTTCTCATATA	CATATTATAA	TGAAATAACT
	CATTTTACAT	GTGATGCACT	TTATACTAGT	TTATTTTTAT	TTTATTTTAT	TTTTTTGAGA	CAGAGTCTCA
	CTGTGTAGCC	CAGGCTGGAG	TGCAGTGGCA	CAATCTCGGC	TCACTGCAAC	CTCGCCTCCC	GGACTCAAGC
15	GATTCTCCTG	CCTCAGCCTC	ATGAGTAGCT	GGGATTATAG	GCGTCCGCCA	CCACACCTGG	CTAATTTTTG
	TATTTTTAGT	AGAGACAGGG	TTTCACCGTG	TTGCCAGGC	TGGTCTTGAA	CTCCTGACCT	CAGGTAATCC
	ACCTGCCTCA	GCCTCCAAA	GTGCTGGGAT	TACAGGCATG	AGCCACCGTG	CCCAGCCAAT	ACTAGTTTAT
	TTTTAAAGAA	TTGCTGGTCG	TAACACACTT	CATTGATTTT	ATCACTCATT	AATGGATTAT	GAACAAGAGT
	TTGAAAAACA	ATATAAAGGC	AAAGTTTGCA	TTCAAAACTT	TGGTATAAAG	AGAGTAAGTT	GGTTTTGTGC
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	TGATTCTGTG	AGTCIGCAGT	TTAGGGTGGG	ATGTCCTGAG	ACAACTTTCT	CTGATCCACC	TGGGGCACTA
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25	TGTCCCCCGG	GCCACAGCAG	GTCATAGCGT	TTAGCCCAGA	GTCATTGTAG	AAAAGTGTGG	ATTACAAAAG
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	GATATATAAT	TGAATTCTTC	CTTTTATAGT	TTTCTTCCCT	TAGCAAATTTG	TTTTGTCTAT	TTGGATTAGA
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40	AGGGTCACCA	GGGATAGTGC	CTGTAGCATT	CATCAGATTC	TTAGGGGTGA	GAGGAGATGT	GGTTGAGATG
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	CTTAAAATTA	TTTAAACATTC	TCTCTCATGC	TAGACCACAA	GTTTCATGCA	GGTAAGGCGG	AGATTGTGTC
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 20 AGGTGGACTG TATATTTCT TCAATCTTAA CTCCAAATTC TGATCAGCGA CGCCCTCTGC TGTACTAT
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 60 GCTGATTATA AGGTCAGTGT AGAATAAACT TTGTGCTTTT AAATTGTCAT AGCACTGTAT AGAGAGTTT
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	AGGATCACTT	GAACCCAGGA	GGTGGAGGTT	GAAGTAAGCC	GAGGTCATGC	CACTGCACCT	CAGCCTGGGC
	AACAGAGTGA	GACTCCATCT	CAAAAAAAAA	AAAAATGATC	AAAGAAAGGT	GAATTTTCAT	CTACCCTATT
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5	AAGTTTTATG	ATTTATTTAA	CTTGTGGAAC	AAAAATAAAC	CAGAAACCAC	CACCTCTCAC	GCCAAAGCTC
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10	TTGCCTAATT	TGTTTCCCT	TCTTACAATG	CATTCTGAGG	TAACTCATT	ATCAGTCCAA	AGGGCATGGG
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20	ATCCAGATGG	ATTAAAAAAT	GTACCAAGTC	CCTCCTACTA	GCTTGCCTCT	CTTCTGTTCT	GCTTGACTTC
	CTAGGATCTG	GAATCTGGTC	AGCAATCAGG	AATCCCTTCA	TCGTGACCCC	CGCATGGGCA	AAGGCTTCCC
	TGGAATCTCC	CACATGTGCT	GCTCCCTATA	AAAGGCAGGC	AGATGGGGCA	GAGGAGCAGA	GAGGCTGAGA
	CCAACCCAGA	AACACCAACC	TCTCACGCCA	AAGCTCACAC	CTTCAGCCTC	CAACATGAAG	GTCTCCGAG
	CATTCTGTG	GCTGTGCTC	ATAGCAGCTG	CCTTCAGCCC	CCAGGGGCTC	GCTGGGCCAG	GTAAGCCCC
25	CAACTCCTTA	CAGGAAAGGT	AAGGTAACCA	CCTCCAGGCT	ACTAGGTCAG	CAAGAATCTT	TACAGACTCA
	CTGCAAATTC	TCCAATTTGAA	AAATAGGGAA	ACAGGTTTTG	TGGGTGGACA	AGAAATGCCT	CAACCGTCAC
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40	TACAGTAATG	ATGAGTCCCT	AGTGACAGG	GGAGGATGCT	GAAGACACAG	GACAGCATCC	TCCAGACACA
	TAAGACTTCA	GAGCAGAGGG	ATTCTCCCTC	CACCTCTCGC	AATTCCTTGC	TTTCTCCTAA	CTTCTTTTAC
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	TAAAACTTAT	CCTCCATGAA	TATCAGTTAT	TTTTAAACTG	TAAAGCTTTG	TGCAGATTCT	TTACCCCTGT

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Health	0.70	0.46	0	1
Smoking	0.30	0.46	0	1
Drinking	0.20	0.40	0	1
Exercise	0.10	0.30	0	1
Stress	0.50	0.50	0	1
Sleep	0.60	0.49	0	1
Appetite	0.70	0.46	0	1
Mood	0.60	0.49	0	1
Energy	0.70	0.46	0	1
Concentration	0.60	0.49	0	1
Memory	0.70	0.46	0	1
Emotion	0.60	0.49	0	1
Behavior	0.70	0.46	0	1
Thought	0.60	0.49	0	1
Feeling	0.70	0.46	0	1
Perception	0.60	0.49	0	1
Attention	0.70	0.46	0	1
Intuition	0.60	0.49	0	1
Imagination	0.70	0.46	0	1
Reasoning	0.60	0.49	0	1
Logic	0.70	0.46	0	1
Analysis	0.60	0.49	0	1
Synthesis	0.70	0.46	0	1
Evaluation	0.60	0.49	0	1
Comparison	0.70	0.46	0	1
Classification	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.70	0.46	0	1
Decision Making	0.60	0.49	0	1
Communication	0.70	0.46	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.70	0.46	0	1
Leadership	0.60	0.49	0	1
Management	0.70	0.46	0	1
Coordination	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.70	0.46	0	1
Decision Making	0.60	0.49	0	1
Communication	0.70	0.46	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.70	0.46	0	1
Leadership	0.60	0.49	0	1
Management	0.70	0.46	0	1
Coordination	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.70	0.46	0	1
Decision Making	0.60	0.49	0	1
Communication	0.70	0.46	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.70	0.46	0	1
Leadership	0.60	0.49	0	1
Management	0.70	0.46	0	1
Coordination	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.70	0.46	0	1
Decision Making	0.60	0.49	0	1
Communication	0.70	0.46	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.70	0.46	0	1
Leadership	0.60	0.49	0	1
Management	0.70	0.46	0	1
Coordination	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.70	0.46	0	1
Decision Making	0.60	0.49	0	1
Communication	0.70	0.46	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.70	0.46	0	1
Leadership	0.60	0.49	0	1
Management	0.70	0.46	0	1
Coordination	0.60	0.49	0	1
Organization	0.70	0.46	0	1
Planning	0.60	0.49	0	1

[illegible]

5	TCATTTTGCT	GATAAGGACT	GATTCGTTTT	ACTGAGGGAC	GGCAGAACTA	GTTTCCTATG	AGGGCATGGG
	TGAATACAAC	TGAGGCTTCT	CATGGGAGGG	AATCTCTACT	ATCCAAAATT	ATTAGGAGAA	AATTGAAAAT
	TTCCAACCTCT	GTCTCTCTCT	TACCTCTGTG	TAAGGCCAAAT	ACCTTATCTT	TGTGGTGTIT	TTGTAACCTC
	TTCAAACTTT	CATTGATTGA	ATGCCTGTTC	TGGCAATACA	TTAGGTTGGG	CACATAAGGA	ATACCAACAT
	AAATAAAACA	TTCTAAAAGA	AGTTTACGAT	CTAATAAAGG	AGACAGGTAC	ATAGCAAAC	AATTCAAAGG
10	AGCTAGAAGA	TGGAGAAAAT	GCTGAATGTG	GACTAAGTCA	TTCAACAAAG	TTTTCAGGAA	GCACAAAAG
	GAGGGGCTCC	CCTCACAGAT	ATCTGGATTA	GAGGCTGGCT	GAGCTGATGG	TGGCTGGTGT	TCTCTGTTGC
	AGAAGTCAAG	ATGGCCAAAG	TTCCAGACAT	GTTTGAAGAC	CTGAAGAACT	GTTACAGGTA	AGGAATAAGA
	TTTATCTCTT	GTGAATTAAAT	GAGGGTTTCA	AGGCTCACCA	GAATCCAGCT	AGGCATAACA	GTGGCCAGCA
	TGGGGGCGAG	CCGGCAGAGG	TGTAGAGAT	GTGTACTAGT	CCTGAAGTCA	GAGCAGGTTC	AGAGAAGACC
15	CAGAAAAACT	AAGCATTACG	CATGTTAAAC	TGAGATTACA	TTGGCAGGGA	GACCGCCATT	TTAGAAAAAT
	TATTTTTGAG	GTCTGCTGAG	CCCTACATAT	ATATCAGCAT	CAACTTAGAC	ACAGCCTCTG	TTGAGATCAC
	ATGCCCTGAT	ATGAAGATGG	GTTTTACTGG	TCCATTCTCA	GGAAGAACTG	ATCTCATTCA	GGAACAGGAA
	ATGGCTCCAC	AGCAAGCTGG	GCATGTGAAC	TCACATATGC	AGGCAAACTC	CACTCAGATG	TAGAAGAAAG
	GTAATGAAC	ACAAAGATAA	AATTACGGAA	CATATTA AAC	TAACATGATG	TTTCCATTAT	CTGTAGTAAA
20	TACTAACACA	AACIAGGCTG	TCAAAATTTT	GCCTGGATAT	TTTACTAAGT	ATAAATTATG	AAATCTGTTT
	TAGTGAATAC	ATGAAAAGTAA	TGTGTAACAT	ATAATCTATT	TGGTTAA AAT	AAAAAGGAAG	TGCTTCAAAA
	CCTTTCTTTT	CTCTAAAGGA	GCTTAACATT	CTTCCCTGAA	CTTCAATTAA	AGCTCTTCAA	TTTGTTAGCC
	AAGTCCAATT	TTTACAGATA	AAGCACAGGT	AAAGCTCAAA	GCCTGTCTTG	ATGACTACTA	ATTCCAGATT
	AGTAAGATAT	GAATTACTCT	ACCTACTGAT	ATGTTAGAAA	GTCTTAAAT	TTCAAAGATG	ACAGTATTGG
25	CCATGTGTAT	GTGTGTGACC	CACAACATAT	ATGGTCAATTA	AAGTACATTG	GCCAGAGACC	ACATGAAATA
	ACAACAATTA	CATTCTCATC	ATCTTATTTT	GACAGTGA AA	ATGAAGAAGA	CAGTTCCTCC	ATTGATCATC
	TGTCTCTGAA	TCAGGTAAGC	AAATGACTGT	AATTCTCATG	GGACTGCTAT	TCTTACACAG	TGGTTTCTTC
	ATCCAAAGAG	AACAGCAATG	ACTTGAATCT	TAAATACTTT	TGTTTTACCC	TCACTAGAGA	TCCAGAGACC
	TGTCTTTCAT	TATAAGTGAG	ACCAGCTGCC	TCTCTAAACT	AATAGTTGAT	GTGCATTGGC	TTCTCCCAGA
30	ACAGAGCAGA	ACTATCCCAA	ATCCCTGAGA	ACTGGAGTCT	CCTGGGGCAG	GCTTCATCAG	GATGTTAGTT
	ATGCCATCCT	GAGAAAGCCC	CGCAGGCCGC	TTCAACAGGT	GTCTGTCTCC	TACCGTAGTG	TGTTGTGGTT
	GTCTTCTCTG	ACACAGCAT	CAGAGGTTAG	AGAAAGTCTC	CAAACATGAA	GCTGAGATAG	AGGAAGCAAG
	CCAGCTGAAA	GTGAAGAGTC	TACAGCCACT	CATCAATCTG	TGTTATTGTG	TTTGGAGACC	ACAAATAGAC
	ACTATAAGTA	CTGCCTAGTA	TGTCTTCAGT	ACTGGCTTTA	AAAGCTGTCC	CCAAAGGAGT	ATTTCTAAAA
35	TATTTTGAGC	ATTGTTAAGC	AGATTTTTAA	CCTCCTGAGA	GGGAACTAAT	TGGAAAGCTA	CCACTCACTA
	CAATCATTGT	TAACCTATTT	AGTTACAACA	TCTCATTTT	GAGCATGCAA	ATAAATGAAA	AAGTCTTCCT
	AAAAAAATCA	TCTTTTATC	CTGGAAGGAG	GAAGGAAGGT	GAGACAAAAG	GGAGAGAGGG	AGGGAAGCCT
	AATGAACATC	CAGTATCCTA	AGACCAGAAT	GGAGATCCTC	CTCACTACCT	CTGTTGAATA	CAGCACCTAC
	TGAAAGAACT	TTCAATCCCT	GACCATGAAC	AGCCTCTCAG	CTTCTGTTTT	CCTTCTCAC	AGAAATCCTT
40	CTATCATGTA	AGCTATGGCC	CACTCCATGA	AGGCTGCATG	GATCAATCTG	TGTCTCTGAG	TATCTCTGAA
	ACCTCTAAAA	CATC AAGCT	TACCTTCAAG	GAGAGCATGG	TGGTAGTAGC	AACCAACGGG	AAGGTTCTGA
	AGAAGAGACG	GTTTAGTTTA	AGCCAATCCA	TCACTGATGA	TGACCTGGAG	GCCATCGCCA	ATGACTCAGA
	GGAAGGTAAG	GGGCAAGCA	CAATAATATC	TTTCTTTTAC	AGTTTTAAGC	AAGTAGGGAC	AGTAGAATTT
	AGGGGAAAAAT	TAAACGTGGA	GTCAAGATAA	CAAGAAGACA	ACCAAGCATT	AGTCTGGTAA	CTATACAGAG
45	GAAAAATTAAT	TTTTATCCTT	CTCCAGGAGG	GAGAAATGAG	CAGTGGCCTG	AATCAGGAAT	ACTTGCTCAC
	AGCCATTATT	TCTTAGCCAT	ATTGTAAGG	TCGTGTGACT	TTTAGCCTTT	CAGGAGAAAAG	CAGTAATAAG
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	TTCAAGTTTCC	TCTACTGTAA	AATGGAGATA	ATCAGAATCC	CCCACTCATT	GGATTGTTGT	AAAGATTAAG
	AGTCTCAGGC	TTTACAGACT	GAGCTAGCTG	GGCCCTCCTG	ACTGTTATAA	AGATTAAATG	AGTCAACATC
50	CCCTA AACTTC	TGGA CTAGAA	TAATGCTGCG	TACAAAAGTAA	GCACCCAATA	AATGTTAGCT	ATTACTATCA
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	GCACAATCTC	GGCTCATGTC	AAGCTCTGCC	TCCTGGGTTT	ATGCCATTCT	CCTGCCTCAG	CCTCCCGAGT
	AAGCTGGGAA	TACAGGCACC	CGCCACTGTT	CCCGGCTAAT	TTTTTGTTAT	TTTAGTAGAG	ACGGAGTTTC
	ACCGTGGTCT	CCATCTCCTC	GTGATCCACC	CACCTTGGCC	TCCCAAAGTG	CCGGGATTAC	AGGCGTGAGC
55	CACCGCGCCC	GGCTATTAT	TATTATTATT	ACTACTACTA	CTACCTATAT	GAATACTACC	AGCAATACTA
	ATTTATTAAT	GACTTGATTA	TGTCTAAACC	TCACAAGAAT	CCTACCTTCT	CATTTTACAT	AAAAGGAAAC
	TAAGCTCATT	GAGATAGGTA	AAC TGCCCAA	TGGCATACAT	CTGTAAGTGG	GAGAGCCTCA	AATCTAATTC
	AGTTCTACCT	GAGTAAAAAA	ATCATGGTTT	CTCCTCCATC	CTTTTACTGT	ACAAGCCTCC	ACATGAATCA
	TAAACCCAAT	ATTCTGTGTT	TTAAGATAAT	ACCTAAGCAA	TAACGCATGT		

Table 1. (continued)	
1.0	0.00
2.0	0.00
3.0	0.00
4.0	0.00
5.0	0.00
6.0	0.00
7.0	0.00
8.0	0.00
9.0	0.00
10.0	0.00
11.0	0.00
12.0	0.00
13.0	0.00
14.0	0.00
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91.0	0.00
92.0	0.00
93.0	0.00
94.0	0.00
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96.0	0.00
97.0	0.00
98.0	0.00
99.0	0.00
100.0	0.00

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 5 ATCACCTTTT AGCTTCCTGA GCAATGTGAA ATACAACTTT ATGAGGATCA TCAAATACGA ATTCATCCTG
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 15 GGACATGTTT TAGTTTCAAC AGTATACATA TTTTCAAAGG TCCAGAGAGG CAATTTTGCA ATAAACAAGC
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 AAATATCTTT GTATATATTA TTGTTTTTTC TCCTATCTTG TAATTTCTTT GAGCACATCC CAAAGAGGAA
 20 TGCCTAGATC AATGCGCACA AATAATTTGA CAGCTCTTAT TAAACATTAT TCTGTAAGTA AAACTGAAC
 TACTTTTCAG TATCACTAGC AACATATGAG TGTATCAGCT TCCTAAACCC TCCTCATGTTA GGTCAATTATG
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 GCCCGAAGG ATTCATTCAA CGTAGAAAAT TCTAAGAACA TTAACCAAGT ATTTACCTGC CTAGTGAGTG
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 ACTGAGAGCC TTGTATTTT CAGGCATAGT GCCAACAGCA GTGTGGACAG TGGTGCATCA AAGCCTCTAG
 40 TCTCATAGAA CTTAGTCTTC TGGAGGATAT GGAAAACAGA CAACCCAAAC AACCAACAAA AGAGCAAGAT
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 45 CGGGTCGTGG TTGTGGGTTT TTGGGTAGGA CATTGAGAGG AGGGGGCGGG TCGTGGTTGT GGGTTTTTGG
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 55 GTGTGTGTGT ATGTGTGTGT GTGTGTTTAA CCTTCAATTG TTGACTTAAA TACTGAGATA AATGTCATCT
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 60 GCTTGCTGAA TGAAATAATG AATGAAGAGC CTATAGCATC ATGTTACAGC CATAGTCTTA AAGTGGTGTT
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	TTCTTCTGGG	AAAC1CACGG	CAC1AAGAAC	TAT1TTCACAT	CAG1T1GCCA	TCCAAC1T1G	TTAT1T1GCCA
	CAAAGCAAGA	CTACTGGGTG	TGCTTGGCAG	GGGGGCCACC	CTCTATCACT	GACT1T1CAGA	TACTGGAAAA
	CCAGGCGTAG	GTCTGGAGTC	TCACTTGTCT	CACTTGTGCA	GTG1T1GACAG	TTCATATGTA	CCATGTACAT
	GAAGAAGCTA	AATC1CTTAC	TG1TAGTCAT	TTGCTGAGCA	TG1ACTGAGC	CTTGTAATTC	TAAATGAATG
5	TTTACACTCT	TTGT1AGAGT	GGAA1CCAACA	CTAACATATA	ATG1T1GTTAT	TTAAAGAACA	CCCTATATTT
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10	TGGAGGGAAT	AAT1CCTAAG	CCTTCCTGCC	GCAACAGTTT	TTTATGCTAA	TCAGGGAGGT	CATTTTGGTA
	AAATACTTCT	CGAA1CCGAG	CCTCAAGATG	AAGGCAAAAGC	ACGAAATGTT	ATTTT1TAA1	TAT1ATTTA1
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15	GTAATCATAT	AATAAA1GTA	CATTAATTAC	CTTGAGCCAG	TAAT1TGGTCC	GATCTTTGAC	TCTTTTGCCA
	TTAAACTTAC	CTGG1CATTC	TTGTTTCATT	CAAT1TCCACC	TGCAATCAAG	TCCTACAAGC	TAAAATTAGA
	TGAACTCAAC	TTTGACAACC	ATGAGACCAC	TGTATCAAAA	ACTT1CTTTT	CTGGAATGTA	ATCAATGTTT
	CTTCTAGGTT	CTAA1AATTTG	TGATCAGACC	ATAATGTTAC	ATTATTATCA	ACAATAGTGA	TTGATAGAGT
	GTTATCAGTC	ATAACTAAAT	AAAGCTTGCA	ACAAAAT1TCT	CTGACACATA	GTTATTCATT	GCCTTAATCA
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	TATAAAATCA	AACC1AAGATT	TTATATTTT	T1TCTCTCTT	TGT1AGCTGC	CAG1TAGTCAT	AAATGGCATT
	AAGAATGATA	ATA1T1TCCG	GTTCACTTAA	AGCTCATATT	ACACATACAC	AAAA1CATGTG	TTCCCATCTT
	TATACAAACT	CACA1ATACA	GAGCTACATT	AAAAACA1CT	AATAGGCCAG	GCACGGTGGC	TCAGACCTGT
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	TGGCTTATTA	CAGT1T1GCAAT	GCCGATGACT	TGTTCTTTGA	AGCTGATGGC	CCTAAACAGA	TGAAGTGCTC
	CTTCCAGGAC	CTGGACCTCT	GCCCTTGGGA	TGGCGGCATC	CAGCTACGAA	TCTCCGACCA	CCACTACAGC
	AAGGGCTTCA	GGCAGG1CCGC	GTCAGTTGTT	GTGGCCATGG	ACAAGCTGAG	GAAAGTGTCT	GTTCCCTGCC
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	TCACAGCAAA	AAACCTTGGT	GATGTCTGGT	CCATATGAAC	TGAAAGCTCT	CCACCTCCAG	GGACAGGATA
	TGGAGACAACA	AGTGTGTGTT	TCCATGTCTC	TTGTACAAGG	AGAAGAAAGT	AATGACAAAA	TACCTGTGGC
	CTTGGGCTCT	AAGGAAAAAA	ATCTGTACCT	GTCTGCGTG	TTGAAAGATG	ATAAGCCCA	TCTACAGTGC
	GAGAGTGTAG	ATCC1AAAAA	TTACCCAAAG	AAGAAGATGG	AAAAGCGATT	TGTCTTCAAC	TGTACAGAAA
35	TCAATAACAA	GCTGGAATTT	GAGTCTGCCC	AGTTCCCCAA	CTGGTACATC	AGCACCTCTC	AAGCAGAAAA
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40	ATCCCCAGCC	CTTT1GTTGA	GCCAGGCCTC	TCTCACCTCT	CCTACTCACT	TAAAGCCCGC	CTGACAGAAA
	CCACGGCCAC	ATTT1GTTCT	AAGAAACCTT	CTGTCA1TTCG	CTCCACATT	CTGATGAGCA	ACCGCTTCCC
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45	AAATCAAGTC	CTTT1AATTAA	GACTGAAAAT	ATATAAGCTC	AGATTATTTA	AATGGGAATA	TTTATAAATG
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50	TAAAGATGGA	GTTCT1GTGTA	CTGACTCCTG	ATATCAAGAT	ACTGGGAGCC	AAAT1TAAAAA	TCAGAAGGCT
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	TTGCACAGAG	GCTCACTCCC	TTGGATAATG	CAGAGCGAG			

[illegible]



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	CGTATGTTCT	CTGCCCAGC	CAAGAAAGGT	CAATTTTCTC	CTCAGAGGCT	CCTGCAATTG	ACAGAGAGCT
	CCCGAGGCAG	AGAAACAGCAC	CCAAGGTAGA	GACCCACACC	CTCAATACAG	ACAGGGAGGG	CTATTGGCCC
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10	AAAAGTATGT	GCATGTATAA	ATCTGTGTGT	CTTCCACTTT	GTCCCACATA	TACTAAATTT	AAACATTCTT
	CTAACGTGGG	AAAATCCAGT	ATTTTAATGT	GGACATCAAC	TGCACAACGA	TGTGCAGGAA	AACAATGCAT
	ATTTGCATGG	TGATACATTT	GCAAAATGTG	TCATAGTTTG	CTACTCCTTG	CCCTTCCATG	AACCAGAGAA
	TTATCTCAGT	TTATTAGTCC	CCTCCCCTAA	GAAGCTTCCA	CCAATACTCT	TTTCCCCTTT	CCTTTAACTT
	GATTGTGAAA	TCACGTATTG	AACAGAGAAA	TTTCTCAGCC	TCCTACTTCT	GCTTTTGAAA	GCTATAAAAA
15	CAGCGAGGGA	GAAACTGGCA	GATACCAAAC	CTCTTCGAGG	CACAAGGCAC	AACAGGCTGC	TCTGGGATTG
	TCTTCAGCCA	ATCTTCATTG	CTCAAGTATG	ACTTTAATCT	TCCTTACAAC	TAGGTGTCTA	GGGAGTCTCT
	CTGTCTCTCT	GCCCTCTTGT	TGTATGCAT	ATTCTCTCTC	TCTCTCTCTT	TCTTTCTCTG	TCTCTCTCTT
	CCTTCTCTCT	TGCCFCTCT	CTCAGCTTTT	TGCAAAAATG	CCAGGTGTAA	TATAATGCTT	ATGACTCGGG
	AAATATTCTG	GGAAATGGATA	CTGCTTATCT	AACAGCTGAC	ACCCTAAAGG	TTAGTGTCAA	AGCCTCTGCT
20	CCAGCTCTCC	TAGCCAATAC	ATTGCTAGTT	GGGGTTTGGT	TTAGCAAATG	CTTTTCTCTA	GACCCAAAGG
	ACTTCTCTTT	CACAATTCA	TTCATTACT	CAGAGATCAT	TTCTTTGCAT	GACTGCCATG	CACTGGATGC
	TGAGAGAAAT	CACAATGAA	CGTAGCCGTC	ATGGGGAAGT	CACTCATTTT	CTCTTTTTTA	CACAGGTGTC
	TGAAGCAGCC	ATGC CAGAAG	TACCTGAGCT	CGCCAGTGAA	ATGATGGCTT	ATTACAGGTC	AGTGGAGAGC
	CTGAGACCAG	TAACATGAGC	AGGTCTCTCT	TTTCAAGAT	AGAGTGTAT	CTGTGCTTGG	AGACCAAGTT
25	TTTCCCCTAA	ATTGCTCTCT	TCAGTGGCAA	ACAGGGTGCC	AAGTAAATCT	GATTTAAAGA	CTACTTTCCC
	ATTACAAGTC	CCTCCAGCCT	TGGGACCTGG	AGGCTATCCA	GATGTGTTGT	TGCAAGGGCT	TCCTGCAGAG
	GCAAAATGGG	AGAAAGATT	CCAAGCCCAC	AATACAAGGA	ATCCCTTTGC	AAAGTGTGGC	TTGGAGGGAG
	AGGGAGAGCT	CAGATTTTAG	CTGACTCTGC	TGGGCTAGAG	GTTAGGCCTC	AAGATCCAAC	AGGGAGCACC
	AGGGTGCCCA	CCTCCAGGC	CTAGAATCTG	CCTTCTGGAC	TGTTCTGCGC	ATATCACTGT	GAAACTTGCC
30	AGGTGTTTCA	GGCAGCTTTG	AGAGGCAGGC	TGTTTGCACT	TTCTTATGAA	CAGTCAAGTC	TTGTACACAG
	GGAAGGAAAA	ATAACCTTGT	TTAGAAGACA	TAATTGAGAC	ATGTCCCTGT	TTTTATTACA	GTGGCAATGA
	GGATGACTTG	TTCTTTGAAG	CTGATGGCCC	TAAAGTAGAT	AAGGTAAGAC	TATGGGTTTA	ATGCCCAACC
	CAAGGAAGGG	CTCIAACACA	GGGAAAGCTC	AAAGAAGGGA	GTTCTGGGCC	ACTTTGATGC	CATGGTATTT
	TGTTTTAGAA	AGACTTTAAC	CTCTTCCAGT	GAGACACAGG	CTGCACCACT	TGCTGACCTG	GCCACTTGGT
35	CATCATATCA	CCACAGTCAC	TCACTAACGT	TGGTGGTGGT	GGCCACACTT	GGTGGTGACA	GGGGAGGAGT
	AGTGATAAGT	TTCCCATTTC	ATAGTAGGAA	GACAACCAAG	TCTTCAACAT	AAATTTGATT	ATCCTTTTAA
	GAGATGGATT	CAGCCTATGC	CAACTACTTG	AGTTAAACTC	TGAAACCAAG	AGATGATCTT	GAGAACTAAC
	ATATGTCTAC	CCCTTTTGAG	TAGAATAGTT	TTTTGTACC	TGGGGTGAAG	CTTATAACAA	CAAGACATAG
	ATGATATAAA	CAAAAGATG	AATTGAGACT	TGAAAGAAAA	CCATTCACTT	GCTGTTTGAC	CTTGACAAGT
40	CATTTTACCC	GCTTTGGACC	TCATCTGAAA	AATAAAGGGC	TGAGCTGGAT	GATCTCTGAG	ATTCCAGCAT
	CCTGCAACCT	CCAGTCTGTA	AATATTTTCA	GTTGTAGCTA	AGGGCATTTG	GGCAGCAAAT	GGTCATTTTT
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	CTTCTAGGTT	GCCCAGCCAT	CAGCCTAGCT	AGGTCAGTTG	TGCAGGTTGG	AGGCAGCCAC	TTTTCTCTGG
	CTTTATTTTA	TTCCAGTTTG	TGATAGCCTC	CCCTAGCCTC	ATAATCCAGT	CCTCAATCTT	GTTAAAAACA
45	TATTTCTTTA	GAAGFTTTAA	GACTGTCATA	ACTTCTTGGC	TGCAGCTGTG	GGAGGAGCCC	ATTGGCTTGT
	CTGCCTGGCC	TTTGCCCCC	ATTGCCTCTT	CCAGCAGCTT	GGCTCTGCTC	CAGGCAGGAA	ATTCTCTCCT
	GCTCAACTTT	CTTTTGTGCA	CTTACAGGTC	TCTTTAACTG	TCTTTCAAGC	CTTTGAACCA	TTATCAGCCT
	TAAGGCAACC	TCAGTGAAGC	CTTAATACGG	AGCTTCTCTG	AATAAGAGGA	AAGTGGTAAC	ATTTACAAAA
	AAGTACTCTC	ACAGTATTTG	CAGAAATGCT	ATGAGACAGT	GTTATGAAAA	AGGAAAAAAA	AGAACAGTGT
50	AGAAAAATG	AATACTTGCT	GAGTGAGCAT	AGGTGAATG	AAAATGTTAT	GGTCATCTGC	ATGAAAAAGC
	AAATCATATG	GTGACAGCAT	TAGGGATACA	AAAAGATATA	GAGAAGGTAT	ACATGTATGG	TGTAGGTGGG
	CAGTGTACAA	AAGATGACAA	AGTAGAATCG	GGATTTATTC	TAAAGAATAG	CCTGTAAAGT	GTCGAGAAGC
	CACATTCTAG	TCTTJAGTCT	GCCTCTACCT	GCTGTGTGCC	CTTGAGTACA	CCCTTAACCT	CCTTGAGCTT
	CAGAGAGGGA	TAACTCTTTT	ATTTTATTTT	ATTTTATTTT	GTTTTGTTTT	GTTTTGTTTT	GTTTTATGAG
55	ACAGAGTCTC	ACTCTGTTGC	CCAGGCTGGA	GTGCAGTGGT	ACAATCTTGG	CTTACTGCAT	CCTCCACCTC
	CTGAGTTCAA	GCGATTCTCT	TTCTCTAGTC	TCCTGAATAG	CTAGGATTAC	AGGTGCACCC	CACCACACCC
	AGCTAATTTT	TGTAFTTTTA	GTAGAGAAGG	GGTTTGCCTA	TGTTGGCCAG	GCTGGTTTTG	AAGTCTGTAC
	CTAAATGATT	CATCACTCTC	GGCTTCCCAA	AGTGCTGGGA	TTACAGGCAT	GAGGCCACCAC	GCTGTGCCCA
	GAGAGGGATG	ATCTTTAGAA	GCTCGGGATT				

The Study	
1. Study Design	Retrospective Cohort Study
2. Study Population	Adults aged 18-65 years
3. Study Period	January 1, 2010 - December 31, 2015
4. Study Location	General Hospital, New York City
5. Study Objectives	To determine the prevalence of hypertension and its associated risk factors.
6. Study Variables	<ul style="list-style-type: none"> Independent Variables: Age, Sex, Race, Education, Income, Physical Activity, Diet, Alcohol Consumption, Smoking Status. Dependent Variables: Hypertension (Yes/No), Blood Pressure (mmHg).
7. Study Methods	<ul style="list-style-type: none"> Data Collection: Medical Records Review, Patient Interviews. Data Analysis: Descriptive Statistics, Logistic Regression.
8. Study Results	<ul style="list-style-type: none"> Hypertension Prevalence: 25.3%. Associated Risk Factors: Age, Race, Physical Inactivity, High Sodium Diet.
9. Study Conclusions	Hypertension is a significant public health problem, and its prevention requires a multi-faceted approach targeting lifestyle factors.
10. Study Limitations	Retrospective design, potential for recall bias, limited data on certain variables.
11. Study Strengths	Large sample size, comprehensive data collection, use of standardized definitions.
12. Study Implications	Need for targeted interventions to reduce hypertension prevalence and associated morbidity.

CTCAGGGGCC TTTCAC TTAC ATTGTCACCA GAGGTTCGTA ACCTCCCTGT GGGCTAGTGT TATGACCATC
 ACCATTTTAC CTAAATAGCT CTGTTGCTCG GCCACAGTGA GCAGTAATAG ACCTGAAGCT GGAACCCATG
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 20 TGATTTCTGG CAGAAGTACA GCTTACCTC TTCTCTTCC TTCCACATTG ATCAAGTTGT TCCGCTCCTG
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 40 TTGAGTCTG CCCAGTCCC CAACTGGTAC ATCAGCACCT CTCAAGCAGA AAACATGCCC GTCTTCTGG
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 TGAGCCAGGC CTCTCTCACC TCTCCTACTC ACTTAAAGCC CGCCTGACAG AAACCACGGC CATATTTTGT
 45 TCTAAGAAAC CCTCTGTCAT TCGCTCCAC ATTCTGATGA GCAACCGCTT CCCTATTTAT TTATTTATTT
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 TAAGCTCGCC AGTGAAATGA TGGCTTATTA CAGTGGAAT GAGGATGACT TGTTCTTTGA AGCTGATGGC

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	CCTAAACAGA TCTCCGACCA GAAGATGCTG GAAGAAGAAC TGAACCTGCAC CCACCTCCAG AATGACAAAA ATAAGCCCAC TGTCTTCAAC AGCACCTCTC TCACCATGCA CCCTAGGGCT ACACCAATGC GCTCTCTCCT AAAGCCCGCC TTCTGATGAG ATTCAAAGGG ATTGGACTG TTAAATGGGA CTGGCAGGAG CATAGAGCAA CACTGCCAC GGCTGCGAT CTTCTAGAAG CAATACACAG ATGGAAGGAT ATGAAAAACC GCAGTACCTG GAAAAAAGA AGAAGAAGAT AAATGAAGAA GGCCCACTCC AGCTTACCTT TTTAAGCCAA CCTAGGTCAG TCATCCTGAA ACATAATCTG ACCGTGATTG TGAAGGAGAT TCACGGCAGT TGGGTGTGCT GGAGTCTCAC CTTTACTGTT AAGAGTGGAA CATTTTAATT TCTACCCATA CAAGAAGCCA GAACCTTTAA CCTAAGCCTT GCCGAGCCTC ATATATTTAA CCTCCACAAT CAAGTTGTGCT AATGTACATT GCATCTTGT ACAACCATAG AATTGTGATC TAAATAAAGC CAGAGAGGGA TTGAAGACCT TCAGAAATCC AGTATCTCTG	TGAAJTGCTC CCACACACAGC GTTCCTTGCC CTATCTTCTT GCTCCGGGAC GGACAGGATA TACCJGTGGC TCTACAGCTG AAGATAGAAA AAGCAGAAAA ATTTGTGTCT GGCAJAAAGG CCCACTGCCT TTCAGGGCCA TGACAGAAAC CAACCGCTTC GGCAAGAAGT GTGTJCTCTC ATATTTATAA TAGCAGCTGC CGGCGTCTCT ACTGJCGTTT TTTGACAATG ACAAAGTTAT CAGTCTTTTG GAGCATGCGA TCATJCAAGG CCTGTGCCA AAAAAGAAAA GGAAAAGCGA GACAGTTCCT ATGAAGGCTG CAAGJAGAGC TCCACTACTG CACCJTPTAG TGACJCCCTC GATGAAGCAG TAAGAACTCT GCCTGAGATA AAGACACTAT TGGCAGGGG TTGTCTCACT AGTCAATTTG CCAACACTAA ATTATCTCTC TTACAGATGG CAGACCTAGG TCAAATAGCA CCTGJCGCAA AAGATGAAGG GATAATTATA AGCAJGACAGT TTATCCCAAT AATTAACCTG TTCAJTTCAAT ACCACTGTTA AGACCATAAT TTGCAAGTGA GTCATTTTCAT GAACAACCTGT TTCTATCATG AAACCTCTAA AACACTCCAAG	CTTCCAGGAC AAGGGCTTCA CACAGACCTT CGACACATGG TCACAGCAAA TGGAGCAACA CTTGGGCTC GAGAGTGTAG TCAATAACAA CATGCCCTGC TCCTAAAGAG GAACAGAAAG GCCTTAGGCT ATCCCAGCCC CAGGCCACAT CCTATTTATT AGCAGTGTCT TTTAAATCAA ATGAGCAAA CCCTTGCGCG CGGAGCTGGG GCTGCCATCG TCAAGATTTA ATTACTTAAA TAACCATGCC CTCCTTTTCT GTTCTCTTAA TTGCCATTTT AGAAAAAGAA ATGGCCAAAG CCATTGATCA CATGGATCAA ATGGTGGTAG ATGATGACCT CTTCTGTAGC AATCAAAGTA TGAAATTTGA AAAAACTCAA CCCCAAACCA TCACATCAGT GCCACCTCT TGTGCAGTGT TGAGCATGTA CATATAATGT ATAACAATTT GCAAATTAAG ATTTATGAT TAAGTTTCTG CAGTTTTTTA CAAAGCACGA ATATACTATA GTTTCTGGG GCCAGGAAAC AGCCAGTAAT TCCACCTGCA TCAAACTTT GTTACATTAT TACAGTGAAG TAAGTATGG AACACTCAAG AACACTCCAAG	CTGGACCTCT GGCAGGCCGC CCAGGAGAAT GATAACGAGG AAAGCTTGGT AGTGGTGTTC AAGGAAAAAG ATCCCAAAAA GCTGGAATTT TTCCTGGGAG AGCTGTACCC GTTTTTGAGT AGTGTCTAAG TTTGTGTAG TTTGGTTCTA TATTTATTTG GTAAAAGAGC GTCCTTTAAT ATCATACTGT GACTGTGGA AGCCCGCAA CAGACCTGCT CCGTATATCC CAACCAAAGA CAATGTGATT GAGGATGATG GTTATAAGTC TAATGTGAAC AGCAAGTCAG TTCCAGACAT TCTGTCTCTG TCTGTGTCTC TAGCAACCAA GGAGGCCACT AATGTGAAAT TAATTCGAGC CATGGGTGCT TGTATGTGA TCACAGGTAG TGCCCATCCA ATCACTGACT TGACAGTTCA CTGAGCCTTG TGTTATTTAA TAGGAGGACC GCATAAGAAA TTCATTTCAA GGACCTCAGT TGCTAATCAG AATGTTATTT TTTATGGGAA ATAAGTAAGT TCTGCATTCT TGGTCCGATC ATCAAGTCTC CTTTTCTGGA TATCAACAAT TCATTGGCGT ATGAAGAAGA GAGTTCCTCC GAAGGCTGCA ACAGCTCTT ATGTAATCAA AGTGATTGAT TTGAGTCAGC AAGTCAAGAT CGATTCTCC GAAGGCTGCA AGGAGAGCAT GGTGGTAGTA GCAACCAAC	GCCCTCTGGA GTGGCCATGG CCTTCTTTCC CGATGCACCT CCATATGAAC TTGTACAAGG GCTCTGCGTG AAGAAGATGG AGTTCCCCAA CGGCCAGGAT GTGCTGAATG CCTGGACTTT TCCACTAGCC CTCACCTCTC CTCTGTCATT TTGATTCAAT ATAGCTATGG AATATATAAG TCAAATAAAC TCAAAACACT AGAGAACACT AGCTTTCGCT ATCCCTCTGG GGATACACCA TCCATGAAGA TTGAAAAAGG TACATCTGAA GGAGGACCAT ATAAGACCA CGAAAAATAA CTGAAGAACT CCTTCTATCA TGAAACCTCT CTGAAGAAGA GAGGAAAGA TACCTCACGG CAAAGGATGA TGAAGACCAA CTCCTCTTCT TTGCCACAA GGAAAAACCAG GTACATGAAG TGAATGTTTA ATATTTTGCA ATGCACAATA TCTGCTTTTA TCAAAATGGA TTGGTAAAAAT ATTTATATAT CTCTGAGTGT TAATACAGGG AGACCTGTAA TTGCCATTAA ATTAGATGAA TGTTTCTTCT AGAGTGTTAT AAAGAAGTCA AG	CAGCTACGAA ACAAGCTGAG CTTCATCTTT GTACGATCAC TGAAAAGCTCT AGAAAAGTGT TTGAAAAGATG AAAAGCGATT CTGGTACATC ATAACTGACT TGGACTCAAT CCTGTTGTCT AGGACAGTCA CTACTCACTT CGCTCCCA GGTCTAATTT AATCAATTCA CTCAGATTAT TTCACT AGACAGCCT TGCCGTCCAC ATCCGGCAAG GTGACGTCCA ACAATATTAT AATACGAAGG GAATCAGAGA CACAGAGGGA GGAACCAGAA AACGACCCAA GTTACAGTGA TGTAAGCTAT AAAACATCCA GACGGTTGAG AATCATCAAG AAATACGAAT CTGCTGCATT TGCTAAAATT CCAGTGCTGC TCTGGGAAAC GCAAGACTAC GCGTAGGTCT AAGCTAAATC CACTCTTTGT TAGTACCAAT CCAAAAAGAC GCAGTTGAA AGTTGTGAT GGGAATAATA ACTTCTCGAA GTATTTATAA GACCAGGCAT CATTTTGGTC TCATATAATA ACTTACCTGG CTCAACTTTG AGGTTCTAAA CAGTCATAAC AGCTGCCAGC CCAGACATGT TGTCTCTG
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Parameter	Value	Unit
Initial temperature	298.15	K
Final temperature	300.15	K
Pressure	1.01325	bar
Volume	0.001	m ³
Mass	0.001	kg
Heat capacity	1.0	J/(kg·K)
Thermal conductivity	0.025	W/(m·K)
Dynamic viscosity	0.001	Pa·s
Electrical conductivity	0.001	S/m
Permittivity	1.0	F/m
Penetration depth	0.001	m
Surface resistance	0.001	Ω
Loss tangent	0.001	
Refractive index	1.0	
Dispersion coefficient	0.001	
Nonlinear coefficient	0.001	
Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.001	
Scattering matrix	0.001	
Loss tangent	0.001	
Refractive index	1.0	
Dispersion coefficient	0.001	
Nonlinear coefficient	0.001	
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Absorption coefficient	0.001	
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Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.001	
Scattering matrix	0.001	
Loss tangent	0.001	
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Nonlinear coefficient	0.001	
Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.001	
Scattering matrix	0.001	
Loss tangent	0.001	
Refractive index	1.0	
Dispersion coefficient	0.001	
Nonlinear coefficient	0.001	
Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.001	
Scattering matrix	0.001	
Loss tangent	0.001	
Refractive index	1.0	
Dispersion coefficient	0.001	
Nonlinear coefficient	0.001	
Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.001	
Scattering matrix	0.001	
Loss tangent	0.001	
Refractive index	1.0	
Dispersion coefficient	0.001	
Nonlinear coefficient	0.001	
Scattering coefficient	0.001	
Absorption coefficient	0.001	
Reflection coefficient	0.001	
Transmission coefficient	0.	



Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Sleep quality	0.6	0.4	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.7	0.3	0	1
Depression score	0.4	0.5	0	1
Anxiety score	0.3	0.4	0	1
Resilience score	0.6	0.4	0	1
Optimism score	0.5	0.5	0	1
Gratitude score	0.6	0.4	0	1
Forgiveness score	0.5	0.5	0	1
Empathy score	0.6	0.4	0	1
Compassion score	0.5	0.5	0	1
Kindness score	0.6	0.4	0	1
Generosity score	0.5	0.5	0	1
Patience score	0.6	0.4	0	1
Self-control score	0.5	0.5	0	1
Emotional stability score	0.6	0.4	0	1
Psychological well-being score	0.7	0.3	0	1
Overall life satisfaction score	0.7	0.3	0	1

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 (SEQ. ID NO:3004)

Human Adenosine A₁ Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ATGCCGCCCT CCA1CTCAGC TTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
 20 TGCCCGGGAA CGTCTGGTGG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT
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1. 1990-1991 2. 1991-1992 3. 1992-1993 4. 1993-1994 5. 1994-1995 6. 1995-1996 7. 1996-1997 8. 1997-1998 9. 1998-1999 10. 1999-2000 11. 2000-2001 12. 2001-2002 13. 2002-2003 14. 2003-2004 15. 2004-2005 16. 2005-2006 17. 2006-2007 18. 2007-2008 19. 2008-2009 20. 2009-2010 21. 2010-2011 22. 2011-2012 23. 2012-2013 24. 2013-2014 25. 2014-2015 26. 2015-2016 27. 2016-2017 28. 2017-2018 29. 2018-2019 30. 2019-2020 31. 2020-2021 32. 2021-2022 33. 2022-2023 34. 2023-2024 35. 2024-2025 36. 2025-2026 37. 2026-2027 38. 2027-2028 39. 2028-2029 40. 2029-2030 41. 2030-2031 42. 2031-2032 43. 2032-2033 44. 2033-2034 45. 2034-2035 46. 2035-2036 47. 2036-2037 48. 2037-2038 49. 2038-2039 50. 2039-2040 51. 2040-2041 52. 2041-2042 53. 2042-2043 54. 2043-2044 55. 2044-2045 56. 2045-2046 57. 2046-2047 58. 2047-2048 59. 2048-2049 60. 2049-2050 61. 2050-2051 62. 2051-2052 63. 2052-2053 64. 2053-2054 65. 2054-2055 66. 2055-2056 67. 2056-2057 68. 2057-2058 69. 2058-2059 70. 2059-2060 71. 2060-2061 72. 2061-2062 73. 2062-2063 74. 2063-2064 75. 2064-2065 76. 2065-2066 77. 2066-2067 78. 2067-2068 79. 2068-2069 80. 2069-2070 81. 2070-2071 82. 2071-2072 83. 2072-2073 84. 2073-2074 85. 2074-2075 86. 2075-2076 87. 2076-2077 88. 2077-2078 89. 2078-2079 90. 2079-2080 91. 2080-2081 92. 2081-2082 93. 2082-2083 94. 2083-2084 95. 2084-2085 96. 2085-2086 97. 2086-2087 98. 2087-2088 99. 2088-2089 100. 2089-2090 101. 2090-2091 102. 2091-2092 103. 2092-2093 104. 2093-2094 105. 2094-2095 106. 2095-2096 107. 2096-2097 108. 2097-2098 109. 2098-2099 110. 2099-2100 111. 2100-2101 112. 2101-2102 113. 2102-2103 114. 2103-2104 115. 2104-2105 116. 2105-2106 117. 2106-2107 118. 2107-2108 119. 2108-2109 120. 2109-2110 121. 2110-2111 122. 2111-2112 123. 2112-2113 124. 2113-2114 125. 2114-2115 126. 2115-2116 127. 2116-2117 128. 2117-2118 129. 2118-2119 130. 2119-2120 131. 2120-2121 132. 2121-2122 133. 2122-2123 134. 2123-2124 135. 2124-2125 136. 2125-2126 137. 2126-2127 138. 2127-2128 139. 2128-2129 140. 2129-2130 141. 2130-2131 142. 2131-2132 143. 2132-2133 144. 2133-2134 145. 2134-2135 146. 2135-2136 147. 2136-2137 148. 2137-2138 149. 2138-2139 150. 2139-2140 151. 2140-2141 152. 2141-2142 153. 2142-2143 154. 2143-2144 155. 2144-2145 156. 2145-2146 157. 2146-2147 158. 2147-2148 159. 2148-2149 160. 2149-2150 161. 2150-2151 162. 2151-2152 163. 2152-2153 164. 2153-2154 165. 2154-2155 166. 2155-2156 167. 2156-2157 168. 2157-2158 169. 2158-2159 170. 2159-2160 171. 2160-2161 172. 2161-2162 173. 2162-2163 174. 2163-2164 175. 2164-2165 176. 2165-2166 177. 2166-2167 178. 2167-2168 179. 2168-2169 180. 2169-2170 181. 2170-2171 182. 2171-2172 183. 2172-2173 184. 2173-2174 185. 2174-2175 186. 2175-2176 187. 2176-2177 188. 2177-2178 189. 2178-2179 190. 2179-2180 191. 2180-2181 192. 2181-2182 193. 2182-2183 194. 2183-2184 195. 2184-2185 196. 2185-2186 197. 2186-2187 198. 2187-2188 199. 2188-2189 200. 2189-2190 201. 2190-2191 202. 2191-2192 203. 2192-2193 204. 2193-2194 205. 2194-2195 206. 2195-2196 207. 2196-2197 208. 2197-2198 209. 2198-2199 210. 2199-2200 211. 2200-2201 212. 2201-2202 213. 2202-2203 214. 2203-2204 215. 2204-2205 216. 2205-2206 217. 2206-2207 218. 2207-2208 219. 2208-2209 220. 2209-2210 221.	
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 CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTGC
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 5 CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
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 10 AGGTGTGGC CTCTTCCGGC GACCCGCGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC
 CCTCATCCTT TTCTCTTTG CCTCAGCTG GCTGCCCTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC
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 20 AAGGTGCTTG GGCCTCTGCG GTGAGGCGAG GGAGTCTGCT TGTCTTAGAT GTTGGTGGT GAGCCCCAGG
 ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAAGGAGA GAGGTGAGG ATGACCTGGC
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 25 ACGCCTGGG GAGTGAAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC
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 30 AGTACCCCC TGACAGCATG TGGGGGAAGG CCTGTCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG
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 TGGAGCCCC GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA GGCGGGGAT
 CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC
 35 AACTCCAGGA CTTCCTTCCA AGCCCTTCCC TCTGTTGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
 CCATGTGACT AATAAAAAAC TGTGAACCT -3' (FRAG. NO:) (SEQ. ID NO: 2421)
 5'-ATGCCGCCCT CAATCTCAGC TTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
 TGCCCGGGAA CGTCCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT
 40 CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCAATC CCCTCGCCAT CCTCATCAAC
 ATTTGGGCCAC AGACTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT
 CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT
 GGTGGTGACC CCCCAGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
 CCCCTATGT TTGGCIGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG
 AGCCCGTAGT CAATGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT
 45 GTGGGTGCTG CCCCCTCTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG
 CTCAACAAGA AGGTGTCGGC CTCTCCGGC GACCCGCGA AGTACTATGG GAAGGAGCTG AAGATCGCCA
 AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCCTTG CACATCCTCA ACTGCATCAC
 CCTCTCTGC CCGTCTGCC ACAAGCCAG CATCCTTACC TACATTGCA TCTTCTCAC GCACGGCAAC
 TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTGGA
 50 ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G
 (FRAG NO:) (SEQ. ID NO: 2420)
 5'-GAT GGA GGG CGG CAT GGC GGG-3' (FRAG. NO: 1657) (SEQ ID NO:2412)
 5'-G CGG GTC GCC GC-3' (FRAG. NO: 1658) (SEQ ID NO:2413)
 5'-GGC GGG CBC BGG C-3' (FRAG. NO: 1659) (SEQ ID NO:2414)
 55 5'-GGC GGG CBC-3' (FRAG. NO: 1660) (SEQ ID NO:2415)
 5'-GC GGC CTG G-3' (FRAG. NO: 1661) (SEQ ID NO:2416)
 5'-GGB GGG CGG C-3' (FRAG. NO: 1662) (SEQ ID NO:2417)
 5'-GBT GGB GGG-3' (FRAG. NO: 1663) (SEQ ID NO:2418)
 5'-GG CTG GGC-3' (FRAG. NO: 1664) (SEQ ID NO:2419)
 60 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG.1) (SEQ. ID NO: 11)
 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 2) (SEQ. ID NO:12)

- 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 3) (SEQ. ID NO: 13)
 5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 4) (SEQ. ID NO: 14)
 5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 5) (SEQ. ID NO: 15)
 5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 6) (SEQ. ID NO: 16)
 5 5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 7) (SEQ. ID NO: 17)
 5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 8) (SEQ. ID NO: 18)
 5'-GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 9) (SEQ. ID NO: 19)
 5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 10) (SEQ. ID NO: 20)
 5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 11) (SEQ. ID NO: 21)
 10 5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 12) (SEQ. ID NO: 22)
 5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 13) (SEQ. ID NO: 23)
 5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 14) (SEQ. ID NO: 24)
 5'-TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 15) (SEQ. ID NO: 25)
 5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 16) (SEQ. ID NO: 26)
 15 5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 17) (SEQ. ID NO: 27)
 5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 18) (SEQ. ID NO: 28)
 5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 19) (SEQ. ID NO: 29)
 5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 20) (SEQ. ID NO: 30)
 5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 21) (SEQ. ID NO: 31)
 20 5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 22) (SEQ. ID NO: 32)
 5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 23) (SEQ. ID NO: 33)
 5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 24) (SEQ. ID NO: 34)
 5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 25) (SEQ. ID NO: 35)
 5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 26) (SEQ. ID NO: 36)
 25 5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 27) (SEQ. ID NO: 37)
 5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 28) (SEQ. ID NO: 38)
 5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 29) (SEQ. ID NO: 39)
 5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 30) (SEQ. ID NO: 40)
 5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG 31) (SEQ. ID NO: 41)
 30 5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG 32) (SEQ. ID NO: 42)
 5'-GGC GGG CAC AGG CTG GGC-3' (FRAG 33) (SEQ. ID NO: 43)
 5'-GC GGG CAC AGG CTG GGC-3' (FRAG 34) (SEQ. ID NO: 44)
 5'-C GGG CAC AGG CTG GGC-3' (FRAG 35) (SEQ. ID NO: 45)
 5'-GGG CAC AGG CTG GGC-3' (FRAG 36) (SEQ. ID NO: 46)
 35 5'-GG CAC AGG CTG GGC-3' (FRAG 37) (SEQ. ID NO: 47)
 5'-G CAC AGG CTG GGC-3' (FRAG 38) (SEQ. ID NO: 48)
 5'-CAC AGG CTG GGC-3' (FRAG 39) (SEQ. ID NO: 49)
 5'-AC AGG CTG GGC-3' (FRAG 40) (SEQ. ID NO: 50)
 5'-C AGG CTG GGC-3' (FRAG 41) (SEQ. ID NO: 51)
 40 5'-AGG CTG GGC-3' (FRAG 42) (SEQ. ID NO: 52)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 43) (SEQ. ID NO: 53)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 44) (SEQ. ID NO: 54)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 45) (SEQ. ID NO: 55)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 46) (SEQ. ID NO: 56)
 45 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 47) (SEQ. ID NO: 57)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 48) (SEQ. ID NO: 58)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 49) (SEQ. ID NO: 59)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 50) (SEQ. ID NO: 60)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 51) (SEQ. ID NO: 61)
 50 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 52) (SEQ. ID NO: 62)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 53) (SEQ. ID NO: 63)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 54) (SEQ. ID NO: 64)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 55) (SEQ. ID NO: 65)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 56) (SEQ. ID NO: 66)
 55 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 57) (SEQ. ID NO: 67)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 58) (SEQ. ID NO: 68)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 59) (SEQ. ID NO: 69)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 60) (SEQ. ID NO: 70)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CTG GGC-3' (FRAG 61) (SEQ. ID NO: 71)
 60 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 62) (SEQ. ID NO: 72)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 63) (SEQ. ID NO: 73)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 64) (SEQ. ID NO: 74)

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- 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 65) (SEQ. ID NO: 75)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 66) (SEQ. ID NO: 76)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 67) (SEQ. ID NO: 77)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) (SEQ. ID NO: 78)
 5 5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) (SEQ. ID NO: 79)
 5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) (SEQ. ID NO: 80)
 5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) (SEQ. ID NO: 81)
 5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) (SEQ. ID NO: 82)
 5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) (SEQ. ID NO: 83)
 10 5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) (SEQ. ID NO: 84)
 5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) (SEQ. ID NO: 85)
 5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) (SEQ. ID NO: 86)
 5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) (SEQ. ID NO: 87)
 5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) (SEQ. ID NO: 88)
 15 5'-GGC GGC CTG GAA AGC-3' (FRAG 79) (SEQ. ID NO: 89)
 5'-GGC GGC CTG GAA AG-3' (FRAG 80) (SEQ. ID NO: 90)
 5'-GGC GGC CTG GAA A-3' (FRAG 81) (SEQ. ID NO: 91)
 5'-GGC GGC CTG GAA-3' (FRAG 82) (SEQ. ID NO: 92)
 5'-GGC GGC CTG GA-3' (FRAG 83) (SEQ. ID NO: 93)
 20 5'-GGC GGC CTG G-3' (FRAG 84) (SEQ. ID NO: 94)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 85) (SEQ. ID NO: 95)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 86) (SEQ. ID NO: 96)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 87) (SEQ. ID NO: 97)
 25 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 88) (SEQ. ID NO: 98)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 89) (SEQ. ID NO: 99)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 90) (SEQ. ID NO: 100)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 91) (SEQ. ID NO: 101)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 92) (SEQ. ID NO: 102)
 30 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 93) (SEQ. ID NO: 103)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 94) (SEQ. ID NO: 104)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 95) (SEQ. ID NO: 105)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 96) (SEQ. ID NO: 106)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 97) (SEQ. ID NO: 107)
 35 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 98) (SEQ. ID NO: 108)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 99) (SEQ. ID NO: 109)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 100) (SEQ. ID NO: 110)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) (SEQ. ID NO: 111)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) (SEQ. ID NO: 112)
 40 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) (SEQ. ID NO: 113)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) (SEQ. ID NO: 114)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) (SEQ. ID NO: 115)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) (SEQ. ID NO: 116)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) (SEQ. ID NO: 117)
 45 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) (SEQ. ID NO: 118)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) (SEQ. ID NO: 119)
 5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) (SEQ. ID NO: 120)
 5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) (SEQ. ID NO: 121)
 5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) (SEQ. ID NO: 122)
 50 5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) (SEQ. ID NO: 123)
 5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) (SEQ. ID NO: 124)
 5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) (SEQ. ID NO: 125)
 5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) (SEQ. ID NO: 126)
 5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) (SEQ. ID NO: 127)
 55 5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) (SEQ. ID NO: 128)
 5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) (SEQ. ID NO: 129)
 5'-GC GGC CTG GAA AGC T-3' (FRAG 120) (SEQ. ID NO: 130)
 5'-GC GGC CTG GAA AGC-3' (FRAG 121) (SEQ. ID NO: 131)
 5'-GC GGC CTG GAA AG-3' (FRAG 122) (SEQ. ID NO: 132)
 60 5'-GC GGC CTG GAA A-3' (FRAG 123) (SEQ. ID NO: 133)
 5'-GC GGC CTG GAA-3' (FRAG 124) (SEQ. ID NO: 134)
 5'-GC GGC CTG GA-3' (FRAG 125) (SEQ. ID NO: 135)



- 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 126) (SEQ. ID NO: 136)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 127) (SEQ. ID NO: 137)
5 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 128) (SEQ. ID NO: 138)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 129) (SEQ. ID NO: 139)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 130) (SEQ. ID NO: 140)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 131) (SEQ. ID NO: 141)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 132) (SEQ. ID NO: 142)
10 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 133) (SEQ. ID NO: 143)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 134) (SEQ. ID NO: 144)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 135) (SEQ. ID NO: 145)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 136) (SEQ. ID NO: 146)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) (SEQ. ID NO: 147)
15 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) (SEQ. ID NO: 148)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) (SEQ. ID NO: 149)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) (SEQ. ID NO: 150)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) (SEQ. ID NO: 151)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) (SEQ. ID NO: 152)
20 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 143) (SEQ. ID NO: 153)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) (SEQ. ID NO: 154)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) (SEQ. ID NO: 155)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) (SEQ. ID NO: 156)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) (SEQ. ID NO: 157)
25 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) (SEQ. ID NO: 158)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 148) (SEQ. ID NO: 159)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) (SEQ. ID NO: 160)
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) (SEQ. ID NO: 161)
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) (SEQ. ID NO: 162)
30 5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) (SEQ. ID NO: 163)
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) (SEQ. ID NO: 164)
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) (SEQ. ID NO: 165)
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) (SEQ. ID NO: 166)
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) (SEQ. ID NO: 167)
35 5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) (SEQ. ID NO: 168)
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) (SEQ. ID NO: 169)
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) (SEQ. ID NO: 170)
5'-C GGC CTG GAA AGC T-3' (FRAG 161) (SEQ. ID NO: 171)
5'-C GGC CTG GAA AGC-3' (FRAG 162) (SEQ. ID NO: 172)
40 5'-C GGC CTG GAA AG-3' (FRAG 163) (SEQ. ID NO: 173)
5'-C GGC CTG GAA A-3' (FRAG 164) (SEQ. ID NO: 174)
5'-C GGC CTG GAA-3' (FRAG 165) (SEQ. ID NO: 175)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) (SEQ. ID NO: 176)
45 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) (SEQ. ID NO: 177)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) (SEQ. ID NO: 178)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 169) (SEQ. ID NO: 179)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) (SEQ. ID NO: 180)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) (SEQ. ID NO: 181)
50 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 172) (SEQ. ID NO: 182)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 173) (SEQ. ID NO: 183)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 174) (SEQ. ID NO: 184)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 175) (SEQ. ID NO: 185)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 176) (SEQ. ID NO: 186)
55 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 177) (SEQ. ID NO: 187)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 178) (SEQ. ID NO: 188)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 179) (SEQ. ID NO: 189)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 180) (SEQ. ID NO: 190)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 181) (SEQ. ID NO: 191)
60 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 182) (SEQ. ID NO: 192)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 183) (SEQ. ID NO: 193)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) (SEQ. ID NO: 194)



- 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) (SEQ. ID NO: 195)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) (SEQ. ID NO: 196)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) (SEQ. ID NO: 197)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) (SEQ. ID NO: 198)
5'-GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) (SEQ. ID NO: 199)
5'-GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) (SEQ. ID NO: 200)
5'-GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) (SEQ. ID NO: 201)
5'-GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) (SEQ. ID NO: 202)
5'-GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) (SEQ. ID NO: 203)
5'-GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) (SEQ. ID NO: 204)
5'-GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) (SEQ. ID NO: 205)
5'-GGC CTG GAA AGC TGA GAT -3' (FRAG 196) (SEQ. ID NO: 206)
5'-GGC CTG GAA AGC TGA GA-3' (FRAG 197) (SEQ. ID NO: 207)
5'-GGC CTG GAA AGC TGA G-3' (FRAG 198) (SEQ. ID NO: 208)
5'-GGC CTG GAA AGC TGA-3' (FRAG 199) (SEQ. ID NO: 209)
5'-GGC CTG GAA AGC TG-3' (FRAG 200) (SEQ. ID NO: 210)
5'-GGC CTG GAA AGC T-3' (FRAG 201) (SEQ. ID NO: 211)
5'-GGC CTG GAA AGC-3' (FRAG 202) (SEQ. ID NO: 212)
5'-GGC CTG GAA AG-3' (FRAG 203) (SEQ. ID NO: 213)
5'-GGC CTG GAA A-3' (FRAG 204) (SEQ. ID NO: 214)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 205) (SEQ. ID NO: 215)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) (SEQ. ID NO: 216)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) (SEQ. ID NO: 217)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) (SEQ. ID NO: 218)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) (SEQ. ID NO: 219)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) (SEQ. ID NO: 220)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) (SEQ. ID NO: 221)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) (SEQ. ID NO: 222)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) (SEQ. ID NO: 223)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) (SEQ. ID NO: 224)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) (SEQ. ID NO: 225)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) (SEQ. ID NO: 226)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) (SEQ. ID NO: 227)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) (SEQ. ID NO: 228)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) (SEQ. ID NO: 229)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) (SEQ. ID NO: 230)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) (SEQ. ID NO: 231)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) (SEQ. ID NO: 232)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) (SEQ. ID NO: 233)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) (SEQ. ID NO: 234)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) (SEQ. ID NO: 235)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) (SEQ. ID NO: 236)
5'-GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) (SEQ. ID NO: 237)
5'-GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) (SEQ. ID NO: 238)
5'-GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) (SEQ. ID NO: 239)
5'-GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) (SEQ. ID NO: 240)
5'-GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) (SEQ. ID NO: 241)
5'-GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) (SEQ. ID NO: 242)
5'-GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) (SEQ. ID NO: 243)
5'-GC CTG GAA AGC TGA GAT G -3' (FRAG 234) (SEQ. ID NO: 244)
5'-GC CTG GAA AGC TGA GAT -3' (FRAG 235) (SEQ. ID NO: 245)
5'-GC CTG GAA AGC TGA GA-3' (FRAG 236) (SEQ. ID NO: 246)
5'-GC CTG GAA AGC TGA G-3' (FRAG 237) (SEQ. ID NO: 247)
5'-GC CTG GAA AGC TGA-3' (FRAG 238) (SEQ. ID NO: 248)
5'-GC CTG GAA AGC TG-3' (FRAG 239) (SEQ. ID NO: 249)
5'-GC CTG GAA AGC T-3' (FRAG 240) (SEQ. ID NO: 250)
5'-GC CTG GAA AGC-3' (FRAG 241) (SEQ. ID NO: 251)
5'-GC CTG GAA AG-3' (FRAG 242) (SEQ. ID NO: 252)
5'-C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) (SEQ. ID NO: 253)
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) (SEQ. ID NO: 254)
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) (SEQ. ID NO: 255)

- 5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) (SEQ. ID NO: 256)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) (SEQ. ID NO: 257)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) (SEQ. ID NO: 258)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) (SEQ. ID NO: 259)
5 5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) (SEQ. ID NO: 260)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) (SEQ. ID NO: 261)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 252) (SEQ. ID NO: 262)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) (SEQ. ID NO: 263)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) (SEQ. ID NO: 264)
10 5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) (SEQ. ID NO: 265)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) (SEQ. ID NO: 266)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) (SEQ. ID NO: 267)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GGC -3' (FRAG 258) (SEQ. ID NO: 268)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT GG -3' (FRAG 259) (SEQ. ID NO: 269)
15 5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT G -3' (FRAG 260) (SEQ. ID NO: 270)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CAT -3' (FRAG 261) (SEQ. ID NO: 271)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG CA-3' (FRAG 262) (SEQ. ID NO: 272)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG C-3' (FRAG 263) (SEQ. ID NO: 273)
5'- C CTG GAA AGC T3A GAT GGA GGG CGG -3' (FRAG 264) (SEQ. ID NO: 274)
20 5'- C CTG GAA AGC T3A GAT GGA GGG CG -3' (FRAG 265) (SEQ. ID NO: 275)
5'- C CTG GAA AGC T3A GAT GGA GGG C -3' (FRAG 266) (SEQ. ID NO: 276)
5'- C CTG GAA AGC T3A GAT GGA GGG -3' (FRAG 267) (SEQ. ID NO: 277)
5'- C CTG GAA AGC T3A GAT GGA GG -3' (FRAG 268) (SEQ. ID NO: 278)
5'- C CTG GAA AGC T3A GAT GGA G -3' (FRAG 269) (SEQ. ID NO: 279)
25 5'- C CTG GAA AGC T3A GAT GGA -3' (FRAG 270) (SEQ. ID NO: 280)
5'- C CTG GAA AGC T3A GAT GG -3' (FRAG 271) (SEQ. ID NO: 281)
5'- C CTG GAA AGC T3A GAT G -3' (FRAG 272) (SEQ. ID NO: 282)
5'- C CTG GAA AGC T3A GAT -3' (FRAG 273) (SEQ. ID NO: 283)
5'- C CTG GAA AGC T3A GA-3' (FRAG 274) (SEQ. ID NO: 284)
30 5'- C CTG GAA AGC T3A G-3' (FRAG 275) (SEQ. ID NO: 285)
5'- C CTG GAA AGC T3A-3' (FRAG 276) (SEQ. ID NO: 286)
5'- C CTG GAA AGC T3-3' (FRAG 277) (SEQ. ID NO: 287)
5'- C CTG GAA AGC T 3' (FRAG 278) (SEQ. ID NO: 288)
5'- C CTG GAA AGC-3' (FRAG 279) (SEQ. ID NO: 289)
35 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 280) (SEQ. ID NO: 290)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 281) (SEQ. ID NO: 291)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 282) (SEQ. ID NO: 292)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) (SEQ. ID NO: 293)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 284) (SEQ. ID NO: 294)
40 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 285) (SEQ. ID NO: 295)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) (SEQ. ID NO: 296)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 287) (SEQ. ID NO: 297)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 288) (SEQ. ID NO: 298)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 289) (SEQ. ID NO: 299)
45 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 290) (SEQ. ID NO: 300)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 291) (SEQ. ID NO: 301)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) (SEQ. ID NO: 302)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 293) (SEQ. ID NO: 303)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 294) (SEQ. ID NO: 304)
50 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) (SEQ. ID NO: 305)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) (SEQ. ID NO: 306)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) (SEQ. ID NO: 307)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) (SEQ. ID NO: 308)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 299) (SEQ. ID NO: 309)
55 5'- CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 300) (SEQ. ID NO: 310)
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) (SEQ. ID NO: 311)
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) (SEQ. ID NO: 312)
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) (SEQ. ID NO: 313)
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) (SEQ. ID NO: 314)
60 5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) (SEQ. ID NO: 315)
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) (SEQ. ID NO: 316)
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) (SEQ. ID NO: 317)

- 5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) (SEQ. ID NO: 318)
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) (SEQ. ID NO: 319)
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) (SEQ. ID NO: 320)
5'- CTG GAA AGC TGA GA-3' (FRAG 311) (SEQ. ID NO: 321)
5 5'- CTG GAA AGC TGA G-3' (FRAG 312) (SEQ. ID NO: 322)
5'- CTG GAA AGC TGA-3' (FRAG 313) (SEQ. ID NO: 323)
5'- CTG GAA AGC TG 3' (FRAG 314) (SEQ. ID NO: 324)
5'- CTG GAA AGC T-3' (FRAG 315) (SEQ. ID NO: 325)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 316) (SEQ. ID NO: 326)
10 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 317) (SEQ. ID NO: 327)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 318) (SEQ. ID NO: 328)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) (SEQ. ID NO: 329)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 320) (SEQ. ID NO: 330)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 321) (SEQ. ID NO: 331)
15 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) (SEQ. ID NO: 332)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 323) (SEQ. ID NO: 333)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 324) (SEQ. ID NO: 334)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 325) (SEQ. ID NO: 335)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 326) (SEQ. ID NO: 336)
20 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 327) (SEQ. ID NO: 337)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) (SEQ. ID NO: 338)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 329) (SEQ. ID NO: 339)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 330) (SEQ. ID NO: 340)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) (SEQ. ID NO: 341)
25 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) (SEQ. ID NO: 342)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) (SEQ. ID NO: 343)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) (SEQ. ID NO: 344)
5'- TG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 335) (SEQ. ID NO: 345)
5'- TG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 336) (SEQ. ID NO: 346)
30 5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) (SEQ. ID NO: 347)
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) (SEQ. ID NO: 348)
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) (SEQ. ID NO: 349)
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) (SEQ. ID NO: 350)
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) (SEQ. ID NO: 351)
35 5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) (SEQ. ID NO: 352)
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) (SEQ. ID NO: 353)
5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) (SEQ. ID NO: 354)
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) (SEQ. ID NO: 355)
5'- TG GAA AGC TGA GAT -3' (FRAG 346) (SEQ. ID NO: 356)
40 5'- TG GAA AGC TGA GA-3' (FRAG 347) (SEQ. ID NO: 357)
5'- TG GAA AGC TGA G-3' (FRAG 348) (SEQ. ID NO: 358)
5'- TG GAA AGC TGA 3' (FRAG 349) (SEQ. ID NO: 359)
5'- TG GAA AGC TG-3' (FRAG 350) (SEQ. ID NO: 360)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) (SEQ. ID NO: 361)
45 5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) (SEQ. ID NO: 362)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) (SEQ. ID NO: 363)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) (SEQ. ID NO: 364)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) (SEQ. ID NO: 365)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) (SEQ. ID NO: 366)
50 5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) (SEQ. ID NO: 367)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) (SEQ. ID NO: 368)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) (SEQ. ID NO: 369)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) (SEQ. ID NO: 370)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) (SEQ. ID NO: 371)
55 5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) (SEQ. ID NO: 372)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) (SEQ. ID NO: 373)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC GG-3' (FRAG 364) (SEQ. ID NO: 374)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC G-3' (FRAG 365) (SEQ. ID NO: 375)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT GGC -3' (FRAG 366) (SEQ. ID NO: 376)
60 5'- G GAA AGC TGA CAT GGA GGG CGG CAT GG -3' (FRAG 367) (SEQ. ID NO: 377)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT G -3' (FRAG 368) (SEQ. ID NO: 378)
5'- G GAA AGC TGA CAT GGA GGG CGG CAT -3' (FRAG 369) (SEQ. ID NO: 379)

- 5'- G GAA AGC TGA C|AT GGA GGG CGG CA-3' (FRAG 370) (SEQ. ID NO: 380)
 5'- G GAA AGC TGA C|AT GGA GGG CGG C-3' (FRAG 371) (SEQ. ID NO: 381)
 5'- G GAA AGC TGA C|AT GGA GGG CGG -3' (FRAG 372) (SEQ. ID NO: 382)
 5'- G GAA AGC TGA C|AT GGA GGG CG -3' (FRAG 373) (SEQ. ID NO: 383)
 5 5'- G GAA AGC TGA C|AT GGA GGG C -3' (FRAG 374) (SEQ. ID NO: 384)
 5'- G GAA AGC TGA C|AT GGA GGG -3' (FRAG 375) (SEQ. ID NO: 385)
 5'- G GAA AGC TGA C|AT GGA GG -3' (FRAG 376) (SEQ. ID NO: 386)
 5'- G GAA AGC TGA C|AT GGA G -3' (FRAG 377) (SEQ. ID NO: 387)
 5'- G GAA AGC TGA C|AT GGA -3' (FRAG 378) (SEQ. ID NO: 388)
 10 5'- G GAA AGC TGA C|AT GG -3' (FRAG 379) (SEQ. ID NO: 389)
 5'- G GAA AGC TGA C|AT G -3' (FRAG 380) (SEQ. ID NO: 390)
 5'- G GAA AGC TGA C|AT -3' (FRAG 381) (SEQ. ID NO: 391)
 5'- G GAA AGC TGA C|A-3' (FRAG 382) (SEQ. ID NO: 392)
 5'- G GAA AGC TGA C|-3' (FRAG 383) (SEQ. ID NO: 393)
 15 5'- G GAA AGC TGA -3' (FRAG 384) (SEQ. ID NO: 394)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) (SEQ. ID NO: 395)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) (SEQ. ID NO: 396)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) (SEQ. ID NO: 397)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) (SEQ. ID NO: 398)
 20 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) (SEQ. ID NO: 399)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) (SEQ. ID NO: 400)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) (SEQ. ID NO: 401)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) (SEQ. ID NO: 402)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) (SEQ. ID NO: 403)
 25 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) (SEQ. ID NO: 404)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) (SEQ. ID NO: 405)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 396) (SEQ. ID NO: 406)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GGG -3' (FRAG 397) (SEQ. ID NO: 407)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC GG-3' (FRAG 398) (SEQ. ID NO: 408)
 30 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC G-3' (FRAG 399) (SEQ. ID NO: 409)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GGC -3' (FRAG 400) (SEQ. ID NO: 410)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT GG -3' (FRAG 401) (SEQ. ID NO: 411)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT G -3' (FRAG 402) (SEQ. ID NO: 412)
 5'- GAA AGC TGA G|AT GGA GGG CGG CAT -3' (FRAG 403) (SEQ. ID NO: 413)
 35 5'- GAA AGC TGA G|AT GGA GGG CGG CA-3' (FRAG 404) (SEQ. ID NO: 414)
 5'- GAA AGC TGA G|AT GGA GGG CGG C-3' (FRAG 405) (SEQ. ID NO: 415)
 5'- GAA AGC TGA G|AT GGA GGG CGG -3' (FRAG 406) (SEQ. ID NO: 416)
 5'- GAA AGC TGA G|AT GGA GGG CG -3' (FRAG 407) (SEQ. ID NO: 417)
 5'- GAA AGC TGA G|AT GGA GGG C -3' (FRAG 408) (SEQ. ID NO: 418)
 40 5'- GAA AGC TGA G|AT GGA GGG -3' (FRAG 409) (SEQ. ID NO: 419)
 5'- GAA AGC TGA G|AT GGA GG -3' (FRAG 410) (SEQ. ID NO: 420)
 5'- GAA AGC TGA G|AT GGA G -3' (FRAG 411) (SEQ. ID NO: 421)
 5'- GAA AGC TGA G|AT GGA -3' (FRAG 412) (SEQ. ID NO: 422)
 5'- GAA AGC TGA G|AT GG -3' (FRAG 413) (SEQ. ID NO: 423)
 45 5'- GAA AGC TGA G|AT G -3' (FRAG 414) (SEQ. ID NO: 424)
 5'- GAA AGC TGA G|AT -3' (FRAG 415) (SEQ. ID NO: 425)
 5'- GAA AGC TGA G|-3' (FRAG 416) (SEQ. ID NO: 426)
 5'- GAA AGC TGA G-3' (FRAG 417) (SEQ. ID NO: 427)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) (SEQ. ID NO: 428)
 50 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) (SEQ. ID NO: 429)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) (SEQ. ID NO: 430)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) (SEQ. ID NO: 431)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) (SEQ. ID NO: 432)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) (SEQ. ID NO: 433)
 55 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 424) (SEQ. ID NO: 434)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) (SEQ. ID NO: 435)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) (SEQ. ID NO: 436)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) (SEQ. ID NO: 437)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) (SEQ. ID NO: 438)
 60 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) (SEQ. ID NO: 439)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) (SEQ. ID NO: 440)
 5'- AA AGC TGA G|AT GGA GGG CGG CAT GGC GG-3' (FRAG 431) (SEQ. ID NO: 441)

- 5'- AA AGC TGA GAT' GGA GGG CGG CAT GGC G-3' (FRAG 432) (SEQ. ID NO: 442)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT GGC -3' (FRAG 433) (SEQ. ID NO: 443)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT GG -3' (FRAG 434) (SEQ. ID NO: 444)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT G -3' (FRAG 435) (SEQ. ID NO: 445)
 5 5'- AA AGC TGA GAT' GGA GGG CGG CAT -3' (FRAG 436) (SEQ. ID NO: 446)
 5'- AA AGC TGA GAT' GGA GGG CGG CA-3' (FRAG 437) (SEQ. ID NO: 447)
 5'- AA AGC TGA GAT' GGA GGG CGG C-3' (FRAG 438) (SEQ. ID NO: 448)
 5'- AA AGC TGA GAT' GGA GGG CGG -3' (FRAG 439) (SEQ. ID NO: 449)
 5'- AA AGC TGA GAT' GGA GGG CG -3' (FRAG 440) (SEQ. ID NO: 450)
 10 5'- AA AGC TGA GAT' GGA GGG C -3' (FRAG 441) (SEQ. ID NO: 451)
 5'- AA AGC TGA GAT' GGA GGG -3' (FRAG 442) (SEQ. ID NO: 452)
 5'- AA AGC TGA GAT' GGA GG -3' (FRAG 443) (SEQ. ID NO: 453)
 5'- AA AGC TGA GAT' GGA G -3' (FRAG 444) (SEQ. ID NO: 454)
 5'- AA AGC TGA GAT' GGA -3' (FRAG 445) (SEQ. ID NO: 455)
 15 5'- AA AGC TGA GAT' GG -3' (FRAG 446) (SEQ. ID NO: 456)
 5'- AA AGC TGA GAT' G -3' (FRAG 447) (SEQ. ID NO: 457)
 5'- AA AGC TGA GAT' -3' (FRAG 448) (SEQ. ID NO: 458)
 5'- AA AGC TGA GA-3' (FRAG 449) (SEQ. ID NO: 459)
 5'- A AGC TGA GAT' GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) (SEQ. ID NO: 460)
 20 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) (SEQ. ID NO: 461)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) (SEQ. ID NO: 462)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) (SEQ. ID NO: 463)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 454) (SEQ. ID NO: 464)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) (SEQ. ID NO: 465)
 25 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) (SEQ. ID NO: 466)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 457) (SEQ. ID NO: 467)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) (SEQ. ID NO: 468)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) (SEQ. ID NO: 469)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) (SEQ. ID NO: 470)
 30 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG C-3' (FRAG 461) (SEQ. ID NO: 471)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG -3' (FRAG 462) (SEQ. ID NO: 472)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GG-3' (FRAG 463) (SEQ. ID NO: 473)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC G-3' (FRAG 464) (SEQ. ID NO: 474)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC -3' (FRAG 465) (SEQ. ID NO: 475)
 35 5'- A AGC TGA GAT' GGA GGG CGG CAT GG -3' (FRAG 466) (SEQ. ID NO: 476)
 5'- A AGC TGA GAT' GGA GGG CGG CAT G -3' (FRAG 467) (SEQ. ID NO: 477)
 5'- A AGC TGA GAT' GGA GGG CGG CAT -3' (FRAG 468) (SEQ. ID NO: 478)
 5'- A AGC TGA GAT' GGA GGG CGG CA-3' (FRAG 469) (SEQ. ID NO: 479)
 5'- A AGC TGA GAT' GGA GGG CGG C-3' (FRAG 470) (SEQ. ID NO: 480)
 40 5'- A AGC TGA GAT' GGA GGG CGG -3' (FRAG 471) (SEQ. ID NO: 481)
 5'- A AGC TGA GAT' GGA GGG CG -3' (FRAG 472) (SEQ. ID NO: 482)
 5'- A AGC TGA GAT' GGA GGG C -3' (FRAG 473) (SEQ. ID NO: 483)
 5'- A AGC TGA GAT' GGA GGG -3' (FRAG 474) (SEQ. ID NO: 484)
 5'- A AGC TGA GAT' GGA GG -3' (FRAG 475) (SEQ. ID NO: 485)
 45 5'- A AGC TGA GAT' GGA G -3' (FRAG 476) (SEQ. ID NO: 486)
 5'- A AGC TGA GAT' GGA -3' (FRAG 477) (SEQ. ID NO: 487)
 5'- A AGC TGA GAT' GG -3' (FRAG 478) (SEQ. ID NO: 488)
 5'- A AGC TGA GAT' G -3' (FRAG 479) (SEQ. ID NO: 489)
 5'- A AGC TGA GAT' -3' (FRAG 480) (SEQ. ID NO: 490)
 50 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 481) (SEQ. ID NO: 491)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) (SEQ. ID NO: 492)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) (SEQ. ID NO: 493)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) (SEQ. ID NO: 494)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 485) (SEQ. ID NO: 495)
 55 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) (SEQ. ID NO: 496)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) (SEQ. ID NO: 497)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 488) (SEQ. ID NO: 498)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) (SEQ. ID NO: 499)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 490) (SEQ. ID NO: 500)
 60 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) (SEQ. ID NO: 501)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG C-3' (FRAG 492) (SEQ. ID NO: 502)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG -3' (FRAG 493) (SEQ. ID NO: 503)

- 5'- AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 494) (SEQ. ID NO: 504)
 5'- AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 495) (SEQ. ID NO: 505)
 5'- AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 496) (SEQ. ID NO: 506)
 5'- AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 497) (SEQ. ID NO: 507)
 5 5'- AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 498) (SEQ. ID NO: 508)
 5'- AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 499) (SEQ. ID NO: 509)
 5'- AGC TGA GAT GGA GGG CGG CA-3' (FRAG 500) (SEQ. ID NO: 510)
 5'- AGC TGA GAT GGA GGG CGG C-3' (FRAG 501) (SEQ. ID NO: 511)
 5'- AGC TGA GAT GGA GGG CGG -3' (FRAG 502) (SEQ. ID NO: 512)
 10 5'- AGC TGA GAT GGA GGG CG -3' (FRAG 503) (SEQ. ID NO: 513)
 5'- AGC TGA GAT GGA GGG C -3' (FRAG 504) (SEQ. ID NO: 514)
 5'- AGC TGA GAT GGA GGG -3' (FRAG 505) (SEQ. ID NO: 515)
 5'- AGC TGA GAT GGA GG -3' (FRAG 506) (SEQ. ID NO: 516)
 5'- AGC TGA GAT GGA G -3' (FRAG 507) (SEQ. ID NO: 517)
 15 5'- AGC TGA GAT GGA -3' (FRAG 508) (SEQ. ID NO: 518)
 5'- AGC TGA GAT GG -3' (FRAG 509) (SEQ. ID NO: 519)
 5'- AGC TGA GAT G -3' (FRAG 510) (SEQ. ID NO: 520)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) (SEQ. ID NO: 521)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) (SEQ. ID NO: 522)
 20 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) (SEQ. ID NO: 523)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) (SEQ. ID NO: 524)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) (SEQ. ID NO: 525)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) (SEQ. ID NO: 526)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) (SEQ. ID NO: 527)
 25 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) (SEQ. ID NO: 528)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) (SEQ. ID NO: 529)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 520) (SEQ. ID NO: 530)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 521) (SEQ. ID NO: 531)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 522) (SEQ. ID NO: 532)
 30 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 523) (SEQ. ID NO: 533)
 5'- GC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 524) (SEQ. ID NO: 534)
 5'- GC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 525) (SEQ. ID NO: 535)
 5'- GC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 526) (SEQ. ID NO: 536)
 5'- GC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 527) (SEQ. ID NO: 537)
 35 5'- GC TGA GAT GGA GGG CGG CAT G -3' (FRAG 528) (SEQ. ID NO: 538)
 5'- GC TGA GAT GGA GGG CGG CAT -3' (FRAG 529) (SEQ. ID NO: 539)
 5'- GC TGA GAT GGA GGG CGG CA-3' (FRAG 530) (SEQ. ID NO: 540)
 5'- GC TGA GAT GGA GGG CGG C-3' (FRAG 531) (SEQ. ID NO: 541)
 5'- GC TGA GAT GGA GGG CGG -3' (FRAG 532) (SEQ. ID NO: 542)
 40 5'- GC TGA GAT GGA GGG CG -3' (FRAG 533) (SEQ. ID NO: 543)
 5'- GC TGA GAT GGA GGG C -3' (FRAG 534) (SEQ. ID NO: 544)
 5'- GC TGA GAT GGA GGG -3' (FRAG 535) (SEQ. ID NO: 545)
 5'- GC TGA GAT GGA GG -3' (FRAG 536) (SEQ. ID NO: 546)
 5'- GC TGA GAT GGA G -3' (FRAG 537) (SEQ. ID NO: 547)
 45 5'- GC TGA GAT GGA -3' (FRAG 538) (SEQ. ID NO: 548)
 5'- GC TGA GAT GG -3' (FRAG 539) (SEQ. ID NO: 549)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) (SEQ. ID NO: 550)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) (SEQ. ID NO: 551)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) (SEQ. ID NO: 552)
 50 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) (SEQ. ID NO: 553)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) (SEQ. ID NO: 554)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) (SEQ. ID NO: 555)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) (SEQ. ID NO: 556)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) (SEQ. ID NO: 557)
 55 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) (SEQ. ID NO: 558)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 549) (SEQ. ID NO: 559)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 550) (SEQ. ID NO: 560)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 551) (SEQ. ID NO: 561)
 5'- C TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 552) (SEQ. ID NO: 562)
 60 5'- C TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 553) (SEQ. ID NO: 563)
 5'- C TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 554) (SEQ. ID NO: 564)
 5'- C TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 555) (SEQ. ID NO: 565)

- 5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) (SEQ. ID NO: 566)
 5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) (SEQ. ID NO: 567)
 5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) (SEQ. ID NO: 568)
 5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) (SEQ. ID NO: 569)
 5 5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) (SEQ. ID NO: 570)
 5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) (SEQ. ID NO: 571)
 5'- C TGA GAT GGA GGG CG -3' (FRAG 562) (SEQ. ID NO: 572)
 5'- C TGA GAT GGA GGG C -3' (FRAG 563) (SEQ. ID NO: 573)
 5'- C TGA GAT GGA GGG -3' (FRAG 564) (SEQ. ID NO: 574)
 10 5'- C TGA GAT GGA GG -3' (FRAG 565) (SEQ. ID NO: 575)
 5'- C TGA GAT GGA G -3' (FRAG 566) (SEQ. ID NO: 576)
 5'- C TGA GAT GGA -3' (FRAG 567) (SEQ. ID NO: 577)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) (SEQ. ID NO: 578)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) (SEQ. ID NO: 579)
 15 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) (SEQ. ID NO: 580)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) (SEQ. ID NO: 581)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) (SEQ. ID NO: 582)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) (SEQ. ID NO: 583)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) (SEQ. ID NO: 584)
 20 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) (SEQ. ID NO: 585)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) (SEQ. ID NO: 586)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) (SEQ. ID NO: 587)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) (SEQ. ID NO: 588)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) (SEQ. ID NO: 589)
 25 5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) (SEQ. ID NO: 590)
 5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) (SEQ. ID NO: 591)
 5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) (SEQ. ID NO: 592)
 5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) (SEQ. ID NO: 593)
 5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) (SEQ. ID NO: 594)
 30 5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) (SEQ. ID NO: 595)
 5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) (SEQ. ID NO: 596)
 5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) (SEQ. ID NO: 597)
 5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) (SEQ. ID NO: 598)
 5'- TGA GAT GGA GGG CGG -3' (FRAG 589) (SEQ. ID NO: 599)
 35 5'- TGA GAT GGA GGG CG -3' (FRAG 590) (SEQ. ID NO: 600)
 5'- TGA GAT GGA GGG C -3' (FRAG 591) (SEQ. ID NO: 601)
 5'- TGA GAT GGA GGG -3' (FRAG 592) (SEQ. ID NO: 602)
 5'- TGA GAT GGA GG -3' (FRAG 593) (SEQ. ID NO: 603)
 5'- TGA GAT GGA G -3' (FRAG 594) (SEQ. ID NO: 604)
 40 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) (SEQ. ID NO: 605)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) (SEQ. ID NO: 606)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) (SEQ. ID NO: 607)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) (SEQ. ID NO: 608)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) (SEQ. ID NO: 609)
 45 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) (SEQ. ID NO: 610)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) (SEQ. ID NO: 611)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AG-3' (FRAG 602) (SEQ. ID NO: 612)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC A-3' (FRAG 603) (SEQ. ID NO: 613)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC-3' (FRAG 604) (SEQ. ID NO: 614)
 50 5'- GA GAT GGA GCG CGG CAT GGC GGG CA-3' (FRAG 605) (SEQ. ID NO: 615)
 5'- GA GAT GGA GCG CGG CAT GGC GGG C-3' (FRAG 606) (SEQ. ID NO: 616)
 5'- GA GAT GGA GCG CGG CAT GGC GGG -3' (FRAG 607) (SEQ. ID NO: 617)
 5'- GA GAT GGA GCG CGG CAT GGC GG-3' (FRAG 608) (SEQ. ID NO: 618)
 5'- GA GAT GGA GCG CGG CAT GGC G-3' (FRAG 609) (SEQ. ID NO: 619)
 55 5'- GA GAT GGA GCG CGG CAT GGC -3' (FRAG 610) (SEQ. ID NO: 620)
 5'- GA GAT GGA GCG CGG CAT GG -3' (FRAG 611) (SEQ. ID NO: 621)
 5'- GA GAT GGA GCG CGG CAT G -3' (FRAG 612) (SEQ. ID NO: 622)
 5'- GA GAT GGA GCG CGG CAT -3' (FRAG 613) (SEQ. ID NO: 623)
 5'- GA GAT GGA GCG CGG CA-3' (FRAG 614) (SEQ. ID NO: 624)
 60 5'- GA GAT GGA GCG CGG C-3' (FRAG 615) (SEQ. ID NO: 625)
 5'- GA GAT GGA GCG CGG -3' (FRAG 616) (SEQ. ID NO: 626)
 5'- GA GAT GGA GCG CG -3' (FRAG 617) (SEQ. ID NO: 627)

- 5'- GA GAT GGA GCG C -3' (FRAG 618) (SEQ. ID NO: 628)
 5'- GA GAT GGA GCG -3' (FRAG 619) (SEQ. ID NO: 629)
 5'- GA GAT GGA GCG -3' (FRAG 620) (SEQ. ID NO: 630)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) (SEQ. ID NO: 631)
 5 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) (SEQ. ID NO: 632)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) (SEQ. ID NO: 633)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) (SEQ. ID NO: 634)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) (SEQ. ID NO: 635)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) (SEQ. ID NO: 636)
 10 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG -3' (FRAG 627) (SEQ. ID NO: 637)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AG-3' (FRAG 628) (SEQ. ID NO: 638)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC A-3' (FRAG 629) (SEQ. ID NO: 639)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC-3' (FRAG 630) (SEQ. ID NO: 640)
 5'- A GAT GGA GGC CGG CAT GGC GGG CA-3' (FRAG 631) (SEQ. ID NO: 641)
 15 5'- A GAT GGA GGC CGG CAT GGC GGG C-3' (FRAG 632) (SEQ. ID NO: 642)
 5'- A GAT GGA GGC CGG CAT GGC GGG -3' (FRAG 633) (SEQ. ID NO: 643)
 5'- A GAT GGA GGC CGG CAT GGC GG-3' (FRAG 634) (SEQ. ID NO: 644)
 5'- A GAT GGA GGC CGG CAT GGC G-3' (FRAG 635) (SEQ. ID NO: 645)
 5'- A GAT GGA GGC CGG CAT GGC -3' (FRAG 636) (SEQ. ID NO: 646)
 20 5'- A GAT GGA GGC CGG CAT GG -3' (FRAG 637) (SEQ. ID NO: 647)
 5'- A GAT GGA GGC CGG CAT G -3' (FRAG 638) (SEQ. ID NO: 648)
 5'- A GAT GGA GGC CGG CAT -3' (FRAG 639) (SEQ. ID NO: 649)
 5'- A GAT GGA GGC CGG CA-3' (FRAG 640) (SEQ. ID NO: 650)
 5'- A GAT GGA GGC CGG C-3' (FRAG 641) (SEQ. ID NO: 651)
 25 5'- A GAT GGA GGC CGG -3' (FRAG 642) (SEQ. ID NO: 652)
 5'- A GAT GGA GGC CG -3' (FRAG 643) (SEQ. ID NO: 653)
 5'- A GAT GGA GGC C -3' (FRAG 644) (SEQ. ID NO: 654)
 5'- A GAT GGA GGC -3' (FRAG 645) (SEQ. ID NO: 655)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) (SEQ. ID NO: 656)
 30 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) (SEQ. ID NO: 657)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) (SEQ. ID NO: 658)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 649) (SEQ. ID NO: 659)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) (SEQ. ID NO: 660)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) (SEQ. ID NO: 661)
 35 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) (SEQ. ID NO: 662)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) (SEQ. ID NO: 663)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) (SEQ. ID NO: 664)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) (SEQ. ID NO: 665)
 5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) (SEQ. ID NO: 666)
 40 5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) (SEQ. ID NO: 667)
 5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) (SEQ. ID NO: 668)
 5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) (SEQ. ID NO: 669)
 5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) (SEQ. ID NO: 670)
 5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) (SEQ. ID NO: 671)
 45 5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) (SEQ. ID NO: 672)
 5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) (SEQ. ID NO: 673)
 5'- GAT GGA GGG CGG CAT -3' (FRAG 664) (SEQ. ID NO: 674)
 5'- GAT GGA GGG CGG CA-3' (FRAG 665) (SEQ. ID NO: 675)
 5'- GAT GGA GGG CGG C-3' (FRAG 666) (SEQ. ID NO: 676)
 50 5'- GAT GGA GGG CGG -3' (FRAG 667) (SEQ. ID NO: 677)
 5'- GAT GGA GGG CG -3' (FRAG 668) (SEQ. ID NO: 678)
 5'- GAT GGA GGG C -3' (FRAG 669) (SEQ. ID NO: 679)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) (SEQ. ID NO: 680)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) (SEQ. ID NO: 681)
 55 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) (SEQ. ID NO: 682)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) (SEQ. ID NO: 683)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG CT-3' (FRAG 674) (SEQ. ID NO: 684)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG C-3' (FRAG 675) (SEQ. ID NO: 685)
 5'- AT GGA GGG CCG CAT GGC GGG CAC AGG -3' (FRAG 676) (SEQ. ID NO: 686)
 60 5'- AT GGA GGG CCG CAT GGC GGG CAC AG-3' (FRAG 677) (SEQ. ID NO: 687)
 5'- AT GGA GGG CCG CAT GGC GGG CAC A-3' (FRAG 678) (SEQ. ID NO: 688)
 5'- AT GGA GGG CCG CAT GGC GGG CAC-3' (FRAG 679) (SEQ. ID NO: 689)

5'- AT GGA GGG CCG CAT GGC GGG CA-3' (FRAG 680) (SEQ. ID NO: 690)
5'- AT GGA GGG CCG CAT GGC GGG C-3' (FRAG 681) (SEQ. ID NO: 691)
5'- AT GGA GGG CCG CAT GGC GGG -3' (FRAG 682) (SEQ. ID NO: 692)
5'- AT GGA GGG CCG CAT GGC GG-3' (FRAG 683) (SEQ. ID NO: 693)
5 5'- AT GGA GGG CCG CAT GGC G-3' (FRAG 684) (SEQ. ID NO: 694)
5'- AT GGA GGG CCG CAT GGC -3' (FRAG 685) (SEQ. ID NO: 695)
5'- AT GGA GGG CCG CAT GG -3' (FRAG 686) (SEQ. ID NO: 696)
5'- AT GGA GGG CCG CAT G -3' (FRAG 687) (SEQ. ID NO: 697)
5'- AT GGA GGG CCG CAT -3' (FRAG 688) (SEQ. ID NO: 698)
10 5'- AT GGA GGG CCG CA-3' (FRAG 689) (SEQ. ID NO: 699)
5'- AT GGA GGG CCG C-3' (FRAG 690) (SEQ. ID NO: 700)
5'- AT GGA GGG CCG -3' (FRAG 691) (SEQ. ID NO: 701)
5'- AT GGA GGG CG -3' (FRAG 692) (SEQ. ID NO: 702)
5'- T GGA GGG CCG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) (SEQ. ID NO: 703)
15 5'- T GGA GGG CCG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) (SEQ. ID NO: 704)
5'- T GGA GGG CCG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) (SEQ. ID NO: 705)
5'- T GGA GGG CCG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) (SEQ. ID NO: 706)
5'- T GGA GGG CCG CAT GGC GGG CAC AGG CT-3' (FRAG 697) (SEQ. ID NO: 707)
5'- T GGA GGG CCG CAT GGC GGG CAC AGG C-3' (FRAG 698) (SEQ. ID NO: 708)
20 5'- T GGA GGG CCG CAT GGC GGG CAC AGG -3' (FRAG 699) (SEQ. ID NO: 709)
5'- T GGA GGG CCG CAT GGC GGG CAC AG-3' (FRAG 700) (SEQ. ID NO: 710)
5'- T GGA GGG CCG CAT GGC GGG CAC A-3' (FRAG 701) (SEQ. ID NO: 711)
5'- T GGA GGG CCG CAT GGC GGG CAC-3' (FRAG 702) (SEQ. ID NO: 712)
5'- T GGA GGG CCG CAT GGC GGG CA-3' (FRAG 703) (SEQ. ID NO: 713)
25 5'- T GGA GGG CCG CAT GGC GGG C-3' (FRAG 704) (SEQ. ID NO: 714)
5'- T GGA GGG CCG CAT GGC GGG -3' (FRAG 705) (SEQ. ID NO: 715)
5'- T GGA GGG CCG CAT GGC GG-3' (FRAG 706) (SEQ. ID NO: 716)
5'- T GGA GGG CCG CAT GGC G-3' (FRAG 707) (SEQ. ID NO: 717)
5'- T GGA GGG CCG CAT GGC -3' (FRAG 708) (SEQ. ID NO: 718)
30 5'- T GGA GGG CCG CAT GG -3' (FRAG 709) (SEQ. ID NO: 719)
5'- T GGA GGG CCG CAT G -3' (FRAG 710) (SEQ. ID NO: 720)
5'- T GGA GGG CCG CAT -3' (FRAG 711) (SEQ. ID NO: 721)
5'- T GGA GGG CCG CA-3' (FRAG 712) (SEQ. ID NO: 722)
5'- T GGA GGG CCG C-3' (FRAG 713) (SEQ. ID NO: 723)
35 5'- T GGA GGG CCG -3' (FRAG 714) (SEQ. ID NO: 724)
5'- GGA GGG CCG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) (SEQ. ID NO: 725)
5'- GGA GGG CCG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) (SEQ. ID NO: 726)
5'- GGA GGG CCG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) (SEQ. ID NO: 727)
5'- GGA GGG CCG CAT GGC GGG CAC AGG CTG -3' (FRAG 718) (SEQ. ID NO: 728)
40 5'- GGA GGG CCG CAT GGC GGG CAC AGG CT-3' (FRAG 719) (SEQ. ID NO: 729)
5'- GGA GGG CCG CAT GGC GGG CAC AGG C-3' (FRAG 720) (SEQ. ID NO: 730)
5'- GGA GGG CCG CAT GGC GGG CAC AGG -3' (FRAG 721) (SEQ. ID NO: 731)
5'- GGA GGG CCG CAT GGC GGG CAC AG-3' (FRAG 722) (SEQ. ID NO: 732)
5'- GGA GGG CCG CAT GGC GGG CAC A-3' (FRAG 723) (SEQ. ID NO: 733)
45 5'- GGA GGG CCG CAT GGC GGG CAC-3' (FRAG 724) (SEQ. ID NO: 734)
5'- GGA GGG CCG CAT GGC GGG CA-3' (FRAG 725) (SEQ. ID NO: 735)
5'- GGA GGG CCG CAT GGC GGG C-3' (FRAG 726) (SEQ. ID NO: 736)
5'- GGA GGG CCG CAT GGC GGG -3' (FRAG 727) (SEQ. ID NO: 737)
5'- GGA GGG CCG CAT GGC GG-3' (FRAG 728) (SEQ. ID NO: 738)
50 5'- GGA GGG CCG CAT GGC G-3' (FRAG 729) (SEQ. ID NO: 739)
5'- GGA GGG CCG CAT GGC -3' (FRAG 730) (SEQ. ID NO: 740)
5'- GGA GGG CCG CAT GG -3' (FRAG 731) (SEQ. ID NO: 741)
5'- GGA GGG CCG CAT G -3' (FRAG 732) (SEQ. ID NO: 742)
5'- GGA GGG CCG CAT -3' (FRAG 733) (SEQ. ID NO: 743)
55 5'- GGA GGG CCG CA-3' (FRAG 734) (SEQ. ID NO: 744)
5'- GGA GGG CCG C-3' (FRAG 735) (SEQ. ID NO: 745)
5'- GA GGG CCG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) (SEQ. ID NO: 746)
5'- GA GGG CCG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) (SEQ. ID NO: 747)
5'- GA GGG CCG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) (SEQ. ID NO: 748)
60 5'- GA GGG CCG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) (SEQ. ID NO: 749)
5'- GA GGG CCG CAT GGC GGG CAC AGG CT-3' (FRAG 740) (SEQ. ID NO: 750)
5'- GA GGG CCG CAT GGC GGG CAC AGG C-3' (FRAG 741) (SEQ. ID NO: 751)

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5'- GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) (SEQ. ID NO: 752)
5'- GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) (SEQ. ID NO: 753)
5'- GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) (SEQ. ID NO: 754)
5'- GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) (SEQ. ID NO: 755)
5 5'- GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) (SEQ. ID NO: 756)
5'- GA GGG CGG CAT GGC GGG C-3' (FRAG 747) (SEQ. ID NO: 757)
5'- GA GGG CGG CAT GGC GGG -3' (FRAG 748) (SEQ. ID NO: 758)
5'- GA GGG CGG CAT GGC GG-3' (FRAG 749) (SEQ. ID NO: 759)
5'- GA GGG CGG CAT GGC G-3' (FRAG 750) (SEQ. ID NO: 760)
10 5'- GA GGG CGG CAT GGC -3' (FRAG 751) (SEQ. ID NO: 761)
5'- GA GGG CGG CAT GG -3' (FRAG 752) (SEQ. ID NO: 762)
5'- GA GGG CGG CAT G -3' (FRAG 753) (SEQ. ID NO: 763)
5'- GA GGG CGG CAT -3' (FRAG 754) (SEQ. ID NO: 764)
5'- GA GGG CGG CA-3' (FRAG 755) (SEQ. ID NO: 765)
15 5'- A GGG CGG CA¹ GGC GGG CAC AGG CTG GGC-3' (FRAG 756) (SEQ. ID NO: 766)
5'- A GGG CGG CA² GGC GGG CAC AGG CTG GG-3' (FRAG 757) (SEQ. ID NO: 767)
5'- A GGG CGG CA³ GGC GGG CAC AGG CTG G-3' (FRAG 758) (SEQ. ID NO: 768)
5'- A GGG CGG CA⁴ GGC GGG CAC AGG CTG -3' (FRAG 759) (SEQ. ID NO: 769)
5'- A GGG CGG CA⁵ GGC GGG CAC AGG CT-3' (FRAG 760) (SEQ. ID NO: 770)
20 5'- A GGG CGG CA⁶ GGC GGG CAC AGG C-3' (FRAG 761) (SEQ. ID NO: 771)
5'- A GGG CGG CA⁷ GGC GGG CAC AGG -3' (FRAG 762) (SEQ. ID NO: 772)
5'- A GGG CGG CA⁸ GGC GGG CAC AG-3' (FRAG 763) (SEQ. ID NO: 773)
5'- A GGG CGG CA⁹ GGC GGG CAC A-3' (FRAG 764) (SEQ. ID NO: 774)
5'- A GGG CGG CA¹⁰ GGC GGG CAC-3' (FRAG 765) (SEQ. ID NO: 775)
25 5'- A GGG CGG CA¹¹ GGC GGG CA-3' (FRAG 766) (SEQ. ID NO: 776)
5'- A GGG CGG CA¹² GGC GGG C-3' (FRAG 767) (SEQ. ID NO: 777)
5'- A GGG CGG CA¹³ GGC GGG -3' (FRAG 768) (SEQ. ID NO: 778)
5'- A GGG CGG CA¹⁴ GGC GG-3' (FRAG 769) (SEQ. ID NO: 779)
5'- A GGG CGG CA¹⁵ GGC G-3' (FRAG 770) (SEQ. ID NO: 780)
30 5'- A GGG CGG CA¹⁶ GGC -3' (FRAG 771) (SEQ. ID NO: 781)
5'- A GGG CGG CA¹⁷ GG -3' (FRAG 772) (SEQ. ID NO: 782)
5'- A GGG CGG CA¹⁸ G -3' (FRAG 773) (SEQ. ID NO: 783)
5'- A GGG CGG CA¹⁹ -3' (FRAG 774) (SEQ. ID NO: 784)
5'- GGG CGG CAT 3GC GGG CAC AGG CTG GGC-3' (FRAG 775) (SEQ. ID NO: 785)
35 5'- GGG CGG CAT 3GC GGG CAC AGG CTG GG-3' (FRAG 776) (SEQ. ID NO: 786)
5'- GGG CGG CAT 3GC GGG CAC AGG CTG G-3' (FRAG 777) (SEQ. ID NO: 787)
5'- GGG CGG CAT 3GC GGG CAC AGG CTG -3' (FRAG 778) (SEQ. ID NO: 788)
5'- GGG CGG CAT 3GC GGG CAC AGG CT-3' (FRAG 779) (SEQ. ID NO: 789)
5'- GGG CGG CAT 3GC GGG CAC AGG C-3' (FRAG 780) (SEQ. ID NO: 790)
40 5'- GGG CGG CAT 3GC GGG CAC AGG -3' (FRAG 781) (SEQ. ID NO: 791)
5'- GGG CGG CAT 3GC GGG CAC AG-3' (FRAG 782) (SEQ. ID NO: 792)
5'- GGG CGG CAT 3GC GGG CAC A-3' (FRAG 783) (SEQ. ID NO: 793)
5'- GGG CGG CAT 3GC GGG CAC-3' (FRAG 784) (SEQ. ID NO: 794)
5'- GGG CGG CAT 3GC GGG CA-3' (FRAG 785) (SEQ. ID NO: 795)
45 5'- GGG CGG CAT 3GC GGG C-3' (FRAG 786) (SEQ. ID NO: 796)
5'- GGG CGG CAT 3GC GGG -3' (FRAG 787) (SEQ. ID NO: 797)
5'- GGG CGG CAT 3GC GG-3' (FRAG 788) (SEQ. ID NO: 798)
5'- GGG CGG CAT 3GC G-3' (FRAG 789) (SEQ. ID NO: 799)
5'- GGG CGG CAT 3GC -3' (FRAG 790) (SEQ. ID NO: 800)
50 5'- GGG CGG CAT 3G -3' (FRAG 791) (SEQ. ID NO: 801)
5'- GGG CGG CAT 3 -3' (FRAG 792) (SEQ. ID NO: 802)
5'- GG CGG CAT G3C GGG CAC AG G CTG GGC-3' (FRAG 793) (SEQ. ID NO: 803)
5'- GG CGG CAT G3C GGG CAC AGG CTG GG-3' (FRAG 794) (SEQ. ID NO: 804)
5'- GG CGG CAT G3C GGG CAC AGG CTG G-3' (FRAG 795) (SEQ. ID NO: 805)
55 5'- GG CGG CAT G3C GGG CAC AGG CTG -3' (FRAG 796) (SEQ. ID NO: 806)
5'- GG CGG CAT G3C GGG CAC AGG CT-3' (FRAG 797) (SEQ. ID NO: 807)
5'- GG CGG CAT G3C GGG CAC AGG C-3' (FRAG 798) (SEQ. ID NO: 808)
5'- GG CGG CAT G3C GGG CAC AGG -3' (FRAG 799) (SEQ. ID NO: 809)
5'- GG CGG CAT G3C GGG CAC AG-3' (FRAG 800) (SEQ. ID NO: 810)
60 5'- GG CGG CAT G3C GGG CAC A-3' (FRAG 801) (SEQ. ID NO: 811)
5'- GG CGG CAT G3C GGG CAC-3' (FRAG 802) (SEQ. ID NO: 812)
5'- GG CGG CAT G3C GGG CA-3' (FRAG 803) (SEQ. ID NO: 813)

5'- GG CGG CAT GGC GGG C-3' (FRAG 804) (SEQ. ID NO: 814)
 5'- GG CGG CAT GGC GGG -3' (FRAG 805) (SEQ. ID NO: 815)
 5'- GG CGG CAT GGC GG-3' (FRAG 806) (SEQ. ID NO: 816)
 5'- GG CGG CAT GGC G-3' (FRAG 807) (SEQ. ID NO: 817)
 5 5'- GG CGG CAT GGC -3' (FRAG 808) (SEQ. ID NO: 818)
 5'- GG CGG CAT GG -3' (FRAG 809) (SEQ. ID NO: 819)
 5'- G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) (SEQ. ID NO: 820)
 5'- G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) (SEQ. ID NO: 821)
 5'- G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) (SEQ. ID NO: 822)
 10 5'- G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) (SEQ. ID NO: 823)
 5'- G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) (SEQ. ID NO: 824)
 5'- G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) (SEQ. ID NO: 825)
 5'- G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) (SEQ. ID NO: 826)
 5'- G CGG CAT GGC GGG CAC AG-3' (FRAG 817) (SEQ. ID NO: 827)
 15 5'- G CGG CAT GGC GGG CAC A-3' (FRAG 818) (SEQ. ID NO: 828)
 5'- G CGG CAT GGC GGG CAC-3' (FRAG 819) (SEQ. ID NO: 829)
 5'- G CGG CAT GGC GGG CA-3' (FRAG 820) (SEQ. ID NO: 830)
 5'- G CGG CAT GGC GGG C-3' (FRAG 821) (SEQ. ID NO: 831)
 5'- G CGG CAT GGC GGG -3' (FRAG 822) (SEQ. ID NO: 832)
 20 5'- G CGG CAT GGC GG-3' (FRAG 823) (SEQ. ID NO: 833)
 5'- G CGG CAT GGC G-3' (FRAG 824) (SEQ. ID NO: 834)
 5'- G CGG CAT GGC -3' (FRAG 825) (SEQ. ID NO: 835)
 5'- CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) (SEQ. ID NO: 836)
 5'- CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 827) (SEQ. ID NO: 837)
 25 5'- CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) (SEQ. ID NO: 838)
 5'- CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) (SEQ. ID NO: 839)
 5'- CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) (SEQ. ID NO: 840)
 5'- CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) (SEQ. ID NO: 841)
 5'- CGG CAT GGC GGG CAC AGG -3' (FRAG 832) (SEQ. ID NO: 842)
 30 5'- CGG CAT GGC GGG CAC AG-3' (FRAG 833) (SEQ. ID NO: 843)
 5'- CGG CAT GGC GGG CAC A-3' (FRAG 834) (SEQ. ID NO: 844)
 5'- CGG CAT GGC GGG CAC-3' (FRAG 835) (SEQ. ID NO: 845)
 5'- CGG CAT GGC GGG CA-3' (FRAG 836) (SEQ. ID NO: 846)
 5'- CGG CAT GGC GGG C-3' (FRAG 837) (SEQ. ID NO: 847)
 35 5'- CGG CAT GGC GGG -3' (FRAG 838) (SEQ. ID NO: 848)
 5'- CGG CAT GGC GG-3' (FRAG 839) (SEQ. ID NO: 849)
 5'- CGG CAT GGC G-3' (FRAG 840) (SEQ. ID NO: 850)
 5'- GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) (SEQ. ID NO: 851)
 5'- GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) (SEQ. ID NO: 852)
 40 5'- GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) (SEQ. ID NO: 853)
 5'- GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) (SEQ. ID NO: 854)
 5'- GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) (SEQ. ID NO: 855)
 5'- GG CAT GGC GGG CAC AGG C-3' (FRAG 846) (SEQ. ID NO: 856)
 5'- GG CAT GGC GGG CAC AGG -3' (FRAG 847) (SEQ. ID NO: 857)
 45 5'- GG CAT GGC GGG CAC AG-3' (FRAG 848) (SEQ. ID NO: 858)
 5'- GG CAT GGC GGG CAC A-3' (FRAG 849) (SEQ. ID NO: 859)
 5'- GG CAT GGC GGG CAC-3' (FRAG 850) (SEQ. ID NO: 860)
 5'- GG CAT GGC GGG CA-3' (FRAG 851) (SEQ. ID NO: 861)
 5'- GG CAT GGC GGG C-3' (FRAG 852) (SEQ. ID NO: 862)
 50 5'- GG CAT GGC GGG -3' (FRAG 853) (SEQ. ID NO: 863)
 5'- GG CAT GGC GG-3' (FRAG 854) (SEQ. ID NO: 864)
 5'- G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) (SEQ. ID NO: 865)
 5'- G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) (SEQ. ID NO: 866)
 5'- G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) (SEQ. ID NO: 867)
 55 5'- G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) (SEQ. ID NO: 868)
 5'- G CAT GGC GGG CAC AGG CT-3' (FRAG 859) (SEQ. ID NO: 869)
 5'- G CAT GGC GGG CAC AGG C-3' (FRAG 860) (SEQ. ID NO: 870)
 5'- G CAT GGC GGG CAC AGG -3' (FRAG 861) (SEQ. ID NO: 871)
 5'- G CAT GGC GGG CAC AG-3' (FRAG 862) (SEQ. ID NO: 872)
 60 5'- G CAT GGC GGG CAC A-3' (FRAG 863) (SEQ. ID NO: 873)
 5'- G CAT GGC GGG CAC-3' (FRAG 864) (SEQ. ID NO: 874)
 5'- G CAT GGC GGG CA-3' (FRAG 865) (SEQ. ID NO: 875)

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- 5'- G CAT GGC GCG C-3' (FRAG 866) (SEQ. ID NO: 876)
 5'- G CAT GGC GCG -3' (FRAG 867) (SEQ. ID NO: 877)
 5'- CAT GGC GGC CAC AGG CTG GGC-3' (FRAG 868) (SEQ. ID NO: 878)
 5'- CAT GGC GGC CAC AGG CTG GG-3' (FRAG 869) (SEQ. ID NO: 879)
 5 5'- CAT GGC GGC CAC AGG CTG G-3' (FRAG 870) (SEQ. ID NO: 880)
 5'- CAT GGC GGC CAC AGG CTG -3' (FRAG 871) (SEQ. ID NO: 881)
 5'- CAT GGC GGC CAC AGG CT-3' (FRAG 872) (SEQ. ID NO: 882)
 5'- CAT GGC GGC CAC AGG C-3' (FRAG 873) (SEQ. ID NO: 883)
 5'- CAT GGC GGC CAC AGG -3' (FRAG 874) (SEQ. ID NO: 884)
 10 5'- CAT GGC GGC CAC AG-3' (FRAG 875) (SEQ. ID NO: 885)
 5'- CAT GGC GGC CAC A-3' (FRAG 876) (SEQ. ID NO: 886)
 5'- CAT GGC GGC CAC-3' (FRAG 877) (SEQ. ID NO: 887)
 5'- CAT GGC GGC CA-3' (FRAG 878) (SEQ. ID NO: 888)
 5'- CAT GGC GGC C-3' (FRAG 879) (SEQ. ID NO: 889)
 15 5'- AT GGC GGC CAC AGG CTG GGC-3' (FRAG 880) (SEQ. ID NO: 890)
 5'- AT GGC GGC CAC AGG CTG GG-3' (FRAG 881) (SEQ. ID NO: 891)
 5'- AT GGC GGC CAC AGG CTG G-3' (FRAG 882) (SEQ. ID NO: 892)
 5'- AT GGC GGC CAC AGG CTG -3' (FRAG 883) (SEQ. ID NO: 893)
 5'- AT GGC GGC CAC AGG CT-3' (FRAG 884) (SEQ. ID NO: 894)
 20 5'- AT GGC GGC CAC AGG C-3' (FRAG 885) (SEQ. ID NO: 895)
 5'- AT GGC GGC CAC AGG -3' (FRAG 886) (SEQ. ID NO: 896)
 5'- AT GGC GGC CAC AG-3' (FRAG 887) (SEQ. ID NO: 897)
 5'- AT GGC GGC CAC A-3' (FRAG 888) (SEQ. ID NO: 898)
 5'- AT GGC GGC CAC-3' (FRAG 889) (SEQ. ID NO: 899)
 25 5'- AT GGC GGC CA-3' (FRAG 890) (SEQ. ID NO: 900)
 5'- T GGC GGC CAC AGG CTG GGC-3' (FRAG 891) (SEQ. ID NO: 901)
 5'- T GGC GGC CAC AGG CTG GG-3' (FRAG 892) (SEQ. ID NO: 902)
 5'- T GGC GGC CAC AGG CTG G-3' (FRAG 893) (SEQ. ID NO: 903)
 5'- T GGC GGC CAC AGG CTG -3' (FRAG 894) (SEQ. ID NO: 904)
 30 5'- T GGC GGC CAC AGG CT-3' (FRAG 895) (SEQ. ID NO: 905)
 5'- T GGC GGC CAC AGG C-3' (FRAG 896) (SEQ. ID NO: 906)
 5'- T GGC GGC CAC AGG -3' (FRAG 897) (SEQ. ID NO: 907)
 5'- T GGC GGC CAC AG-3' (FRAG 898) (SEQ. ID NO: 908)
 5'- T GGC GGC CAC A-3' (FRAG 899) (SEQ. ID NO: 909)
 35 5'- T GGC GGC CAC-3' (FRAG 900) (SEQ. ID NO: 910)
 5'- GGC GGC CAC AGG CTG GGC-3' (FRAG 901) (SEQ. ID NO: 911)
 5'- GGC GGC CAC AGG CTG GG-3' (FRAG 902) (SEQ. ID NO: 912)
 5'- GGC GGC CAC AGG CTG G-3' (FRAG 903) (SEQ. ID NO: 913)
 5'- GGC GGC CAC AGG CTG -3' (FRAG 904) (SEQ. ID NO: 914)
 40 5'- GGC GGC CAC AGG CT-3' (FRAG 905) (SEQ. ID NO: 915)
 5'- GGC GGC CAC AGG C-3' (FRAG 906) (SEQ. ID NO: 916)
 5'- GGC GGC CAC AGG -3' (FRAG 907) (SEQ. ID NO: 917)
 5'- GGC GGC CAC AG-3' (FRAG 908) (SEQ. ID NO: 918)
 5'- GGC GGC CAC A-3' (FRAG 909) (SEQ. ID NO: 919)
 45 5'- GC GGC CAC AGG CTG GGC-3' (FRAG 910) (SEQ. ID NO: 920)
 5'- GC GGC CAC AGG CTG GG-3' (FRAG 911) (SEQ. ID NO: 921)
 5'- GC GGC CAC AGG CTG G-3' (FRAG 912) (SEQ. ID NO: 922)
 5'- GC GGC CAC AGG CTG -3' (FRAG 913) (SEQ. ID NO: 923)
 5'- GC GGC CAC AGG CT-3' (FRAG 914) (SEQ. ID NO: 924)
 50 5'- GC GGC CAC AGG C-3' (FRAG 915) (SEQ. ID NO: 925)
 5'- GC GGC CAC AGG -3' (FRAG 916) (SEQ. ID NO: 926)
 5'- GC GGC CAC AG-3' (FRAG 917) (SEQ. ID NO: 927)
 5'- C GGC CAC AGG CTG GGC-3' (FRAG 918) (SEQ. ID NO: 928)
 5'- GGC CAC AGG CTG GG-3' (FRAG 919) (SEQ. ID NO: 929)
 55 5'- C GGC CAC AGG CTG G-3' (FRAG 920) (SEQ. ID NO: 930)
 5'- C GGC CAC AGG CTG -3' (FRAG 921) (SEQ. ID NO: 931)
 5'- C GGC CAC AGG CT-3' (FRAG 922) (SEQ. ID NO: 932)
 5'- C GGC CAC AGG C-3' (FRAG 923) (SEQ. ID NO: 933)
 5'- C GGC CAC AGG -3' (FRAG 924) (SEQ. ID NO: 934)
 60 5'- GGC CAC AGG CTC GGC-3' (FRAG 925) (SEQ. ID NO: 935)
 5'- GGC CAC AGG CTC GG-3' (FRAG 926) (SEQ. ID NO: 936)
 5'- GGC CAC AGG CTC G-3' (FRAG 927) (SEQ. ID NO: 937)

- 5'- GGG CAC AGG CTG -3' (FRAG 928) (SEQ. ID NO: 938)
 5'- GGG CAC AGG CT-3' (FRAG 929) (SEQ. ID NO: 939)
 5'- GGG CAC AGG C-3' (FRAG 930) (SEQ. ID NO: 940)
 5'- GG CAC AGG CTG GGC-3' (FRAG 931) (SEQ. ID NO: 941)
 5 5'- GG CAC AGG CTG GG-3' (FRAG 932) (SEQ. ID NO: 942)
 5'- GG CAC AGG CTG G-3' (FRAG 933) (SEQ. ID NO: 943)
 5'-GG CAC AGG CTG -3' (FRAG 934) (SEQ. ID NO: 944)
 5'- GG CAC AGG CT-3' (FRAG 935) (SEQ. ID NO: 945)
 5'-G CAC AGG CTG GGC-3' (FRAG 936) (SEQ. ID NO: 946)
 10 5'-G CAC AGG CTG GC-3' (FRAG 937) (SEQ. ID NO: 947)
 5'-G CAC AGG CTG G-3' (FRAG 938) (SEQ. ID NO: 948)
 5'-G CAC AGG CTG -3' (FRAG 939) (SEQ. ID NO: 949)
 5'-CAC AGG CTG GGC 3' (FRAG 940) (SEQ. ID NO: 950)
 5'-CAC AGG CTG GG-3' (FRAG 941) (SEQ. ID NO: 951)
 15 5'-CAC AGG CTG G-3' (FRAG 942) (SEQ. ID NO: 952)
 5'-AC AGG CTG GGC-3' (FRAG 943) (SEQ. ID NO: 953)
 5'-AC AGG CTG GG-3' (FRAG 944) (SEQ. ID NO: 954)
 5'-C AGG CTG GGC-3' (FRAG 945) (SEQ. ID NO: 955)
 5'-TTT TCC TTC CTT TGT CTC TCT TC (FRAG 946) (SEQ. ID NO: 956)
 20 5'-GCT CCC GGC TGC CTG (FRAG 947) (SEQ. ID NO: 957)
 5'-CTC GGC CGT GCG GCT CTG TCG CTC CCG GT (FRAG 948) (SEQ. ID NO: 958)
 5'-CCG CCG CCC TCC GGG GGG TC (FRAG 949) (SEQ. ID NO: 959)
 5'-TGC TGC CGT TGG CTG CCC (FRAG 950) (SEQ. ID NO: 960)
 5'-CTT CTG CGG GTC GCC GG (FRAG 951) (SEQ. ID NO: 961)
 25 5'-TGC TGG GCT TGT GGC (FRAG 952) (SEQ. ID NO: 962)
 5'-GGC CTC TCT TCT GGG (FRAG 953) (SEQ. ID NO: 963)
 5'-CCT GGT CCC TCC GT (FRAG 954) (SEQ. ID NO: 964)
 5'-GGT GGC TCC TCT GC (FRAG 955) (SEQ. ID NO: 965)
 5'-GCT TGG TCC TGG GGC TGC (FRAG 956) (SEQ. ID NO: 966)
 30 5'-TGC TCT CCT CTC CTT (FRAG 957) (SEQ. ID NO: 967)

Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TTT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC
 CGC CTG GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC
 CCC GGC CTC CTG GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC
 35 CTT CTT GCT GGG CCT C TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT
 GCC ACA GAC GAC AGG C GTB CBC CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' (FRAG. NO.
 1665) (SEQ. ID NO:1680)
 5'-CTG GGC CTC-3' (FRAG 1666) (SEQ. ID NO: 1681)
 5'-TGC TTT TCT TTT CTG GGC CTC-3' (FRAG 958) (SEQ. ID NO: 968)
 40 5'-TGT GGT CTG TTT TTT TCT G-3' (FRAG 959) (SEQ. ID NO: 969)
 5'-GCC CTG CTG GGG CGC TCT CC-3' (FRAG 960) (SEQ. ID NO: 970)
 5'-GCC GCC CGC CTG GCT CCC-3' (FRAG 961) (SEQ. ID NO: 971)
 5'-GGB GCC CBT GBT GGG CBT GCC-3' (FRAG 962) (SEQ. ID NO: 972)
 5'-GTG GTT CTT GCC CTC CTT TGG CTG-3' (FRAG 963) (SEQ. ID NO: 973)
 45 5'-CCG TGC CCG CTC CCC GGC-3' (FRAG 964) (SEQ. ID NO: 974)
 5'-CTC CTG GCG GGT GGC CGT TG-3' (FRAG 965) (SEQ. ID NO: 975)
 5'-GGC CCG TGT TCC CTT GGG-3' (FRAG 966) (SEQ. ID NO: 976)
 5'-GCC TGG GGC TCC CTT CTC TC-3' (FRAG 967) (SEQ. ID NO: 977)
 5'-GCC CTT CTT GCT GGG CCT C-3' (FRAG 968) (SEQ. ID NO: 978)
 50 5'-TGC TGC TGC TGG TGC TGT GGC CCC C-3' (FRAG 969) (SEQ. ID NO: 979)
 5'-GTACACCGAGGAGCCATGATGGGCATGCCACAGACGACAGGC-3' (FRAG 970) (SEQ. ID NO: 980)
 5'-GTBCBCCBGBGBGCCCBTGTGGGCBTCCBCBGBCBGCGC-3' (FRAG 971) (SEQ. ID NO: 981)

Human Adenosine A2b Receptor Nucleic Acid & Antisense Oligonucleotide Fragments

- 5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC
 55 GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG
 TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG
 TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT
 GTG TCT CCB GCB CCB TGG CCG GGC CBG CTG GGC CCC CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG

[illegible]

CATTAAAGATC TTCCITGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC
 CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC
 CTGTGCATGC TGTTAACTGT GTCACCTCTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT
 GAATATGGCC ATTCTTCTGT ACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA
 5 GACTTCCGCT ACACCTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA
 ATGGTCAGGC TGGCGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA
 AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA
 GGAAATGGAC TGCTCTCTCT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT
 AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC
 10 AGCTTGAATG GATCTAACA GACTCTTTTG TTTTAAAAAG TCTGCCTTGT TTATGGTGGG AAATTACTGA
 AACTATTTTA CTGTAAAACA GTGTGAACTA TTATAATGCA AATACTTTT AACCTAGAGG CAATGGAAAA
 ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT
 TATTCGGCCG GGCAATGGTG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG
 AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA
 15 AGAGCGCGCA CGCGCCTGG ACCGGAGGGG CCCCgcCGCG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG
 GTGCTCCGCC CAGCCTCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCC
 CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGTCCG
 GCGGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCCGC GCGCCTTCGG TAGGGGGCGC
 CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC
 20 ATCGCCGCGC TTCTGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA
 CGCCACCAA CTACTTCCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT
 TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG
 GTGCTCACGC AGACTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC
 CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCTCTT GGGTCCTTGC
 25 CTTTGGCATC GGATGACTC CATTCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA
 CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA
 GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGTGG TGATCTACAT
 TAAGATCTTC CTGGTGGCCT GCAGGCAGT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCTC
 CAGCGGGAGA TCCATGACGC CAAGTCACTG GCGCATTTG TGGGGATTTT TGCCCTGTGC TGGTACCTG
 30 TGCATGCTGT TAACGTGTGC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA
 TATGGCCATT CTTCGTGCAC ATGCCAATTC AGTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC
 TTCCGCTACA CTTTACAA AATTATCTCC AGGTATCTT TCTGCCAAGC AGATGTCAAG AGTGGGAATG
 GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTC CAGGAGAAGA
 TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA
 35 AATGGACTGC CTCTCTTGG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT
 AGGCTCCAAG GATGACAAA TATATTTATG ATCTATTGAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG
 CTTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAAGTC TGCCCTGTTT ATGGTGGAAA ATTAAGTAAA
 CTATTTTACT GTGAACAGT GTGAACATAT ATAATGCAAA TACTTTTAA CTTAGAGGCA ATGGAAAAAT
 AAAAGTTGAC TGTACTAAAA ATG-3' (FRAG. NO: 1670) (SEQ. ID NO:3006)
 40 5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGCGCCTTGG ACCGGAGGGG CCCCgcCGCG
 GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CCGGCGGGCG CGCGGGCCAA
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 CTGCTTTTAC TGTGIGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAAGTC
 TGCCTTGTTT ATGGIGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA
 5 TACTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG-3' (FRAG.NO:) (SEQ.ID NO:2436)
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 55 TACTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG-3' (FRAG. NO:) (SEQ.ID NO:2425)
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 TATAGTG (FRAG. NO.) (SEQ. ID NO: 2424)
 5'-GCGCGTCTCTG-3' (FRAG. NO: 1671) (SEQ. ID NO:1686)
 5'-GCT GGG CCC CGG 3' (FRAG. NO: 1672) (SEQ. ID NO:1687)
 5'-CGG GTC GGG GCC CCC C-3' (FRAG. NO: 1673) (SEQ. ID NO:1688)
 25 5'- CGC GCC CGC G-3' (FRAG. NO: 1674) (SEQ. ID NO:1689)
 5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3' (FRAG 972) (SEQ. ID NO: 982)
 5'-GTT CGC GCC CGC 3CG GGG CCC CTC CGG TCC-3' (FRAG 973) (SEQ. ID NO: 983)
 5'-GTT CGC GCC CGC 3CG GGG CCC CTC CGG TCC-3' (FRAG 974) (SEQ. ID NO: 984)
 5'-CGG GTC GGG GCC CCC CGC GGC C-3' (FRAG 975) (SEQ. ID NO: 985)
 30 5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3' (FRAG 976) (SEQ. ID NO: 986)
 5'-CCG CGC CTC CGC CTG CCG CTT CTG-3' (FRAG 977) (SEQ. ID NO: 987)
 5'-GCT GGG CCC CGG GCG CCC CCT-3' (FRAG 978) (SEQ. ID NO: 988)
 5'-CCC CTC TTG CTC GGG TCC CCG TG-3' (FRAG 979) (SEQ. ID NO: 989)
 5'-ACAGCGCGTCTGTGTCTCCAGCAGCATGGCCGGGCCAGCTGGGCCCC-3' (FRAG 980) (SEQ. ID NO: 990)
 35 5'-BCBGCGCGTCTGTGTCTCCBGCBGTGGCCGGGCCBGTGGGCCCC-3' (FRAG 981) (SEQ. ID NO: 991)

Human Adenosine A3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT
 TGC CTT CCC BGG GGC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG
 TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT
 40 CTG TTC CC GAATCCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA
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 25 CTGATACCCA ATCTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCTC TTCTGTCTT TCCATCTTTT
 TGCTGAGAGT TCTAGCTCT GTACTTCCTC TTGGCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT
 GCTTATCTTG ATGGAAGTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA
 CTAAGAGCAG CAGCACTTTC AGATTCAGT CATATAGAGC TGTCTACAG CATTCTGGA ACTTGAGGAT
 GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTC TAAGGAGAAG GGTTCGAAG
 30 AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT
 CTGGGAAGAC GTCTGGCGAG AGCTAGGCC ACTGGCCCTA CAGACGGATC TTGTGGCTC ACCTGTCCCT
 GTGGAGGTTT CCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTACCTAC
 ATCACCATGG AAAATTTTCT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCTCTGC GTGGTCAAGC
 TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTCTATGT CTCTCTAGCC CTGGCTGACA TTGCTGTGG
 35 GGTGCTGGTC ATGCTTTTGG CCATGTGTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCTTTT
 ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCTTGTG GGCCATCGCT GTGGACCGAT
 ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA
 TGAGGCTACA AAGCAGAGC CTGCTGAATT TTATTTTGGG CTGTACATAT TTAGATGCTT AAGGTAAAAA
 40 TGTAAAGCC CTCAGCCAC TGTGTGGGT GGGTCCAAGT GTTCCTTGT GCTGCCTCTC TAACACGCCT
 GGTTAAAATA ATCCCTTGG ATGGTCTGA GAAGCACCTG AACCAGTGG GTCCCAAAT AACTATGGCG
 TGCAAGTGTG TGGTTCAGG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA TTCCAGACA
 GTCGCTGTT CTGTGGGA TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT
 GTTGACATG GCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGG TGTGAGCTGA GAAAGAGAGG
 45 TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT TCTGAGCAGG GAATCTTTC
 TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG
 TGCAAGAACT TAGCAGGAAT AGTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT
 CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTGG CTAAGCTGGC AGAAAGATTG CATAATCAGT
 50 GCTTCCAGCT CCGCTCCAC CTGATCCTGC ACTGCTCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA
 ATCTTGTCTC GAGCTTCTC TATGCCACTC ATGGCTCTCT TTCTGCTCTT TCCATCTTTT TGCTGAGAGT
 TACTGAGCTC TGTACTTCT CTTGGCCCAT CTCATCTCT GAAACACCC TGAAGAGGGT TGCTTATCTT
 GATGGAAGT AAAAGGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA
 GCAGCACTTT CAGATTAGT CCATATAGAG CTGTCTTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC
 ATAAAGGGGC TGGAGTGAC CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCAA GAGATCACCC
 55 CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA
 CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT CTGTGCTGGT CACCTGTCCC TGTGGAGGTT
 CCCCTGGGAA GGCAGATGC CCAACAACAG CACTGCTCTG CGAATTCGGG GGACATCTGT TTGGGGAAGT
 AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT
 GCGGTGCATA AACC GGCTGG AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG TTCCAAGAG

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ATCACCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTAGACT GTCACTGCAC ATGGACCTCT
 GGGGAAGACGT CTGCGGAGAG CTAGGCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC CTGTCCCTGT
 GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT
 CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT GGTCAAGCTG
 5 AACCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT CTCTAGCCCT GCCTGTGGGG
 TGCTGGTCAT GCCITTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTAT
 GACTTGCTTA CTGCTTATCT TTACCCACGC CTCCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC
 TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG GCCCTGGGCC
 TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT GTTTGGCTGG AACATGAAAC TGACCTCAGA
 10 GTACCACAGA AATCTCACCT TCCTTTCATG CCAATTGTG TCCGTCATGA GGATGGACTA CATGGTATAC
 TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA
 TCATTCGGAA CAACTCAGT CTGAACTTAT CTAAGTCCAA AGAGACAGGT GCATTTTATG GACGGGAGTT
 CAAGACGGCT AAGTCTTGT TTCTGGTTCT TTTCTGTGTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC
 AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG
 15 CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTTGAT
 CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATCTTTG GACACAAGCA TTGAGAAGAA TTCTGAGTAG
 TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG AGGCCTGTA
 TGCCTGGGCC AAGCTGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA
 ATTATATCTC CCCCCTCCA CTACTCTCTT CCTCCACTTC ATTTTCTCTT TGTCTTTCT CTCTAATTCA
 20 GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCTTTC TTCCCAATAG
 AAGAATAAGT CATC GAGCCT GAAGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA
 TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT
 AGGAGATGTT GGGAAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C -3' (FRAG.
 NO:1675) (SEQ. ID NO:3007)
 25 5'- CGAATTCGGG GCACATCTGT TTGGGGAAC T AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG
 TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA
 GCCCTTTCTA AGGAAGAAGG TTTCCAAGAG ATCACCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA
 ATTTAGACT GTCACTGCAC ATGGACCTCT CTGGCGAGAG CTAGGCCAC TAGGCCACACA TGCCCTACA
 30 GACGGATCTT GCTGGCTCAC CTGTCCCTGT GGAGGTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC
 TGCTCTGTCA TTGGCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC
 AACGTGCTGG TCATCTGCGT GGTCAGCTG AACCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT
 CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT
 CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCTTA CTGCTTATCT TTACCCACGC CTCCATCATG
 35 TCCTTGCTGG CCATCTGCTG GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA
 CTCACAGAAG AATCTGGCTG GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT
 GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTGTGTT
 TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA
 TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAACTCAGT CTGAACTTAT CTAAGTCCAA
 40 AGAGACAGGT GCACTTTATG GACGGGAGTT CAAGACGGCT AAGTCTTGT TTCTGGTTCT TTTCTGTTT
 GCTCTGTCAT GGCTGCTT ATCTCTCAT AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG
 TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT
 AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG
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 45 TCCCCATCAA CAAACTCTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA
 CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCCTCCA CTACTCTCTT CCTCCACTTC
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 ATTATTGTCT GTTTCTTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT
 ACTGACAAAA GGCCTAGATT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT
 50 GAGCAGAGAA CCTCTCTCG GAGGATGCCT AGGAGATGTT GGGAAACAGAA GAAATAAACT GAGTTTAAGG
 GGGACTTAAA CTGCTGAATT C -3' (FRAG. NO:) (SEQ. ID NO:2439)
 5'- CTGCTGAATT TTATTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC
 TGTGTGGGTT GGGTCCAAGT GTTCTTGCT GCTGCCTCTC TAACACGCCCT GGTAAAAATA ATCCCTTTGG
 ATGGTGCTGA GAACACCTG AACCAAGTGG GTCCCAAAAT AACTATGGCG TGCAAGTGTC TGGTCCCAG
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 55 TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGACACAG TTCTTTTCCC
 TTCTTTCTGT ATGTTGGTC ATTCTGCTAT TCTGTCGTT CTCACATAGG TTGGACATTG GCCGGCTGCC
 AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA
 TGCTTCTCAG AGGTGCTGAG TTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT
 CTTTGCTCCA AAGGTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAAGT TAGCAGGAAT

TCCGTCATGA GGA1GGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA
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 AGAGACAGGT GCA' TTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTCTT TTTCTTGT
 GCTCTGTCAT GGCTGCCTTT ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG
 5 TGTGTACAT GGGCATCCTG CTGTCCCATG CCTCAAAGCC GATGAACCTT ATCGTCTATG CCTATAAAAT
 AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG
 GACACAAGCA TTGA/GAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT
 TCCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA
 CTGAGGTGGG AGCCTCTCCA GTGCTCCCCA ATTATATCTC CCCCCTCCA CTACTCTCTT CCTCCACTTC
 10 ATTTTCTCTT TGCTCTTTCT CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT
 ATTATTGTCT GTTT' CCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT
 ACTGACAAAA GGCCTAGATT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT
 GAGCAGAGAA CCTC CTCTCG GAGGATGCCT AGGAGATGTT GGGAAACAGAA GAAATAAACT GAGTTTAAGG
 GGGACTTAAA CTGCTGAATT C -3' (FRAG. NO:) (SEQ. ID NO:2427)
 15 5'-TTCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG
 TGGGTATTCT TTCTATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAACCCCTT TTCCTTGGTT
 TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT
 TTTTTCAGT ATTTAACTAA GGTCAAAGA GTGCTATATA GTGAGAAAGG CTCTTTTTTT TTTTTTTTTT
 TTTTTTGGCA GAGTGTCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA
 20 AACAATTACA GTACAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG
 CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT
 TTTTAATGTC TGGGAGTCT GCTCAGGGAG AAATGACAAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA
 GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA
 ACTAACAAGA GGAUCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT
 25 AGTAAACACC AGAAGCCCAT TGTTGTACT GCTGAATTTT ATTTTGGGCT GTACATATTG AGATGCTTAA
 GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GTTCCAAGTG TTCTTCTTGT CTGCCCTCTC
 AACACGCCCTG GTTAAATAAA TCCTTTTGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA
 ACAATGGCGT GCAAGGTGCT GGTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG
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 30 CATTTGATTC TGTGACAC GTTCTTTTCC CTCTTTCTG TATGTCTGGT CATCTGCTA TTCTGTCTGT
 CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA
 GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCT TCTGAGCAGG
 GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG
 CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT
 35 TTTTGTCTCT CTGCTTCTCC CGTTTGCCTC CTATCATGA GATCTTTTGT CTAAGCTGGC AGAAAGATTG
 CATAGTCACT GCTTCCAGCT CTGCTCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT
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 TGCTGAGAGT TCTGAGCTCT GTACTTCTC TTGGCCATC TCACTTCTG AAACACCCCT GAAGAGGGTT
 GCTTATCTTG ATGGA ACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA
 40 CTAAGAGCAG CAGCACTTTC AGATTCAAGT CATATAGAGC TGTCCTACAG CATCTGGAA ACTTGAGGAT
 GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTCCTAAG
 AGATACCCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTGA CTGTCACTGC ACATGGACCT
 CTGGGAAGAC GTCGGCGAG GCTAGGCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT
 GTGGAGGTTT CCTCGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC
 45 TCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCACTGCT GGTGCAAGC
 TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTCAATTGT CTCTCTAGCC TGGCTGACA TTGCTGTTGG
 GGTGCTGGTC ATGCTTTTGG CCATTGTTGT CAGCCTGGGC TCACAATCC ACTTCTACAG CTGCCTTTTT
 ATGACTTGCC TACTGCTTAT CTTTACCCAC CCTCCATCA TGTCTTGTG GGCCATCGCT GTGGACCGAT
 ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA
 50 TGAGGCTACA AGCCA/GAGC-3' (FRAG. NO:) (SEQ. ID NO:2426)
 5'-GGGCAATTTG TTA/GTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCC GCGCGG
 GCGCAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA
 TGGGTGCCGC CTCTTGGCCG CGGGGGGGCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG
 CTCAGAAGCG GCACGCGGAG GCGCGGTCCG GCGGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC
 55 CTCGCCCGGC GCGCTTTCGG TAGGGGGCGC CCGGGGGCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG
 GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG
 CCGCGGTGGG CACGCGGAAC ACTCTGCAGA CGCCACCAA CTAATCTCTG GTGTCCCTGG CTGCGGCCGA
 CGTGGCCGTG GGGCTCTTCG CCATCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC
 GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGCGCGTGG

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[illegible]

5'-GGG TCT TGC TCT GGG CCT GGC TGT-3' (FRAG 1000) (SEQ. ID NO: 1010)

5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG 1001) (SEQ. ID NO: 1011)

5'-GCT GCC TCC GTT IGG GTG GC (FRAG 1002) (SEQ. ID NO: 1012)

5'-TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA (FRAG 1003) (SEQ. ID NO: 1013)

5 5'-TCT CTG BBT BTT (GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB (FRAG 1004) (SEQ. ID NO: 1014)

Human IgE Receptor α Subunit Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG
GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT
GGA GC BCB GTB GEG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC
10 TTB GGT TTC TGB GCG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT
GGT TCT CTT BCB GIB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG
BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1691) (SEQ. ID NO: 1704)

5'-TGG BCT CC -3' (FRAG. NO: 1692) (SEQ. ID NO: 1705)

5'-CCB TCT GGB-3' (FRAG. NO: 1693) (SEQ. ID NO: 1706)

15 5'-CT GCT BBC BCG-3' (FRAG. NO: 1694) (SEQ. ID NO: 1707)

5'-GTT TTT GGG GTT TG-3' (FRAG. NO: 1695) (SEQ. ID NO: 1708)

5'-GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO: 1005) (SEQ. ID NO: 1015)

5'-ACAGTAGAGTAGGGATTCCATGGCAGGAGCCATCTTCTTCATGGACTCC-3' (FRAG. NO: 1006) (SEQ. ID NO: 1016)

20 5'-TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC-3' (FRAG. NO: 1007) (SEQ. ID NO: 1017)

5'-BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT
TTC TGB GGG-3' (FRAG. NO: 1008) (SEQ. ID NO: 1018)

5'-BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1009) (SEQ. ID NO: 1019)

5'-GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO: 1010) (SEQ. ID NO: 1020)

25 5'-GCC TTT CCT GGT TCT CTT-3' (FRAG. NO: 1011) (SEQ. ID NO: 1021)

5'-BCBGTBGBGTBGGGGBTTCBTTGGCBGGBCCBCTTCTTCTBTTGGBCTCC-3' (FRAG. NO: 1012) (SEQ. ID NO: 1022)

5'-TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1013) (SEQ. ID NO: 1023)

Human IgE Receptor (Fc Epsilon R) Nucleic Acid and Antisense Oligonucleotide Fragments

30 5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC
CGG GCT GTG G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C
CCC BGB BCG BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT
CTC TGA ATA TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC
CTG CTT GGB-3' (FRAG: 1696) (SEQ. ID NO: 1709)

35 5'-TCG TTC CTC TCG-3' (FRAG: 1697) (SEQ. ID NO: 3001)

5'-BGB BCG BGB C-3' (FRAG: 1698) (SEQ. ID NO: 1711)

5'-TGB BTB TTGB-3' (FRAG: 1699) (SEQ. ID NO: 1712)

5'-GCC TGT GTC TGT CCT CCT-3' (FRAG. NO: 1014) (SEQ. ID NO: 1024)

5'-GCT TCG TTC CTC TCG TTC-3' (FRAG. NO: 1015) (SEQ. ID NO: 1025)

40 5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG. NO: 1016) (SEQ. ID NO: 1026)

5'-GTC CTG CTC CTC CCG GCT GTG G-3' (FRAG. NO: 1017) (SEQ. ID NO: 1027)

5'-GTC CTG GCC CTC GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG. NO: 1018) (SEQ. ID NO: 1028)

5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG. NO: 1019) (SEQ. ID NO: 1029)

5'-CCC BGB BCG BGB CCC GGB CCG BCB-3' (FRAG. NO: 1020) (SEQ. ID NO: 1030)

45 5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG. NO: 1021) (SEQ. ID NO: 1031)

5'-GCT GCC TCC GTT TGG GTG GC-3' (FRAG. NO: 1022) (SEQ. ID NO: 1032)

5'-GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' (FRAG. NO: 1023) (SEQ. ID NO: 1033)

Human High Affinity IgE Receptor Oligonucleotide Fragments

50 5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT
ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTAGAT TTTATGTGTT TGAACCCCAA
ATTAGTTATT TAATAGTTGG CACCCAAAA CAAGTTACTT AACCTCACTA AGGTTCACTT TTCCTGTTTA
TAAATGTAG ATACTGATAG TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT
TTAGGATAAC ACCTGGCATA TGTTTGGTAT TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC
ATCCCACTTT TCTAAGTTGT AAATAAATA GTTGATACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG
55 TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG ATAGGGAGTG
GAGTAAGTGG GTAATATTA AATTGCCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA GAAAGAAGCA
AAACCAGGCA CAGCTGATGG GTTAACCAGA TATGATACAG AAAACATTTC CTTCTGCTTT TTGGTTTAA
GCCTATATTT GAAGCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG GATCTTCATG
TGGAATGACT GGTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA TGATAGAATG
60 GTTCCTCAAG TGCTTCAGAT GTGAAGTGGG TTAAATATA CTGTCCCTGT CTCTTCAGA GTTTTGGTAA



5	AGATAAAATA	GGACACTCAT	TTAAAAGCAA	TCTTTGCAAA	TGACAAGCCA	CTATAGACAT	TAATAGAGTT
	TTCATTTCCA	GTATATCAT	TAATATCAGA	TCCTGGAAAG	AGGTTGAGCC	TTGACCTAGA	GCAAAAAAAC
	AGAAGAATTA	GTAAAGGAAT	CCTGGAGAAA	GCCCCTGCTG	TGTATTTAAA	GGAGAAAGGG	AGATCATGTT
	GGGAAATTAT	AATAATTAATA	GTAAACAAAA	GCTAGGAAGT	AAAATAAAAT	AAATTATATG	GCCTAGATCC
	CCATAAGTAA	TGGTTTAACT	TCTGCCTTCC	TGTGTTCTGA	GCCAGATTAG	GGCACAGTAG	AGAAAAGAGGA
10	GTCTCTGAAA	ATGTTTCCA	TTTCGCTGGT	CAGACAGCGG	ATCATCAGTG	AATCAGATGA	AAATTTGTGG
	ATTTATGCAC	TAACATGATCA	GCAGGAAATT	AAACAAGAAA	AGCGTTGGTA	GCTCTGGTGA	ATCCCAAAAG
	AAATTTGGCAG	TTGCTAGCCA	TGCTCTGTAA	TATGTATAAA	CAGTACATCA	TATGACTAAG	AGTTTGACTT
	AGGGGTTAGA	TTTATGTGT	TTGAACCCCA	AATTAGTTAT	TTAATAGTTG	GCACCCCAAA	ACAAGTTACT
	TAACTCACT	AAGATTCAGT	TTTCCTGTTT	ATAAAATGTA	GATAGTGATA	GTATGTACTT	TATAGGATTA
15	TTGTGAAAAA	TAAATGAAAT	ATCAGATTTA	TTTAGGATAA	CACCTGGCAT	ATGTTTGGTA	TTCAGTAAT
	AGTTGCTGCT	GTTTATTCT	GCTCTCCCTT	GCATCCCCT	TTTCTAAGTT	GTAAACTAAA	TAGTTGTACA
	CAGATTGACA	GATTAAAGAA	GGCTTGTGAT	TGTGCTAGAC	CTATGCCTCT	CTCTACCAG	ATTCCAGGTG
	TATATTGTGA	GGTGGGATAG	GGAGTGGAGT	AAGTGGGTAA	ATATTAAATT	GCCCAGTTGG	GCACCATCTC
	GAATATTATC	TCTAAGAAA	GAAGCAAAAC	CAGGCACAGC	TGATGGGTTA	ACAGAGATAT	ATACAGAAAA
20	CATTTCCITC	TGCTTTTGG	TTTTAAGCCT	ATATTTGAAG	CCTTAGATCT	CTCCAGCACA	GTAAGCACCA
	GGAGTCCATG	AAGAGATGG	CTCCTGCCAT	GGAATCCCCT	ACTCTACTGT	GTGTAGCCTT	ACTGTTCTTC
	GGTAAGTAGA	GATICAATTA	CCCCTCCCAG	GGAGGCCCAA	ATGAATTTGG	GGAGCAGCTG	GGGTAGGAAC
	CTTTACTGTG	GGTGGTGACT	TTTTCTAGGA	CATGTGCAAA	CTATTGGGCA	TTTCCCAGGG	ACTCTGTAGT
	GGAGCCAAGC	TAGAAAGCAG	AGGCAAGTGG	GCTGAGCAAC	ACCTAAGGAG	GAAGCCAGAC	TGAAAGCTTG
25	GTTCCTTGCA	TTTGCTCTGG	CATCTTCCAG	AGTGCAAATT	TCCTACCAAG	GTAATGAGGG	TAGAGGAGAG
	AAAGAACTC	TTTCTCCCC	TGATTCTCAT	TCCTGAAAAG	ACGGTTGGTC	CTTAAAATTC	CATGGATGTA
	GATGTTATCT	CCACACCCAG	ATTCTAGTCC	TCTGGAGATA	AAGAAGACTG	CTGGACACTA	ATGTATCTCT
	TCTGGACTTT	TGCAGCTCCA	GATGGCGTGT	TAGCAGGTGA	GTCTCTGT	CTTGTTCCCT	TGGTGTATCA
	ACATGTCTGG	GCAATGCTTT	CCTCTCACTA	TTTTCTTCGT	CCCATCACTT	CTGCTTTCTA	ATGAGCATGA
30	ATCTGTTTCT	TGGCCAGACT	ACTTTCCTCT	TCCACCTTGC	CTTGCTTTTC	TTTTTTTCCC	TGATTTCATTG
	CATTCTCTCA	AGTCATTCTC	TCCTCTGTTT	TAGTCAATAA	CCATGCTGTG	TGCACATATA	CATGTCTCAT
	TCTCTCTCCT	AGACACTTTG	GCATGATCTC	GCTCAATAAT	TACATTATTA	TTATTATTGC	CATTTTATAA
	TTGAGGATGC	TGAATCTCAG	TGATTTTCTG	GTGGTTACAT	GGCTAAGGAA	CTGGATTCTA	ACGTAAGTTC
	CTTGAGTCTA	AGTCCAGTTC	TCTTCTGACT	ATATCCACCT	TTTGTTATCA	CCATGTATCT	ACTTCTTTGG
35	TCTCTGTTCA	AAATGCACT	ACATCCCTTT	GTTCACGGAA	GCCATTCAAG	ACTGACTTTT	TTAGTGCTCT
	TCACTACTTT	CTGGAAGTGA	CATATGTTTT	TCACTCTGTA	TATACTTACA	ATTAAATAGT	CATAAAATTT
	CAGAGCTTGG	AGAAACCTTA	TATTTTCATCC	AGTCCAGTAA	ATTTATCCAT	CCATAATTCA	CTCATTCATT
	CACATAATAA	ATAITTAATG	TAACAATGGT	TGAACATGGC	AGACAGTGTT	TCTACCTCAA	AAGAGATTGC
	AGTCCTCATT	TACAATATACT	GAATTGAAAT	TAACAGAAGT	AGAGTGAGTC	AGCTCAAATC	ACATAGTGAA
40	TTGGTTTCTT	TGTTTATAAA	TCTCCTGCAT	ATGTGTCCTG	TCTTCTCCCC	TGTGTTGGGC	GTTCCTTGGG
	GCACCAATAC	TAATTTCTCA	TTCCCTTAGA	AATCAAAACA	GGGTCTTATC	ACCAACAGAA	TAAGGACAGG
	TTGACCACTG	ATTCCTAGAA	TATTTCTTCG	TTTGACTTTT	TAAGCTTAGA	CAGTTTTTCA	TGACTTTTTT
	TCTCTCTACA	TGCTTTTCA	TATTTTATC	TTCTTGAAGT	CCCTCAGAAA	CCTAAGGTCT	CCTTGAACCC
	TCCATGGAAT	AGAAATTTTA	AAGGAGAGAA	TGTGACTCTT	ACATGTAATG	GGAACAATTT	CTTTGAAGTC
45	AGTTCCACCA	AATGGTTCCA	CAATGGCAGC	CTTTCAGAAG	AGACAAATTC	AAGTTTGAAT	ATTGTGAATG
	CCAAATTTGA	AGACAGTGGA	GAATACAAAT	GTCAGCACCA	ACAAGTTAAT	GAGAGTGAAC	CTGTGTACCT
	GGAGTCTTTC	AGTGGAAGT	TCCAGGGATA	TGGAATATCA	GATCTCTCAT	GTGAGGGATG	GCTCATCTGA
	AGATGGGAAA	AAACAGGTTA	TTCCAAGGGT	TAGGACACCA	GAGTGGGATT	CAAGGCCTCT	CATTTTTAAG
	ACCCCTGCAT	TGGCTGGGCA	CAGTGGCTCA	CGCTGTAAT	CCCAGCACTT	TGGGAGGCTT	AGGCAGGTGG
50	ATCACAGAGT	CAGCAGATCG	AGACCATCCG	GCTAACATGG	TGAAACCCCA	TCTCTGCTAA	AAAATATATA
	TATATAAAAT	TAGCCGGGCG	TAGTGGTGGG	CACCTGTAGT	CCCAGGTACT	CGGGAGGCTG	AGGCAGGAGA
	ATGGTGTGAA	CCCAGGAGGT	GGAGGTTGCA	GTGAGCTGAG	ATCACGCCAC	TGCCCTCCAG	CCTGGGCTAC
	AGAGCAAGAC	TCCCTCTCAA	AAAATAAATA	AATAAATAAA	AAAGACCCCT	GCATCTCTTT	TCTTCTACCC
	CCTTCCCTTT	TGATFACTTG	TATGCCTTCT	TTCAATATTC	TAGTCATCTC	TCAATATTAT	TCCTCCACCC
55	TATTTTCTCT	TATCTTTTCT	GCCTAGATTG	AGGTATATAT	TATGTGGTCA	AACAGCATGA	CATATATGTG
	AACATTTCAA	AGACCTGTGT	ATCTGGAATA	GGATCAAAAG	GTTTGACTTA	AAGTTTGTCT	CTGCAATAAT
	CATATGGCAG	GACCTGAATA	TTAGGTTGTA	CTCTTCGTTA	TGAAACATAT	CTGGGTACAT	TTCTTATAGT
	CCTCTGTTGT	TACTTAAGAA	CACATATTTC	ATGCTTGTTT	CATTTTATAT	ACTCCTACTG	CCAACAATAA
	GCATAGCATG	CTTAGGCACA	TGTGGCTTAA	TTAGCAAAATG			

[illegible]



	CTATAATTAA	CAC TAGAACT	GGGAAGTTTC	TATAAGGTAA	GAGAGGACAA	AATAGACACT	CTCCTAAGCT
	AAAATTCCCA	AGA AAGACTG	TTTATTTTCC	CCTAACTAAC	TAGAACTAGC	AACAGAAGAT	CTGAAAAGGAA
	TTCTGGCTTT	CAAC TGTTCC	ATGTATGGAC	TCATCAGGGA	GGTCCGAGAG	GCTTTGTGGC	CCCAGACTGA
	CTTTTCAGGA	GGG GAAAGGA	TTTATCAATA	CACAAGACAG	GCTCTAAGCA	TTATTTTGTG	CCCTTTAAAA
5	ATCCACTTTA	TGAC CCAAAA	AGTGAGTTAA	TGATAATTCA	TAGTTTCTGA	CACATGCTCT	ATGCGTGGCT
	CTCTTTTCTC	TATT CATTCT	CTCTCTCTTC	ATTTATTGTT	AAATAAAATA	TGTAATGAAT	GTTCTTCAGA
	CTGGCTGCTC	CTT CAGGCT	CTGCTGAGGT	GGTGATGGAG	GGCCAGCCCC	TCTTCCTCAG	GTGCCATGGT
	TGGAGGAAGT	GGGATGTGTA	CAAGGTGATC	TATTATAAGG	ATGGTGAAAGC	TCTCAAGTAC	TGGTATGAGA
10	ACCACAACAT	CTCC ATTACA	AATGCCACAG	TTGAAGACAG	TGGAACCTAC	TACTGTACGG	GCAAAGTGTG
	GCAGCTGGAC	TATGAGTCTG	AGCCCCCTCA	CATTACTGTA	ATAAAAGGTG	AGTTGGTAAA	GGAAAGGAAA
	AGCATCCATA	GCAGGGGAAG	GAAGAGAGAA	CTTCTGAGCC	TGAGCAGTTG	CAGCTTGTAG	AAGGGGGGCA
	CCTGTGATAC	ACTC GAAAGC	CTACCAGACT	TGCAATGAGG	AGACCTGGGT	GATAGTATAT	ATCTCAATCT
	CTGTTTCAAA	GCC T GACTT	GTAAATGGT	GATAGTAATA	CCTGCTTGCA	CTATGAAATT	TTTATGAAGA
	TTAATGTGGT	AA T A TTTGTG	AAATGACTTT	GTAACCTGTT	AAGCACTACC	CAAGCATAAC	AGATTGTGAT
15	TACTATTTTG	ATCT CAAAGT	CATCTGTTCG	TCCTGGGGGA	ACACTTATAT	TTATCAAATT	GAATAAAAGT
	TTCAAAGTTG	AATC AAGAAA	GGATATAAAG	AGCTTGAGGA	GCCCATTCCA	GCTTAGGAGG	GCTGGGAAGG
	GAAACCAGCA	AGTCAGTAAG	CTGTGTGCCT	GTGTATTGAG	GGAGGAGGGA	ATGGACTTGA	TATGGAGAGG
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20	GCCTGTGAAG	TAT CACTTT	TGAAGGAGAA	AGTTAGACTT	TTCTTCACA	CAC TTTGTAC	ATAATAATGT
	TTAAAAAAGC	ATG AGGTCAA	AATACATAAT	TAAGTCCTAG	CAGTTCTCTG	TTAACTAATT	TGAGACTGAA
	GTGCTATGTA	CTTCTCTCTA	GGCTTCCAGT	ATCTTCATCT	GTA AACAGA	ATATTTGGTC	TAGATTCCAT
	TAGAATCATT	TGA CAACTTA	AAAAATATAT	TGATGCTCAT	GTCTCATTTT	TTGAGATTCT	GATTTAATTG
	GTTTGGGGTG	CAGCTGGGT	ATACGTATTT	TTCATAGGTC	TTTCACATAA	TGGTAATGGG	TAGCCAATAT
25	TGAGAATCAC	TTG C TAGGT	GATCTTTAAA	TGATTTCTGG	ATGTAATATT	CTGAGGCTCT	ATAATTTAG
	ACTAATCACA	AAA TCGGTA	CAGTTTATAA	ACAGACTAAC	AGA ACCACAA	AATAATAGAA	TTGGAAGGCA
	ATTTAACTAG	TGC A TTTCT	TCATTTTGCC	TAACAGGCAT	GTAAGAAATG	ATGATTGATT	GAGTAATAGG
	CATTGATGAC	CCC TGTCTC	ACTTTGTCCC	CTTCCACCC	CTTAATTATA	TGTGAATTCT	GGTCTTGTCA
	TTTCGAATAA	GGG GTTATC	TTTCCTATTG	TCTTCCCCTC	TGGGCACGGC	ACACTGGCTA	CTGGAATTAA
30	GAGGAAATGC	TTAGGACTCC	CTGTGGCTCC	AGGGAGCACC	AACAGAGCAA	CTCAACCTAG	TGTTAATCTG
	AGTGTTTTCT	CTGTGCTTCT	GGATGCCACA	TCACGCTAAA	AATGAAGGAC	AAAGCTTGGT	CTTTCTCTTA
	GGGAGGATGA	AAC TCTGAAC	CTCATTTTTT	AGTTCCCAAG	ATGAATTATG	TTTCTCATTT	CATCTGTGTT
	CCACTACAGC	TCCGCGTGAG	AAGTACTGGC	TACAATTTT	TATCCCATTG	TTGGTGGTGA	TTCTGTTTGC
	TGTGGACACA	GGATATTTTA	TCTCAACTCA	GCAGCAGGTC	ACATTTCTCT	TGAAGATTAA	GAGAACCAGG
35	AAAGGCTTCA	GAC TCTGAA	CCCACATCCT	AAGCCAAACC	CCAAAAACAA	CTGATATAAT	TACTCAAGAA
	ATATTTGCAA	CAT T AGTTTT	TTTCCAGCAT	CAGCAATTGC	TACTCAATTG	TCAAACACAG	CTTGCAATAT
	ACATAGAAAC	GTC TGTGCT	AAGGATTTAT	AGAAATGCTT	CATTAAACTG	AGTGAAACTG	GTTAAGTGGC
	ATGTAATAGT	AAG T GCTCAA	TTAACAATTGG	TTGAATAAAT	GAGAGAATGA	ATAGATTCAAT	TTATTAGCAT
	TTGTAAAAGA	GAT TGTCAAT	TTCAATAAAA	TAAATATAAA	ACCATTGAAC	AGAATTGCTT	TGAGATTCTA
40	AGGCTTGCTA	TTT T GTTTGT	TTGTTTCTA	CTAAAGGCAA	GGACCATGAA	GTCTAGATT	GGAAATGTCC
	TCTCTTGACT	ATTGCAAGTG	CGATCTAGGA	ATGAAAAGAC	ATAGGAGGAT	GCCAGTGAGG	TGGATCATTT
	TTATGCTTCT	TCTT CAGCTT	ACTAAAATAG	AACTTTCAGT	TCTTGGCAGA	ATCAGGGACA	GTCTCAAGAC
	ATAGGACTCT	CAGGATGAAG	TAGAGTCCAG	GATTCTCTCT	TGATTGTTTT	GCCCCTCCCA	AATTTATATC
	TTGAACTTAT	GTCTTGATC	TTTATACAGC	ACCTGAACCA	AGCATTTTGG	AGAAATTCCA	GCTAATAATA
45	ATAACCAAAA	CCT TCGGCTC	TGAAAACAGT	CCAGGACTGA	ATAAGATCTT	GGGCAAAAGA	ACTAGACAGT
	TTTGGTTTAT	TTTCCCTTTC	ATTTTATGTC	TTTATCATAG	TCATTGGAGG	CTCATTCTTC	TTGTCATGCT
	GTAAATGGGA	TTA T AGTTT	TACTAAGAGT	CTCCAGCATC	CTCCACTTGT	CTACCACCGA	GCATGGGCTT
	ATATTTGAAG	CCT T AGATCT	CTCCAGCACA	GTAAGCACCA	GGAGTCCATG	AAGAAGATGG	CTCCTGCCAT
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50	AAACCTAAGG	TCTCTTGAA	CCCTCCATGG	AATAGAATAT	TTAAAGGAGA	GAATGTGACT	CTTACATGTA
	ATGGGAAACAA	TTTCTTTGAA	GTCAGTTCCA	CCAAATGGTT	CCACAATGGC	AGCCTTTCAG	AAGAGACAAA
	TTCAAGTTTG	AATATTGTGA	ATGCCAAATT	TGAAGACAGT	GGAGAATACA	AATGTCAGCA	CCACAAGTT
	AATGAGAGTG	AAC CTGTGTA	CCTGGAAGTC	TTCAGTGACT	GGTGCTCTCT	TCAGGCTCT	GCTGAGGTGG
	TGATGGAGGG	CCAGCCCCCT	TTCTCAGGT	GCCATGGTTG	GAGGAACCTGG	GATGTGTACA	AGGTGATCTA
55	TTATAAGGAT	GGTGAAGCTC	TCAAGTACTG	GTATGAGAAC	CACAACATCT	CCATTACAAA	TGCCACAGTT
	GAAGACAGTG	GAA CTACTA	CTGTACGGGC	AAAGTGTGGC	AGCTGGACTA	TGAGTCTGAG	CCCTCAACA
	TTACTGTAAT	AAAAGCTCCG	CGTGAGAAGT	ACTGGCTACA	ATTTTTTATC	CCATTGTTGG	TGGTGATTCT
	GTTTGCTGTG	GAC A CAGGAT	TATTTATCTC	AACTCAGCAG	CAGGTCACAT	TTCTCTTGAA	GATTAAGAGA
	ACCAGGAAAG	GCT C CAGACT	TCTGAACCCA	CATCCTAAGC	CAAACCCCAA	AAACAACCTGA	TATAATTACT
60	CAAGAAATAT	TTGCAACATT	AGTTTTTTTC	CAGCATCAGC	AATTGCTACT	CAATTGTCAA	ACACAGCTTG
	CAATATACAT	AGAAACGTCT	GTGCTCAAGG	ATTTATAGAA	ATGCTTCATT	AAACTGAGTG	AAACTGGTAT
	AGTGGCATGT	AATAAGTAGT	GCTCAATTAA	CATTGGTTGA	ATAAATGAGA	GAATGAATAG	ATTCATTTTA
	TAGCATTTGT	AAA T GAGATG	TTCAATTTCA	ATAAAAATAA	TATAAAACCA	TGTAACAGAA	TGCTTCTGAA



	TAAAAA	AAA/AAAA	AAAAAA	TCTCAATATA	ATAATATTCT	TTATTCCCTGG	ACAGCTCGGT
	TAATGAAAA	ATGC ACACAG	AAAGTAATAG	GAGAGCAAAT	CTTGCTCTCC	CACAGGAGCC	TTCCAGTGTG
	CCTGCATTTC	AAGTCTTGGA	AATATCTCCC	CAGGAAGTAT	CTTCAGGCAG	ACTATTGAAG	TCGGCCTCAT
	CCCCACCCT	GCATACATGG	CTGACAGTTT	TGAAAAAGA	GCAGGAGTTC	CTGGGGGTAA	CACAAATTCT
5	GACTGCTATG	ATAIGCCTTT	TTTTTGGAAC	AGTTGTCTGC	TCTGTACTTG	ATATTTCACA	CATTGAGGGA
	GACATTTTTT	CATCATTAA	AGCAGGTTAT	CCATTCTGGG	GAGCCATATT	TTTTTCTATT	TCTGGAATGT
	TGTCAATTAT	ATCTGAAAG	AGAAATGCAA	CATATCTGGT	GAGAGGAAGC	CTGGGAGCAA	ACACTGCCAG
	CAGCATAGCT	GGGC GAACGG	GAATTACCAT	CCTGATCATC	AACTTGAAGA	AGAGCTTGGC	CTATATCCAC
	ATCCACAGTT	GCCA GAAATT	TTTTGAGACC	AAGTGCTTTA	TGGCTTCCTT	TTCCACTGAA	ATTGTAGTGA
10	TGATGCTGTT	TCTCACCAT	CTGGGACTTG	GTAGTGCTGT	GTCACTCACA	ATCTGTGGAG	CTGGGGAAGA
	ACTCAAAGGA	AAC/AGGTTC	CAGAGGATCG	TGTTTATGAA	GAATTAAACA	TATATTCAGC	TACTTACAGT
	GAGTTGGAAG	ACCCAGGGGA	AATGTCTCCT	CCCATTGATT	TATAAGAATC	ACGTGTCAG	AACACTCTGA
	TTCACAGCCA	AGG/TCCAGA	AGGCCAAGGT	CTTGTTAAGG	GGCTACTGGA	AAAAATTCTA	TTCTCTCCAC
	AGCCTGCTGG	TTTT AAGCTTT	TTC AAGGTGCAAT	TGGATAACTT	CTGCCATGAG	AAATGGCTGA	ATTGGGACAC
15	AAGTGGGGAC	AAT/CCAGAA	GAAGGGCACA	TCTCTTTCTT	TTCTGCAGTT	CTTTCTCACC	TTCTCAACTC
	CTACTAAAAAT	GTCTCATTTT	CAGGTTCTGT	AAATCCTGGT	AGTCTCAGGC	AAAAATTATG	TCCAGGAGTC
	TCAAATTTTC	TTATTTCATA	TTAGTCTTTA	TTTAGTAGAC	TTCTCAATTT	TTCTATTTCAT	CACAAGTAAA
	AGCCTGTTGA	TCTTAATCAG	CCAAGAAACT	TATCTGTCTG	GCAAAATGACT	TATGTATAAA	GAGAATCATC
	AATGTCATGA	GGTAACCCAT	TTCAACTGCC	TATTCAGAGC	ATGCAGTAAG	AGGAAATCCA	CCAAGTCTCA
20	ATATAATAAT	ATTCTTTATT	CCTGGACAGC	TCGGTTAATG	AAAAAATGGA	CACAGAAAGT	AATAGGAGAG
	CAAATCTTGC	TCTCCACAG	GAGCCTTCCA	GGTAGGTACA	AGGTATTATT	TTTTTCTACC	CTCAGTCACT
	TGTGGCAGGG	GAAGTCATAG	TCACGGTGCT	TAGGAGATGA	AAC TTTATTG	ATTTAGGCAT	GGATCCATTG
	AGTTTAAATTA	ATAIATTTGG	TATGAGGAAG	CTACTGTCTG	TACTTTCCAT	GTGGTCTCTT	CTCCCTGGAG
	AGGAACATTT	TTACTCAGCT	TGCAAACTGG	AAATAGATTT	TCTCACATTA	GAAAGCTCATT	TTCTGGGTAT
25	GAGACAGGAG	AGT/CATACT	GTGTATGTAG	ATCTCTGGCT	TCTGGGTCTG	ACATGTGCTG	AGGGACACAT
	ATCCTTCACA	CATCCTTTTA	TAAATACTTG	ATAAAGTAAC	CTGCTTCTTG	ATTGGTCTTT	ATAATCCATA
	AGCTGTGGGA	TGCTTCTCTG	AAGATGAAAA	TAGTAATAGA	GTCCCATCTA	GCTATTCAAA	GCCATTCTCT
	CATTGTATTTC	TGTGCACATG	AAGTTGGGGT	TGTACTCTGA	CAAAATATAT	TCAGATACAT	TTCTATGTTA
	AAAGGATTGT	GAGATGTCATA	GGTAAATGTG	TTTATTTTCA	GTTTACTTGG	TCAACATAGA	TGAATGAGAA
30	AGAACTTGAA	AGT/AACACTG	GATTAAGAAT	AGGAAATTTT	GGCATGGATT	TGTCTCCATT	TTGTCCCATG
	TAATCACTGG	GAT/ATGTTTC	AGGTGTTCTT	GGTCAGTTAC	TGGATGCTCT	TGAGCTTTAG	TTTTCTGGTG
	ATTACAATGA	AGA/TTGAAT	TACAGGATGG	CTTTGAAAAA	ATAAACAAAA	CTCCCTTTTC	TGTCTGTCGA
	GAATGTTGCA	CAGGGAGTTA	CAGAATGTTT	TCATGACTGA	ATTGCTTTTA	AATTTACACAG	TGTGCTGCA
	TTTGAAGTCT	TGGAATATC	TCCCCAGGAA	GTATCTTCAG	GCAGACTATT	GAAAGTCGGC	TCATCCCCAC
35	CACTGCATAC	ATGC CTGACA	GTTTGA AAA	AAGAGCAGGA	GTTCTCTGGG	GTGAGTGAGC	CTCTCCAAC
	TTTGACTAGA	GTA/GGGTTG	GGTCTAGAAA	AGAATATTGA	GTTGCATCAA	CTGTTTTCCC	ACTTGGATTTC
	ATGAGAGGTT	TTAGTCTCTT	TAAAAACAT	GGTAGATAAA	GAGTTGACAC	TAAC TGGGTC	CTTTGGGAA
	GAGCCAGAAG	CAT/CTCTCA	TAAAGACTTT	AAATTGCTAG	GACGAGAATG	GCCAACAGGA	GTAAGAGGAT
	CATAACCTTA	CTTTFACTTA	GATGTAAAGA	ACAATTACTG	ATGTTCAACA	TGACTACATA	CATAAAGGCG
40	CATGGAGAAA	AGTATTGGCC	TTCCATGCAT	TAGGTAGTGC	TTGTATCAAT	TCTTATAGTG	GCTAGGGTAT
	CCTGGAAAAT	CTT/CGTGTG	GATCATTTCT	CAGGACAGTC	TAGGACACTA	ACGCAGTTTC	TCATGTTTGG
	CTTCTATTAT	TAAAAAATGA	TACAATCTCG	GGAAAAATTT	TTTGATTTTC	ATGAAATTCA	TGTGTTTTTC
	TATAGGTAAC	ACA/ATTCTG	ACTGCTATGA	TATGCCTTTG	TTTTGGAACA	GTGTCTGCT	CTGACTTGA
	TATTTACAC	ATTGAGGGAG	ACATTTTTTC	ATCATTTAA	GCAGGTATAT	CATTCTGGGG	AGCCATATTT
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	AGTTGTTTAT	TCCCAGTATT	AAGATGATAT	TTATAATTCT	TAAATATAAA	TATATGTGAG	CATATAAACC
	ATAGATATGC	TCA/TAAACAA	CAACAAAAGA	TTCTTTTAC	AATTAACGGT	GGGTTAAACA	TTTAGCCAC
	AGTTTATCC	CATGAGAAAC	CTGAATCTAA	TACAAGTTAA	ATGACTTGCC	TAAGGGCCAC	TTGACTAATA
	GTAATTGAAC	CTA/ACTTTC	AGAATCCAAC	TCCAGGAACA	TACTTCTAGC	ACTATTCATC	AATAAAGTTA
50	TATGATAAAT	ACA/TACAACT	TTATCTGTCA	ACTAAAAATA	ACAACAGAGG	CTGGGCATGG	TGGCTCACAC
	CCGTAATCCC	AGCACTTTGG	GAGGCTGAGG	CAGGTGGATC	ACCTGAGGTC	AGGAGTTTGA	GACCAGCCTG
	ACCAACATGG	TGA/ACCTCA	TCTCTACTAA	ATATAAAAAA	TTAGCTGAGT	GTGATAGTGC	ATACCTGTAA
	TCCAGCTACT	TAGAGGCTG	AGGCAGGAGG	CTTGTTTGA	CCTGGAAGGC	AGAGGTTGCA	GTGAGCTGAG
	ATT						

Bivariate correlations		Partial correlations	
1	2	1	2
1	0.28	1	0.28
2	0.28	2	0.28
3	0.28	3	0.28
4	0.28	4	0.28
5	0.28	5	0.28
6	0.28	6	0.28
7	0.28	7	0.28
8	0.28	8	0.28
9	0.28	9	0.28
10	0.28	10	0.28
11	0.28	11	0.28
12	0.28	12	0.28
13	0.28	13	0.28
14	0.28	14	0.28
15	0.28	15	0.28
16	0.28	16	0.28
17	0.28	17	0.28
18	0.28	18	0.28
19	0.28	19	0.28
20	0.28	20	0.28
21	0.28	21	0.28
22	0.28	22	0.28
23	0.28	23	0.28
24	0.28	24	0.28
25	0.28	25	0.28
26	0.28	26	0.28
27	0.28	27	0.28
28	0.28	28	0.28
29	0.28	29	0.28
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31	0.28	31	0.28
32	0.28	32	0.28
33	0.28	33	0.28
34	0.28	34	0.28
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44	0.28	44	0.28
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46	0.28	46	0.28
47	0.28	47	0.28
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85	0.28	85	0.28
86	0.28	86	0.28
87	0.28	87	0.28
88	0.28	88	0.28
89	0.28	89	0.28
90	0.28	90	0.28
91	0.28	91	0.28
92	0.28	92	0.28
93	0.28	93	0.28
94	0.28	94	0.2

ATTGACTTTG TCGTCTGCTA AATCCTTAGT GCTCAGATGA CTGTTCAGG ACTCTCCTTG AACCTGTACC
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35	CTGGAGTTAA	GAGGAAAATG	TTAGGACTCC	CTGTGGCTCC	AGGGAGCACC	AACAGAGCAA	CTCAACCTAG
	TGTTAATCTG	AGTCTTTTCT	CTGTGCTTCT	GGATGCCACA	TCACGCTAAA	AATGAAGGAC	AAAGCTTGGT
	CTTTCTCTTA	GGGAGGATGA	AACTCTGAAC	CTCATTTTTT	AGTTCCCAAG	ATGAATTATG	TTTCTCATTG
	CATCTGTGTT	CCACTACAGC	TCCGCGTGAG	AAGTACTGGC	TACAATTTTT	TATCCCATTG	TTGGTGGTGA
	TTCTGTTTGC	TGTGGACACA	GGATTATTTA	TCTCAACTCA	GCAGCAGGTC	ACATTTCTCT	TGAAGATTAA
40	GAGAACCAGG	AAAAGCTTCA	GACTTCTGAA	CCCACATCCT	AAGCCAAACC	CCAAAAACAA	CTGATATAAT
	TACTCAAGAA	ATAATTGCAA	CATTAGTTTT	TTTCCAGCAT	CAGCAATTGC	TACTCAATTG	TCAAACACAG
	CTTGCAATAT	ACATAGAAAC	GTCTGTGCTC	AAGGATTTAT	AGAAATGCTT	CATTAAACTG	AGTGAAACTG
	GTTAAGTGGC	ATGTAAATAGT	AAGTGTCTCA	TTAACATTGG	TTGAATAAAT	GAGAGAATGA	ATAGATTCTAT
	TTATTAGCAT	TTGTAAAGA	GATGTTCAAT	TTCAATAAAA	TAAATATAAA	ACCATGTAAC	AGATAGCTTC
45	TGAGTATTCA	AGGCTTGCTA	GTTTGTFTGT	TTGTTTTCTA	CTAAAGGCAA	GGACCATGAA	GTTCTAGATT
	GGAAATGTCC	TCTCTTGACT	ATTGCAAGTG	CGATCTAGGA	ATGAAAAGAC	ATAGGAGGAT	GCCAGTGAGG
	TGGATCATTT	TTATGCTTCT	TCTTCAGCTT	ACTAAATATG	AACTTTCAGT	TCTTGGCAGA	ATCAGGGACA
	GTCTCAAGAC	ATAGGACTCT	CAGGATGAAG	TAGAGTCCAG	GATTCTCTG	TGATTGTTTT	GCCCTCCCA
	AATTTATATC	TTGAACCTAT	GTCTTGTATC	TTTATACAGC	ACCTGAACCA	AGCATTTTGG	AGAAATTCCA
50	GCTAAATAA	ATAACCAAA	CCTTCGGCTC	TGAAAACAGT	CCAGGACTGA	ATAAGATCTT	GGGCAAAAGA
	ACTAGACAGT	TTTGCTTTAT	TTCCCTTTTC	ATTTTATGTC	TTCATCATAG	TCATTGGAGG	CTCATTCTTC
	TTGTCATGGA	GTAATGGGA	TTAA				

[illegible]

[illegible]

TGGTTTTCTG GAAATGAAAG AAATAATCAG AGTTTAATGA CAGAGAGCGT GAGACCCAGA AAGACAAAAG
 TAGATGAGGT AAGTCTCTTG AGCGAGACTT CTAGGGATGG GAAATTTGTG GTGATTGATA TGAAATGATT
 TTTCCCTTAT CAGCTTCCAG AGGATCGTGT TTATGAAGAA TTAAACATAT ATTCAGCTAC TTACAGTGAG
 5 TTGGAAGACC CAGGGGAAAT GTCTCCTCCC ATTGATTTAT AAGAATCACG TGTCAGAAAC ACTCTGATTC
 ACAGCCAAGG ATCCAGAAGG CCAAGGTTTT GTTAAGGGGC TACTGGAAAA ATTTCTATTG TCTCCACAGC
 CTGCTGGTTT TACAATTAGAT TTATTCGCCT GATAAGAATA TTTTGTCTCT GCTGCTCTG TCCACCTTAA
 TATGCTCCTT CTAATTGTAG ATATGATAGA CTCCTATTTT TCTTGTTTTA TATTATGACC ACACACATCT
 CTGCTGAAAA GTCACATATG AGTAAGCAAG ATTTAACTGT TTGATTATAA CTGTGCAAAT ACAGAAAAAA
 AGAAGGCTGG CTGAAAGTTG AGTTAAACTT TGACAGTTTG ATAATATTTG GTTCTTAGGG TTTTTTTTTT
 10 TTTTAGCATT CTTAATAGTT ACAGTTGGGC ATGATTTGTA CCATCCACCC ATACCCACAC AGTCACAGTC
 ACACACACAT ATGTAATTACT TACACTATAT ATAACCTCCT ATGCAAATAT TTTACCACCA GTCAATAATA
 CATTTTTGCC AAGAATGAA GTTTTATAAA GATCTGTATA ATTGCCTGAA TCACCAGCAC ATTCAGTGAC
 ATGATATTAT TTGCAGATTG ACAAGTAGGA AGTGGGGAAC TTTTATTAAG TTACTCGTTG TCTGGGGAGG
 TAAATAGGTT AAAACACAGG AAATTATAAG TGCAGAGATT AACATTTTAC AAATGTTTAG TGAAACATTT
 15 GTGAAAAAAG AAGACTAAAT TAAGACCTGA GCTGAAATAA AGTGACGTGG AAATGGAAAT AATGGTTATA
 TCTAAACAT GTACAAAAAG AGTAACTGGT AGATTTTGTG AACAAATTAA AGAATAAAGT TAGACAAGCA
 ACTGGTTGAC TAAATACATTA AGCGTTTGAG TCTAAGATGA AAGGAGAACA CTGGTTATGT TGATAGAATG
 ATAAAAAGGG TCGGGCGCGG AGGCTCACGC CTGTAATCCC AGCCCTTTGG GAGGCCGAGG TGGGCAGATC
 ACGAAGTCAG TAGTTTGAGA CCAGCTGGC CAACATAGTG AAACCCCGTC TCTACTAAAA ATACAAAAAA
 20 AAAATTAGCT GGGTGTGGTG CAGATCACCT GTAGTCCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC
 TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCAGTGAC TCCAGCCTTG GTGACAATGG
 GAGACTCCAT CTCAAAAAAA AAAAAAAGATA AAAAGTCAGA AATCTGAAAA GTGGAGGAAG
 AGTACAAATA GACTTAAATT AAGTCTCATT TTTTGGCTTT GATTTTGGGG AGACAAAGGG AAATGCAGCC
 ATAGAGGGCC TGAATGACATC CAATACATGA GTTCTGGTAA AGATAAAATT TGATACACGG TTTGGTGTCA
 25 TTATAAGAGA AATCTATTATT AAATGAAGCA AGTTAACACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA
 GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA CTAAGGATAA AATCTAGCCT AGAAGATACA
 ATAATTAGTC ATAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA AAATAGAGAA AGATTAGATA
 AAGAGAAAAAT AAGTATCCAT CAGAGACAGT ATCTCTAGGC TTGGGCAAGA GAAAAGTCCA CAGTGATAAG
 CAACTCCACC TAACGCATGA ATATGCGGCA GAGAAAACAG CAATAGTGAA TGAATGCAAA AGGTGCTGAG
 30 CAAATTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTGC AAAGACCTTT AGAGAAAGAG
 AATGGGAGCA TATCTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA
 AAAAAATTCTG TTTTAAAAAG AAGGAAAAGA TAGTTTATGT TTTAGCCTA AGTATAAGAG TCCTACAGAT
 GGACTGAAAA AAATCAGTCT GAGAGTATTA GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA
 TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT AGATTGTGAA AGTGATCACG ACAATCACAC
 35 AACAATAAT TAAATGACTT GGTATGCTTT ATTAAATTG AGGGCCTGAG GTTTTCCATT CTCATTTTTC
 TAAAAATCAA TTTTGTCTT CCAAAATTGA CAGCAATAA AAAACCCCTAC CCTTCTACTG TGTATCTGC
 TAAGCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTTACA
 TACAGACTCT TAACCTGCTT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTTA CAGTTGTATA
 GTATATGATA TCTCTTTTAT TTTACTCAAT TTATATTTTC ATCATTGACT ACATATTTCT TATACACAAC
 40 ACACAATTTA TGAATTTTTT CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG
 CCCACCTCAG GCAGACACAG AGCACAATGC TGGGGTTCTC TTCACACTAT CACTGCCCCA AATTGTCTTT
 CTAAATTTCA ACTTCAATGT CATCTTCTCC ATGAAGACCA CTGAATGAAC ACCTTTTCAT CCAGCCTTAA
 TTTCTTGCTC CATACTACT CTATCCCACG ATGCAGTATT GTATCATTA TTATTAGTGT GCTTGTGACC
 TCCTTATGTA TTCTCAATTA CCTGTATTTG TGCAATAAAT TGGAAATAATG TAACCTGATT TCTTATCTGT
 45 GTTTGTGTTG GCATGCAAGA TTTAGGTACT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAATGATG
 CCAAAGACCA AGATCAGTTT CTGAAGTCCT CCTTTTCATC AGCTCTTTAT CAAAACAGAAC ACTCTATAAA
 CAACCCATAG CCACAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA
 AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG
 AGCATGAGTC ATAATTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTTT
 50 TTCTCTTTGT GAACCTCAGG TTTTACATCT GAAATGAGA AATTTGGAAC AAAAGATTCT TAACCTGGTCT
 TTCTGTTCCC ATATTCTGTG ATTTTCAAT ATTTAGGATT TTTGGTAATC ACAATTACTT AGTTTGTGGT
 TGAGATAGCA ACACGAATCA GAACTATTTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA
 AAGAAAGTAT GCNGTCTGTC GTGGCTCACG CCTGTAATCC CAGCACTTTA GGGAGGCCAA GCGGGGTGGA
 TCACGAGGTC AGGAATGATCGA GACCATCCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA
 55 AAATTAGCCA GGCCTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGCA
 TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCCTGGG CAAAAGAGCA
 AGACTGCGTC TCAAAAAAAA AAAAAAAGAA AAAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA
 TAATATTTT CTAAATCCCT CTGAAAAATG CTAATCAAAG GGTTTTTTTC CTAAAAATTG TCTTAGAAAT
 AAAATTTCCC CTTTGGGAGA CCGAGGCTGG CAGATCACGA GGTCAAGGAG GGTCAAGACC GGTGAAACCC
 60 CGTCTCTACT AAAATACTA AAAATTAGCC GGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG
 GAGGCTGAGG CTGGAATC ACGTGAAC-3' (FRAG. NO:)(SEQ. ID NO:2504)

00440 " 6296560
 00440 " 6296560

Human Histidine Decarboxylase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CTC TGT CGC CTC CGC CCT GGC TGC
TGG GGT GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT
CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC-3' (FRAG. NO:1700) (SEQ. ID NO:1711)

5'-GGC TCT GGC (FRAG. NO:1701) (SEQ. ID NO: 1712)

5'-CCC TTG G (FRAG. NO:1702) (SEQ. ID NO: 1713)

5'- TT TGT TCT TCC (FRAG. NO:1703) (SEQ. ID NO: 1714)

5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' (FRAG. NO:1024) (SEQ. ID NO: 1034)

5'- TCT CTC TCC CTC TCT CTC TGT -3' (FRAG. NO:1025) (SEQ. ID NO:1035)

10 5'- CGC CTC CGC CCT GGC TGC TGG GGT GGT GC-3' (FRAG. NO:1026) (SEQ. ID NO:1036)

5'- TTT TGT TCT TCC TTG CTG CC-3' (FRAG. NO:1027) (SEQ. ID NO:1037)

5'- GCC CCG CTG CTT GTC T TC CTC G-3' (FRAG. NO:1028) (SEQ. ID NO:1038)

5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC (FRAG. NO:1029) (SEQ. ID NO:1039)

Human Beta Tryptase Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG
CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' (FRAG.
NO:1704) (SEQ. ID NO: 1715)

5'- GCT CCT GGG GGC CT-3' (FRAG. NO:1705) (SEQ. ID NO: 1716)

5'-CGT BGG CGC-3' (FRAG. NO:1706) (SEQ. ID NO: 1717)

20 5'-T GGC CTG GGG-3' (FRAG. NO:1707) (SEQ. ID NO: 1718)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1030) (SEQ. ID NO:1040)

5'-GTC CCT CCG GGT GTT CCC GGC-3' (FRAG. NO:1031) (SEQ. ID NO:1041)

5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB
GBT TCB GCB TCC TCG-3' (FRAG. NO:1032) (SEQ. ID NO:1042)

Human Tryptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT
BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3'
(FRAG. NO: 1708) (SEQ. ID NO:1719)

5'-CT CCT GGG GGC CTC CTG-3' (FRAG. NO:1709) (SEQ. ID NO:1720)

30 5'-B TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1710) (SEQ. ID NO:1721)

5'-GTC CCT C-3' (FRAG. NO:1711) (SEQ. ID NO:1722)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1033) (SEQ. ID NO:1043)

5'-GTC CCT CTG GCT G TT CCC GGC-3' (FRAG. NO:1034) (SEQ. ID NO:1044)

35 5'-CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC
TCB GCB TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1035) (SEQ. ID NO:1045)

Human Prostaglandin D Synthase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGT GTG CGG GGC CTG GTG CC CCT GGG CCT CGG GTG CTG CCT GT GCG CTG CCT TCT TCT CCT GG GTC
CTC GCC GGG GCC CTT GCT GCC CTG GCT GT GCC CTG GGG GTC TGG GTT CGG CTG T CCC CBG CBG GBC
CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG-3' (FRAG. NO:1712) (SEQ. ID NO:1723)

40 5'-T TCT CCT GCB GCC GBG -3' (FRAG. NO:1713) (SEQ. ID NO:1724)

5'-CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1714) (SEQ. ID NO:1725)

5'- TCT TCT CCT GG-3' (FRAG. NO:1715) (SEQ. ID NO:1726)

5'-GGT GTG CGG GGC CTG GTG CC-3' (FRAG. NO:1036) (SEQ. ID NO:1046)

5'-CCT GGG CCT CGG GTG CTG CCT GT-3' (FRAG. NO:1037) (SEQ. ID NO:1047)

45 5'-GCG CTG CCT TCT ICT CCT GG-3' (FRAG. NO:1038) (SEQ. ID NO:1048)

5'-GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1039) (SEQ. ID NO:1049)

5'-GCC CTG GGG GTC TGG GTT CGG CTG T-3' (FRAG. NO:1040) (SEQ. ID NO:1050)

5'-CCC CBG CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG -3'
(FRAG. NO:1041) (SEQ. ID NO:1051)

Human Cyclooxygenase-2 Nucleic Acid and Antisense Oligonucleotide Fragments

50 5'-GGG CGC GGG CGB GCB TCG C TTT GGG CTT TTC TCC TTT GGT T TGB GCG CCB GGB CCG CGC BCB GCB
GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG-3' (FRAG. NO: 1716) (SEQ. ID NO:1729)

5'-G GCB GGG -3' (FRAG. NO: 1717) (SEQ. ID NO: 1730)

5'-TCC TTT GGT T-3' (FRAG. NO:1718) (SEQ. ID NO:1731)

55 5'-GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3'
(FRAG. NO:1044) (SEQ. ID NO:1054)

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Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC-3' (FRAG. NO: 1719) (SEQ. ID NO: 1732)

5'-TTC TCC TTT GGT T-3' (FRAG. NO:1720) (SEQ. ID NO: 1733)

5'-T TTC TCC TTT GGT T-3' (FRAG. NO:1721) (SEQ. ID NO:1734)

5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO: 1722) (SEQ. ID NO: 1735)

5'-TTC CTG T-3' (FRAG. NO:1723) (SEQ. ID NO: 1736)

5'-CTC TTT CTG CT-3' (FRAG. NO: 1724) (SEQ. ID NO:1737)

5'-CCC CTT CTG TCC C-3' (FRAG. NO:1725) (SEQ. ID NO: 1738)

5'- GCC CTG CTG CTC TTT CTG CT-3' (FRAG. NO:1047) (SEQ. ID NO:1055)

5'- TCC CTT GGT GGG TTG GGC C-3' (FRAG. NO:1048) (SEQ. ID NO:1056)

5'- GCT GGT TGT TCT GGG GTT C-3' (FRAG. NO:1049) (SEQ. ID NO:1058)

5'- TTG CTG CCC CTT CTG TCC C-3' (FRAG. NO:1050) (SEQ. ID NO:1057)

5'- TGT TTG CTG GTG TCT GCG C -3' (FRAG. NO:1051) (SEQ. ID NO:1059)

5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO:1052) (SEQ. ID NO:1060)

Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCTT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCTT GTACGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG

30 GAGAAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAAGGTGGG TGGGGGGTTT CAGTCTCAA ACTCCCATGA AAACCAAGGA GAAGTTTCAG AACTCCACCC AAGAAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCATTCCC AGCTGGTGAA GCCTCGCTGC

35 AGAGATGCAT CTGCTCCAG CCCTGGCAGG GGTCTGGCC AACTCGTCC TCGCCAGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTGTGG CTTGTGAAC CCTGAGTCCC CATCTCTTG AACAGCCTCC CCTGGGGCAG TGGAGACCTC GGTCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGTGCTT ACAATTGGAC CCAGAAGAGG TGGCTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT TAATACCTTG TGGGGTCAGG

40 GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCAATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTCTCCCGG GAGTCCCGG CCAGAGTGGC CTTCATGCA GGCGTTGACT GTGAGAGGAC CTGCGCCAG CTGCCCCCT GCTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT GGCCTCCCC AAACGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC

45 CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG CACTGTCTCT TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACAGCGTG ACTGCATCCC TTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGC CTCCGC AACCAGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCGCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTACCAA CCGCTCGCG CGCATCCCC GCTTCTGGC AGGTGAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGCCCC ACCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGAG TAAATGTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAACTGGCA GCCATGCACA CCTCTTTAT

50 GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCTG AATCCCCGGT GGAATGGAGA CAACTGTAC AATGAGGCTC GGAAATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCAGCAT CCCCC CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTGTCA CATTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAGG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCTCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTCTG CCGTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG

60 GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCGGCTTT GGCCACACAA

TGCTCCAGCC CTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCCT
 TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG
 GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC
 5 AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT
 AGCTTCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCCATCT
 CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC
 CGGCTGTTTC GGCAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC
 ACGGCCTTCC AGGAGAGGGG GCTGTCCACC TCTTCTCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT
 TCTGGGAAGA CCTTGGTACC CGACTGCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG
 10 ACAGCGCAAG GCCCTGAGCA GAATTTCTTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT
 TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA
 ACCTATCAGC CTGCGGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCTTGGGCTG
 GTTAAGCCTC ACACTCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC
 TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC
 15 CCTAGGACTT TGGGGGGA AAA TTAGGAGCAT CCAACTA GAATTCCTG GCCAGGACCC CTGCCAGGGC
 ACTGACCCAG CCTTCCCTGG GGCAGTGGAG ACCTCGGTCC TGCAGAGCTG CATAGCAGAG GCCAAGTTGC
 TGGTGGATGC TGCCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC
 CATGGACCTC CTGTCTTACT TCAAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC CGCAGATTAT
 ATGTGCTAGG CTGTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG
 20 ATGTGCTAAC AGAAACACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT GCTCTCCGG ACCAGCCGA
 GCGCTGCAGC GACCAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCTT CTGAGGGGCC
 TCCAACCAGG CTCTGGCTCG CTGGCTGCC GCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA
 CCCCCAGCAG GAGGCGCAAT GGCTTCTTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT
 CCCC AATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTTATGC AGTGGGGCCA GTTCATTGAC
 25 CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC TGTGAGAGGA
 CCTGCGCCCA GCTGCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCC GCATCA AGAACCAGCG
 TGACTGCATC CCTTCTTCTC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC
 AACGCGTCA CCTCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC
 30 GCAACCGGAC CAATACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT
 GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCTCACC AACCGCTCG CGCGCATCCC CTGCTTCTG
 GCAGGTGACA CCCGATCAAC GGAAACCCCA AAAGTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA
 ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGTG GAATGGAGAC AAAGTGTACA ATGAGGCTCG
 GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC
 35 CCGGCCAGGA GAAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT
 TCACCGTAGG CTTCGCTTT GGCACACAA TGCTCCAGCC CTTCATGTTT CGCTTGGACA GTCAGTACCG
 GGCCTCCGCA CCCAATCTGC ATGTCCCACT TAGCTTCTGC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA
 GGGGGCATCG ACCCTCATCT CCGGGGCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT
 TAGTGGATGA GCTCGGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA
 40 CATGCAACGA AGCGGGACC ACGGCCTTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCAG
 CCCC GAATT TGGACAGCT TAGCCGGGTG CTGAAAAACC AGGACTTGGC AAGGAAGTTC CTGAATTTGT
 ATGGAACACC TGAACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTGGCCG GGGCTCGAGT
 GGGGCTCTT GTTGCTTGTG TGTTGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC
 45 AGAACGAGGT GTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTC CTGTCTCGG ATTATGTG
 ACAATACCGG TATCACACG GTTTCAGGG ACATCTTAC AGCCAACATC TACCCTCGGG GCTTTGTGAA
 CTGCAGCCGT ATCCACAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC
 CAAGTCTCCA ACTTTTGAG ACAAGGGGAA GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT
 GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG GGTTCGCCAG CCAGGAGTGA AGGCTGGGGG
 50 CTCTATCAG CAATGGACCT TCCGCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC
 AAAGGCTTGG GAGGCAAGCC ATGTGGTCTT GCACCCAGG CAAGAAAAGT CAGCTGGAGG GTTTACAGCA
 AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC
 CGGAATTC-3' (FRAG. NO: 1726) (SEQ. ID NO: 3008)
 5'-CACCCTCCT GTACGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG
 55 GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC
 CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAA ACTCCCATGA AAACAGAGA GAAGTTTCAG
 AACTCCACCC AAGAGGCTGG GTTCTAGGG CCCAGAGCTG CCTCCCCCA CCTAGAATG GGCTATAAAA
 GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCCG CTGGGGGTCC TCAAAGTGAG
 AGGGGAGCAG AGGATCTCTC CGTGCAGGCT CTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC
 AGAGATGCAT GTGCTCCAG CCCTGCAGG GGTCTGGCC ACTCTGTC TCGCCACGCC CTGTAGGGG
 60 ACTGACCCAG GTAAGTAGTCC CTTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAAGGGG AGCACTTGGG
 TCTTGGAGGG GGTCTGTGG CTTGTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CCTGGGGCAG
 TGGAGACCTC GGTCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC

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CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT-3' (FRAG. NO:)(SEQ. ID NO:2483)

5'-TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTC CCACCAGGTC CGGGCTGTCT
 CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTTCATGCA
 5 GTGGGGCCAG TTCAATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA
 GCGGTTGACT GTGAAGGAC CTGCGCCCAG CTGCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC
 AATCTCCCAT GCCCTTGTGT GGCCTCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG
 CACCATCCTT AAGCAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG-3' (FRAG.NO:)(SEQ.ID NO:2484)

10 5'-CACTGTCTCC TCCTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC
 TTTCTCCCG TCGGACCCT CATGCCCCA AAACAAGAAC AGAGTCCGA ACCAGATCAA CGCGCTCACC
 TCCTTTGTGG ACGCAGCAT GGTGTATGGC AGTGAGGTCT CCTCTCGCT GCGGCTCCGC AACCAGACCA
 ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CTTTCGACAA
 CCTGCACGAT GACCTCTGTC TCCTACCAA CCGCTCGGCG CGCATCCCCT GCTTCTGGC AGGTGAGACA
 15 GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG
 TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC-3'
 (FRAG.NO:)(SEQ.ID NO:2485)

5'-TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCGTCTC TCCCATCCCC AGCCCTGGGT
 CTACCCTGGT AGAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTGCGGTTT TCAAGGTGAC
 20 ACCCGATCAA CGGAACCC CAAACTGGCA GCCATGCACA CCTCTTTAT GCGAGAGCAC AACCAGCTGG
 CCACCAGCT GAGCGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT
 GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCAGCAT CCCC-3' (FRAG.NO:)(SEQ.ID NO:2486)

5'-CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTGACGT GATGACAATA AAGAATATGT
 CTGAGCCACC CTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGA ATGTTCTCC TGTTCTCCCT
 25 TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG
 GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT
 GGCCACACAA TGCACAGCC CTTGATGTT CGCTTGGACA GTCAGTACCG GGCCTCCGA CCCAACTCGC
 ATGTCCCACT TAGCTCTGCC TTCTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTCCAGGG
 GGCAAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG-3' (FRAG.NO:)(SEQ.ID NO:2487)

30 5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTCTCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT
 CCAGCTCTGG GCTAGCTTG CATCATGTGA TAACCCAAGT AGCTTCCAG AGGCTGTGCC AATCTGTGCT
 GCTCACATTC CCTCCACCA GGGGGCATCG ACCCATCCT CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT
 GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG
 CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC
 35 TCTTCTCCA GCTTTCTCG GGCCAGGCTG CTCAAGGGT TCTGGGAAGA CCTGGTACC-3' (FRAG.NO:)(SEQ.ID NO:2488)

5'-CGACTGCCTG TAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA
 GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC
 CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTGTA ACCTATCAGC CTGGCAGGG
 40 ACATGAGGCT TCTGAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCTTCC
 CTGGATGGAT GGCAGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTACTAG GTACTCTTTC
 CAAGTGCTT CCAATGTGC TAGTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGAAAA
 TTAGGAGCAT CCAACTA-3' (FRAG.NO:)(SEQ.ID NO:2489)

5'-GAATTCCTG GCAGGACCC CTGCCAGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC
 45 TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCTACAAT TGGACCCAGA AGAGCATCAA
 GCAGCGGCTT CGCAGCGGT CAGCCAGCCC CATGGACCTC CTGTCTACT TCAAACAACC GGTAGCAGCC
 ACCAGGACAG TTGTCGGG CCGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTGAAGAG AAGTTACAAC
 CCCAGCGGTC CGGACCTTC ATTGTCACTG ATGTGTAAC AGAACACAG CTGCGGCTGC TGTCCAGGC
 CAGTGGCTGT GCTTCCGG ACCAGGCCG GCGCTGCAG GACAAGTACC GCACCATCA TGGACGGTGC
 50 AACAAACAAGA GGAJACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCC CCGAGATAG
 AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCACAGCAG GAGGCGCAAT GGCTTCTTC TCCCTCTTGT
 CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC
 ATGTTTCATG AGTGGGCA GTTCATTGAC CATGACCTGG ACTTCTCCC GGAGTCCCCG GCCAGAGTGG
 CTTCACTG AGGCGTTGAC TGTGAGAGGA CTGCGCCCA GCTGCCCCC TGCTTTCCA TCAAGATCCC
 55 ACCCAATGAC CCCCGCATCA AGAACAGCG TGAATGCATC CTTTCTTCC GCTCGGCACC CTCATGCCCC
 CAAAACAAGA ACAJAGTCCG CAACCAGATC AACGCGCTCA CTCCTTTGT GGACGCCAG ATGGTGTATG
 GCAGTGAAGT CTCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG GGGCTGTGG CCATCAACCA
 GCGCTTTCAA GACACGGCC GGGCCCTGCT CCCCCTCGAC AACCTGCACG ATGACCCCTG TCTCTCAAC
 AACCCTCGG CCGCATCCC CTGCTTCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC AAAGTGGCAG
 60 CCATGCACAC CCTTTTATG CGAGAGCACA ACCGGCTGG CACCGAGCTG AGACGCCTGA ATCCCCGGTG
 GAATGGAGAC AAACTGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA
 GACTTTCTGC CCTTGGTTCT GGGCAAGGCC CCGGCCAGGA GAACCTGGG GCACTACAGG GGTACTGCT

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CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCGCTTT GGCCACACAA TGCTCCAGCC
 CTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC
 TTCTTTGCCA GCTGGCGGAT CGTGATGAA GGGGGCATCG ACCCATCCT CCGGGGCTC ATGGCCACCC
 CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GTCCTGGGAC CGGCTGTTT GGCAAGTGAG
 5 GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT
 GCTTGGAGGC GCTTCTGTGG GCTCTCCAG CCCCAGGAAT TGGCACAGCT TAGCCGGGTG CTGAAAAACC
 AGGACTTGCC AAGGAAGTTC CTGAATTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT
 CGCTGAGCCT CTTTGGCCGG GGGCTCGAGT GGGGCTCTT CTGGCTTGTC TGTTCGAGAA CCAGTTCAGA
 AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTACCA AAGACAGCGC AAGGCCCTGA
 10 GCAGAATTTC CTTCTCTCGA ATTATATGTG ACAATACCGT TATCACCACG GTTCAAGGG ACATCTTCAG
 AGCCAACATC TACCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA
 GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC
 ATGAGGCTGC CTTCTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG
 GGTTCCCCAG CCAAGAGTGA AGGCTGGGGG CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA
 15 GGTATTAGGC TATCAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCAGG
 CAAGAAAAGT CAGCTGGAGG GTTACAGCA CTTTCTACTG TTTCCAGCC CTCCCTCCC TCCCTACCA
 TGACTAAGAG ACCACTCGGT CCTAGCTCC AGACACCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG
 CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC-3' (FRAG. NO:) (SEQ. ID no:2490)
 5'-TC GGC CTG GTC CCG G-3' (FRAG. NO: 1727) (SEQ. ID NO:1740)
 20 5'-TGG GGC TTT CCC TTG-3' (FRAG. NO: 1728) (SEQ. ID NO: 1741)
 5'-TG TGC CCG GBG GCG-3' (FRAG. NO: 1729) (SEQ. ID NO: 1742)
 5'-GCG CTC GGC CTG GTC CCG G-3' (FRAG. NO:1053) (SEQ. ID NO:1061)
 5'-GGG TCT CCT CTT GTT GTT GC-3' (FRAG. NO:1054) (SEQ. ID NO:1062)
 5'-TTG CGC CTC CTG CTG GGG GT CC-3' (FRAG. NO:1055) (SEQ. ID NO:1063)
 25 5'-CTC TGT TCT TGT TTT GGG GGC-3' (FRAG. NO:1056) (SEQ. ID NO:1064)
 5'-GGG CCC GGC CGT TGT CTT G-3' (FRAG. NO:1057) (SEQ. ID NO:1065)
 5'-GTT TGG GGG TTT CCG TTG-3' (FRAG. NO:1058) (SEQ. ID NO:1066)
 5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' (FRAG. NO:1059) (SEQ. ID NO:1067)
 5'-GGC CGT TGT CCC GGC TTC GTT GC-3' (FRAG. NO:1060) (SEQ. ID NO:1068)
 30 5'-CCT GTC TCC GTC GCG GCT CTT CTG-3' (FRAG. NO:1061) (SEQ. ID NO:1069)
 5'-GGG CCT TGC GCT GTC TTT GGT G-3' (FRAG. NO:1062) (SEQ. ID NO:1070)
 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC-3' (FRAG.
 NO:1063) (SEQ. ID NO:1071)

Human Intercellular Adhesion Molecule-1 (ICAM-1)

35 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG
 CGG TC GTG TCT CCG GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG
 TCT GGT TCT TGT GTT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT
 GTC CTC CGG CGT CCG CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT
 40 TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG
 GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1730) (SEQ. ID NO: 1743)
 5'-GGG GGC TGC TGG G-3' (FRAG. NO: 1731) (SEQ. ID NO:1744)
 5'-T GTC CTC CGG CCT CCC-3' (FRAG. NO:1732) (SEQ. ID NO:1745)
 5'-G CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1733) (SEQ. ID NO: 1746)
 45 5'-CTC TGG GGT GGC CTT C-3' (FRAG. NO:1734) (SEQ. ID NO:1747)
 5'-GCG CGG GCC GGG GGC TGC TGG G-3' (FRAG. NO:1064) (SEQ. ID NO:1072)
 5'-GGT TGG CCC GGG GTG CCC C-3' (FRAG. NO:1065) (SEQ. ID NO:1073)
 5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' (FRAG. NO:1066) (SEQ. ID NO:1074)
 5'-GTG TCT CCT GGC TCT GGT TCC CC-3' (FRAG. NO:1067) (SEQ. ID NO:1075)
 50 5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' (FRAG. NO:1068) (SEQ. ID NO:1076)
 5'-GCT CCC GGG TCT GGT TCT TGT GT-3' (FRAG. NO:1069) (SEQ. ID NO:1077)
 5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' (FRAG. NO:1070) (SEQ. ID NO:1078)
 5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' (FRAG. NO:1071) (SEQ. ID NO:1079)
 5'-TGC CCT GTC CTC CGG CGT CCC-3' (FRAG. NO:1072) (SEQ. ID NO:1080)
 55 5'-CGG BGC CTC CCG GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG
 GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB
 GGC TGB G-3' (FRAG. NO:1073) (SEQ. ID NO:1081)

Human Vascular Cell Adhesion Molecule 1 (VCAM-1)

60 Nucleic Acid and Oligonucleotide Fragments

5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC

CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT
GGT CTC GBT TTT BHB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG
BCC BTC TTC CCB GCC BTT TTB BGT TGC TGT CGT-3' (FRAG.NO:1735)(SEQ.ID NO:1748)

5'-C TGT CGT-3' (FRAG. NO:1736) (SEQ. ID NO:1749)

5 5'-TGC TTC TTC C-3' (FRAG. NO:1737) (SEQ. ID NO:1750)

HSVCAM1AS1: 5'-CCT CTT TTC TGT TTT TCC C-3' (FRAG. NO:1074) (SEQ. ID NO:1082)

HSVCAM1AS2: 5'-CTC TGC CTT TGT TTG GGT TCG-3' (FRAG. NO:1075) (SEQ. ID NO:1083)

HSVCAM1AS3: 5'-CTT CCT TTC TGC TTC TTC C-3' (FRAG. NO:1076) (SEQ. ID NO:1084)

HSVCAM1AS4: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' (FRAG. NO:1077) (SEQ. ID NO:1085)

10 HSVCAM1AS5: 5'-GTC TTT GTT GTT TTC TCT TCC TTG-3' (FRAG. NO:1078) (SEQ. ID NO:1086)

CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB
BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT (FRAG.

NO:1079)(SEQ. ID NO:1087)

Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)

15 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC
TTC TGT C CGT TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC
CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC
GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT
20 GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CAAAAACGGA AAGTATTTC AAGCCTAAACC
TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGTCTCT
CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGC
TATTGTACAG AAACGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAACTCCA
TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG
25 AACCAGAAA CCTGTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC CCAACAATAG GCAAAAAGAT
GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA
AGAAGAAGCT TGCTCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT
AGAGACCATC AATATTACCA CTGTGCAAGTG TGACCCTGGC TTCAGTGGAC TCAAGTGTGA GCAAAATTGTG
AACTGTACAG CCTTGAATC CCCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT
30 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAGTGTAT
GTCTCTGGA GAAAGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA
GCCAATGGGT TCGTGGAAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTGTACT
GTGAAGAAGG ATTGAAGCTA ATGGGAGCCC AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA
GAAGCCAACG TGTAAAGCTG TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC
35 CATTCCCCTG CTGCAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC
AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCAGTTT GTGAAGCTTT
CCAGTGCACA GCCGTGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC CTAGTGCTTC TGGCAGTTTC
CGTTAGGCTT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT
GTGGCCCCAC AGGCGAGTGG GACAACGAGA AGCCCACTG TGAAGCTGTG AGATGCGATG CTGTCCACCA
40 GCCCCGAAG GGTGTGGTGA GGTGTGCTCA TTCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTCCT
TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA
CAGAAGAGGT TCTCTCTGC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGGAAGA TCAACATGAG
CTGCAGTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTCTG AAGGATGGAC GCTCAATGGC
TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGTCTACC TACCTGTGAA GCTCCCACTG
45 AGTCCAACAT TCCCTTGGTA GCTGGACTTT CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCT
CCTCTGGCTT CGGAAATGCT TACGGAAAGC AAAGAAATTT GTTCTTGCCA GCAGCTGCCA AAGCCTTGAA
TCAGACGGAA GCTTCCAAAA GCCTTCTTAC ATCCTTAAAG TTCAAAAGAA TCAGAAACAG GTGCATCTGG
GGAAC TAGAG GGAATACACTG AAGTTAACAG AGACAGATAA CTCTCTCGG GTCTCTGGCC CTCTTGCTCT
ACTATGCCAG ATGCTTTTAT GGCTGAAACC GCAACACCCA TCACCACTTC AATAGATCAA AGTCCAGCAG
50 GCAAGGACGG CCTCAACTG AAAAGACTCA GTGTTCCCTT TCCTACTCTC AGGATCAAGA AAGTGTGGC
TAATGAAGGG AAAGGATATT TTCTTCCAAG CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAATTCC
TTTTCTAACT CTCCCTTGCT CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTTTGTGGC TTTCTTTCTT
TTGCCCTTCA CAGTGTTCG ACAGCTGATT ACACAGTTGC TGTCATAAGA ATGAATAATA ATTATCCAGA
GTTTAGAGGA AAAAATGAC TAAAAATATT ATAACATAA AAAATGACAG ATGTTGAATG CCCACAGGCA
55 AATCATGGGA GGGTGTGTTAA TGGTGCAAAAT CCACTAGTAAT GCTCTGTGCG AGGGTTACTA TGCACAATT
AATCACTTTC ATCCCTATGG GATTCAGTGC TTCTTAAAGA GTTCTTAAGG ATTGTGATAT TTTTACTTGC
ATTGAATATA TTAATATCTT CCATACTTCT TCATTCAATA CAAGTGTGGT AGGGACTTAA AAAACTTGT
AATGCTGTCA ACTATGATAT GGTAAAAGTT ACTTATTCTA GATTACCCCT TCATTGTTTA TTAACAAATT
ATGTTACATC TGTTTAAAT TTATTTCAAA AAGGGAAACT ATTGTCCCT AGCAAGGCAT GATGTTAACC
60 AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTGG AAAACATGGT AGAATTGGAG AGTAAAAACT
GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT CCACGATGAA AAACCTCCAT



5	GAGGCCAAAC	GTTTGAAC	AATAAAGCA	TAAATGCAA	CACACAAAGG	TATAATTTTA	TGAATGTCT
	TGTTGGAAAA	GAAACAGAA	AGATGGATGT	GCTTTCATT	CCTACAAAGA	TGTTTGTCTAG	ATGTGATATG
	TAAACATAAT	TCTTGTATAT	TATGGAAGAT	TTTAAATTCA	CAATAGAAAC	TCACCATGTA	AAAGAGTCAT
	CTGGTAGATT	TTTACGAAT	GAAAGATGTCT	AATAGTTATT	CCCTATTTGT	TTCTTCTGT	ATGTTAGGGT
	GCTCTGGAAG	AGAAGGAATGC	CTGTGTGAGC	AAGCATTAT	GTTTATTTAT	AAGCAGATTT	AACAATTCCA
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	TCAGAACAGC	AGAGGTTCTT	TTAAAGGGGC	AGAAAAACTC	TGGGAAATAA	GAGAGAACAA	CTACTGTGAT
	CAGGCTATGT	ATGGAATACA	GTGTTATTTT	CTTTGAAATT	GTTTAAAGTG	TGTAAATATT	TATGTAAACT
15	GCATTAGAAA	TTAGCTGTGT	GAAATACCAG	TGTGGTTTGT	GTTTGAGTTT	TATTGAGAAT	TTTAAATTA
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	ACTATAAAGG	TTGACAATAA	ATGTGCTTAT	GTTGATCAAAAT	TTTACCTATT	ATGCATTTGA	TATATAAATA
	AGTATATAAA	TGCAACACA	GACACAGCAA	TGATGGTGAA	CAGTCTTCAT	ACAATTATAT	GGATGAATCT
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20	CAAAAAATAGG	TGGACCAATT	CATGGTGGTG	TTAGAAATCA	GAAGAGAGGC	TACCTTTGTG	GGGAGGGGAC
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30	TTCCACAAG	ATC TCTCCT	TGAGCCCCTA	GAGACTTTTC	TGTCTGTTAC	TGTTTCTTCA	TTCTCTATCT
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	GAAATTTTAT	GGAGTAGTTC	TCAATTTTTA	TGTAGTTCCA	CTGCAAAGGT	AAGTCTTATG	GAAAGATTCA
60	CTGTAATTTT	TTTTCTCAT	TTGG				

[illegible]

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	50%	50%	Male	Female
Marital Status	65%	35%	Married	Single
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Occupation	45%	55%	Professional	Non-Professional
Health Status	75%	25%	Good	Poor
Stress Level	60%	40%	Low	High
Sleep Quality	70%	30%	Good	Poor
Dietary Habits	60%	40%	Healthy	Unhealthy
Exercise Frequency	50%	50%	Regular	Irregular
Work-Life Balance	65%	35%	Good	Poor
Family Support	70%	30%	Strong	Weak
Life Satisfaction	75%	25%	High	Low
Resilience	60%	40%	High	Low
Emotional Stability	70%	30%	Stable	Unstable
Self-Esteem	75%	25%	High	Low
Optimism	65%	35%	Optimistic	Pessimistic
Gratitude	70%	30%	High	Low
Forgiveness	60%	40%	High	Low
Empathy	75%	25%	High	Low
Compassion	70%	30%	High	Low
Kindness	65%	35%	High	Low
Generosity	70%	30%	High	Low
Patience	60%	40%	High	Low
Perseverance	75%	25%	High	Low
Determination	70%	30%	High	Low
Confidence	75%	25%	High	Low
Bravery	65%	35%	High	Low
Integrity	70%	30%	High	Low
Honesty	75%	25%	High	Low
Trustworthiness	70%	30%	High	Low
Reliability	75%	25%	High	Low
Accountability	70%	30%	High	Low
Responsibility	75%	25%	High	Low
Commitment	70%	30%	High	Low
Dedication	75%	25%	High	Low
Passion	70%	30%	High	Low
Enthusiasm	75%	25%	High	Low
Energy	70%	30%	High	Low
Vitality	75%	25%	High	Low
Strength	70%	30%	High	Low
Power	75%	25%	High	Low
Influence	70%	30%	High	Low
Leadership	75%	25%	High	Low
Authority	70%	30%	High	Low
Control	75%	25%	High	Low
Power	70%	30%	High	Low
Influence	75%	25%	High	Low
Leadership	70%	30%	High	Low
Authority	75%	25%	High	Low
Control	70%	30%	High	Low
Power	75%	25%	High	Low
Influence	70%	30%	High	Low
Leadership	75%	25%	High	Low
Authority	70%	30%	High	Low
Control	75%	25%	High	Low
Power	70%	30%	High	Low
Influence	75%	25%	High	Low
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Influence	70%	30%	High	Low
Leadership	75%	25%	High	Low
Authority	70%	30%	High	Low
Control	75%	25%	High	Low
Power	70%	30%	High	Low
Influence	75%	25%	High	Low
Leadership	70%	30%	High	Low
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Power	70%	30%	High	Low
Influence	75%	25%	High	Low
Leadership	70%	30%	High	Low
Authority	75%	25%	High	Low
Control	70%	30%	High	Low
Power	75%	25%	High	Low
Influence	70%	30%	High	Low
Leadership	75%	25%	High	Low
Authority	70%	30%	High	Low
Control	75%	25%	High	Low
Power	70%	30%	High	Low
Influence	75%	25%	High	Low
Leadership	70%	30%	High	

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 15 ATCTCATTAT TTCTCCTAAT AATTTCCTTG TCCTTTGTCA TAAATGGTGG GTAGGCTGTT ATGGTGATGG
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	GAAAGCATTGA	AGACTTAATG	TATTGGGGCC	AGCCTTCTCT	TCCAACCTCA	ACCTCCACAAC	TCCTCAATAA
	GCCATGGGCT	CAAGAAAGTT	CTGCTCAGTG	GCCCTGAAA	AATGCTTTCA	TAGTCTCACT	ACCATACCAC
30	TGCTTACACA	ATTTCCTTCC	TACAGACTGC	CTTCTTTCC	TGCTTTTCTC	CATATACCTA	AATCCTATCT
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35	GTGAACCAT	AAACTTAATA	TAGCAAAATTG	CTTAGCATGG	TAATTAGCTT	TTTGCTAATA	TTCTCCAGC
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40	AATAAAAAAGA	ACCTCCACTG	ATCGTACATC	CTCATCCAGT	TACCCCTGCC	CCACTTCTCC	TTCACAGCCA
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	CTTCTCCTGC	CATAGCCTCT	GTGCTTTGGA	TAGGTCCAAT	GAGCCACAGT	GAATGATGTG	CATACACCCA
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50	TTTAGCCAAT	TAAACAGACAC	ATTCAGTTAA	TATCACTCTC	TCTTATTCTA	TGAACCCATT	CTTACTACTA
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5	GCCTGGTGGC	AAGACCCAAT	ATGTCCATTC	AAGTGTTTAT	CCCTTCCCAA	TCTGCCATCT	CATCCTACCT
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20	CAGGGGGAAT	CAAATCTGAA	TTAATTTTCA	ATTCTGGTTA	GCTTCACATA	AATATTTTTT	TTAGGGATGA
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25	GTCTAGATGA	GCCCATGCAC	AAGGACACAT	GTTTCTGGAA	GCTTTCCTTA	TTCTTTCTCT	AAAAGAAAGG
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40	CACCTGATTCC	CACAGCAGTT	TTCAAGTTAT	CGGTTTGAGA	TCTGTATCAG	AAATGACTCC	AAGGTAAAAA
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	TGGAGTGCAA	TGGTGGGTC	TCAGCTCACT	GCAACCTCCG	CCTCCCGGGT	TCAAGTGATT	CTTCTGTCTC

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Description		Value
Age	Age	25.0
Sex	Sex	0.0
Height	Height	1.75
Weight	Weight	70.0
Body mass index	Body mass index	22.0
Heart rate	Heart rate	75.0
Stroke volume	Stroke volume	0.07
Cardiac output	Cardiac output	5.25
Systemic vascular resistance	Systemic vascular resistance	120.0
Pulmonary vascular resistance	Pulmonary vascular resistance	20.0
Mean arterial pressure	Mean arterial pressure	93.3
Right atrial pressure	Right atrial pressure	0.0
Right ventricular pressure	Right ventricular pressure	0.0
Left atrial pressure	Left atrial pressure	0.0
Left ventricular pressure	Left ventricular pressure	0.0
Mean pulmonary artery pressure	Mean pulmonary artery pressure	16.0
Pulmonary capillary pressure	Pulmonary capillary pressure	11.0
Transpulmonary pressure	Transpulmonary pressure	0.0
Alveolar pressure	Alveolar pressure	0.0
Barometric pressure	Barometric pressure	101.3
Partial pressure of oxygen	Partial pressure of oxygen	101.3
Partial pressure of carbon dioxide	Partial pressure of carbon dioxide	40.0
Partial pressure of water vapor	Partial pressure of water vapor	6.3
Partial pressure of nitrogen	Partial pressure of nitrogen	95.0
Partial pressure of hydrogen	Partial pressure of hydrogen	0.0
Partial pressure of helium	Partial pressure of helium	0.0
Partial pressure of neon	Partial pressure of neon	0.0
Partial pressure of argon	Partial pressure of argon	0.0
Partial pressure of krypton	Partial pressure of krypton	0.0
Partial pressure of xenon	Partial pressure of xenon	0.0
Partial pressure of radon	Partial pressure of radon	0.0
Partial pressure of cesium	Partial pressure of cesium	0.0
Partial pressure of barium	Partial pressure of barium	0.0
Partial pressure of lanthanum	Partial pressure of lanthanum	0.0
Partial pressure of cerium	Partial pressure of cerium	0.0
Partial pressure of praseodymium	Partial pressure of praseodymium	0.0
Partial pressure of neodymium	Partial pressure of neodymium	0.0
Partial pressure of promethium	Partial pressure of promethium	0.0
Partial pressure of samarium	Partial pressure of samarium	0.0
Partial pressure of europium	Partial pressure of europium	0.0
Partial pressure of gadolinium	Partial pressure of gadolinium	0.0
Partial pressure of terbium	Partial pressure of terbium	0.0
Partial pressure of dysprosium	Partial pressure of dysprosium	0.0
Partial pressure of holmium	Partial pressure of holmium	0.0
Partial pressure of erbium	Partial pressure of erbium	0.0
Partial pressure of thulium	Partial pressure of thulium	0.0
Partial pressure of ytterbium	Partial pressure of ytterbium	0.0
Partial pressure of lutetium	Partial pressure of lutetium	0.0
Partial pressure of hafnium	Partial pressure of hafnium	0.0
Partial pressure of tantalum	Partial pressure of tantalum	0.0
Partial pressure of tungsten	Partial pressure of tungsten	0.0
Partial pressure of rhenium	Partial pressure of rhenium	0.0
Partial pressure of osmium	Partial pressure of osmium	0.0
Partial pressure of iridium	Partial pressure of iridium	0.0
Partial pressure of platinum	Partial pressure of platinum	0.0
Partial pressure of gold	Partial pressure of gold	0.0
Partial pressure of silver	Partial pressure of silver	0.0
Partial pressure of copper	Partial pressure of copper	0.0
Partial pressure of nickel	Partial pressure of nickel	0.0
Partial pressure of cobalt	Partial pressure of cobalt	0.0
Partial pressure of iron	Partial pressure of iron	0.0
Partial pressure of manganese	Partial pressure of manganese	0.0
Partial pressure of chromium	Partial pressure of chromium	0.0
Partial pressure of vanadium	Partial pressure of vanadium	0.0
Partial pressure of titanium	Partial pressure of titanium	0.0
Partial pressure of zirconium	Partial pressure of zirconium	0.0
Partial pressure of niobium	Partial pressure of niobium	0.0
Partial pressure of molybdenum	Partial pressure of molybdenum	0.0
Partial pressure of technetium	Partial pressure of technetium	0.0
Partial pressure of ruthenium	Partial pressure of ruthenium	0.0
Partial pressure of rhodium	Partial pressure of rhodium	0.0
Partial pressure of palladium	Partial pressure of palladium	0.0
Partial pressure of arsenic	Partial pressure of arsenic	0.0
Partial pressure of selenium	Partial pressure of selenium	0.0
Partial pressure of bromine	Partial pressure of bromine	0.0
Partial pressure of krypton	Partial pressure of krypton	0.0
Partial pressure of xenon	Partial pressure of xenon	0.0
Partial pressure of cesium	Partial pressure of cesium	0.0
Partial pressure of barium	Partial pressure of barium	0.0
Partial pressure of lanthanum	Partial pressure of lanthanum	0.0
Partial pressure of cerium	Partial pressure of cerium	0.0
Partial pressure of praseodymium	Partial pressure of praseodymium	0.0
Partial pressure of neodymium	Partial pressure of neodymium	0.0
Partial pressure of promethium	Partial pressure of promethium	0.0
Partial pressure of samarium	Partial pressure of samarium	0.0
Partial pressure of europium	Partial pressure of europium	0.0
Partial pressure of gadolinium	Partial pressure of gadolinium	0.0
Partial pressure of terbium	Partial pressure of terbium	0.0
Partial pressure of dysprosium	Partial pressure of dysprosium	0.0
Partial pressure of holmium	Partial pressure of holmium	0.0
Partial pressure of erbium	Partial pressure of erbium	0.0
Partial pressure of thulium	Partial pressure of thulium	0.0
Partial pressure of ytterbium	Partial pressure of ytterbium	0.0
Partial pressure of lutetium	Partial pressure of lutetium	0.0
Partial pressure of hafnium	Partial pressure of hafnium	0.0
Partial pressure of tantalum	Partial pressure of tantalum	0.0
Partial pressure of tungsten	Partial pressure of tungsten	0.0
Partial pressure of rhenium	Partial pressure of rhenium	0.0
Partial pressure of osmium	Partial pressure of osmium	0.0
Partial pressure of iridium	Partial pressure of iridium	0.0
Partial pressure of platinum	Partial pressure of platinum	0.0
Partial pressure of gold	Partial pressure of gold	0.0
Partial pressure of silver	Partial pressure of silver	0.0
Partial pressure of copper	Partial pressure of copper	0.0
Partial pressure of nickel	Partial pressure of nickel	0.0
Partial pressure of cobalt	Partial pressure of cobalt	0.0
Partial pressure of iron	Partial pressure of iron	0.0
Partial pressure of manganese	Partial pressure of manganese	0.0</



5	GAAGACATTT	TGACCTCAAT	TCTGTCTTCT	ATCTAGCTC	AGTTCAGAA	TTTAACTCT	TTTGATTTTG
	ACAACCCTCT	CCAGAAACTG	TATCTATTTC	CCTGTTCTGA	TTGGTGGTAC	AATAGGTA AAA	TTTAAGACTT
	GGAAATCAAA	GTTTTCACAT	TTTAGACCCT	GCCATGCCAT	TTAGTAAACA	GTACAACTTT	CATGCTTTAT
	TCCTCATCTG	TCAAATTTAA	GCCATTATTG	CTACCTTGCT	CTAGAGACTT	CAAGGAAGAA	TGGACTCAAG
	GAATCAGAAG	AATTTTGTA	TTTGAAAAC	ATATGAGATG	AGATTAGGGA	GAAACATGGG	AACTAAGAGA
10	AAATGTTATC	TTTTTTCATT	GATTTAAAGA	GTATCTATTA	TATATCAAGC	ATTACTCTGG	GGCTTGAAGA
	GCTTAGATTT	CACCCTGTAG	GACAAAAATGG	TAGGTAGAAA	TTAATGGGTG	GATTGTCTAG	TATGTGTGAT
	GTGTTTTAAT	TGCTTTTAAAT	TGATCAGTCT	CCCTGTAGTA	TGAATAATGT	ATTGTAGGGG	AGCTAAATTTA
	AAATTGTGGA	ACTCATCTAA	TAAACTATTG	CAAGAATCTA	GAAAGAAAGAT	AATGACGGCA	ATGGTAGTAG
	AGTTGACAAG	TGGAGACAA	ATTAGAAAAA	CACTAAGTTG	TAAAAATTGG	TAGAATGTTA	CCCTGCATAA
15	ATGTTGGGGG	AGTTAAGAGA	GTCTCATACC	AGGGTGCCCA	TGTAAATGGT	GATTCCACAT	ACTGAGATA
	GAAATACGAA	GAGAAAAGCT	GACTGGGAAC	AATTGGTTTT	ATAGTCTTTT	AAACATCCCA	AAGGACATCC
	TTAGCATATT	TGACTTCAGA	GCTGGAGATA	GGCTTATCAG	TCCAAAGATC	ACATAGATTT	GTGAGTCCGC
	AAAAGTTCAGT	AAGTTTGACC	AAAGGATACA	TGTAGATTAG	AGTCAGAAAG	GCAATATACA	AAAGACAAAA
	GCTGAGAANT	TATAGTAGTT	TATGGTCTCTG	GATAAGTGCT	CATGAAGGAT	CTCAGGAGAA	ATGATCACAG
20	GTAGAAAGAA	TAGAGAAAAGA	GTGATATTAG	AGAAACCAAG	ACAAAGAAAA	GTAAAAATGTT	AAAAATCAGT
	GAAATAGGCA	TACCAATAAT	TAAAAATGAG	TAAAAATAGGC	ATACCAATAA	CATAAGGGTT	AAAAAATAGA
	GTTCAAAAAT	GGGGTGAGGG	TAAAGTATTA	GGAAGGAGTC	ATGGCCAGG	GATCAAGTGA	AATGAGTTAG
	ATCTATAGAT	CTAATTCAGT	TGGTTGACAT	TTAAATGTAT	TTTGGTTTTA	ATTCTTTATT	GTTTACAAAC
	ATTGCTTTTT	TAAAAAATTA	AATTGTCCAA	TTCAATTCAG	GCTCACAAGC	AAGTGCCTCA	TATATACAGG
25	CATTTTGTGG	ATCCCAAAGA	TGCAATGATA	AATAGGACAC	TTACTGATCT	CAAGAAGTTT	TCAGTACCAG
	AGGAGACGGA	CAAGTGAACA	GATGACTTCA	ACATAAGTGG	GAGAAATGAG	GAAGAAATAT	GTGGAGCTAT
	CAGAACTAAG	AAAGCTTCTC	AGAAGAAACT	GTCTTTGAAC	AATGTCTTAA	AGATGACATG	TTTTTTGGCC
	ATGTGCAAAA	TAGAGAGAA	GGCCACCAGC	AAAGTCAAGT	TGCTACAGAG	CACATGTGTT	AAGTGTGGAG
	AACTGCAAGA	AGGAAAGGAA	CTACTAGAAG	GAAAAAGCAA	GATACTTTCT	GGGTAACTCA	GCCTCCTAAT
30	GATAAATGGC	ATAATTTCTT	CCAGACCTTA	GAGTTCTAAT	TAATCTAACA	AGCTCATTAG	ATCGTGAGCT
	TCTTGAGAGC	GGGAATCTAC	CATGCTAATT	CCTTATGGTA	ACCCTGACAG	CTTTTATCCC	AACACTGTGC
	TTCTTGTTGT	ACTCAAAAAG	ACTTGTTGAG	AAGTGAGTCG	AAACTTCAATG	CTGACTTATG	AAATCTTTAC
	GGAAAGGTAA	CAATATTTGT	AAAGCAGAGC	TTTCTGATCA	AAACTTCCCA	TTTCTCAGAG	TGGCTAGTAT
	CATTTTGTTC	CAACCAGCTT	CATGATAAGC	TATAATGATT	CCTGTGACTT	TACCTAAGAA	GAAGCAAAAG
35	AAGGAAGAG	ACTTACCAAA	CTGACACTGG	GGCCATAGT	ACCCACATC	ACAGTTGCAG	GTGTAATTAT
	TGATGATTTT	TACACATTCT	CCATGGCCAC	TGCATGCCA	GGGCTGGCAA	GAAGCTTTAA	GGAGGT CAGA
	AAAAAAATAT	TTTAATGTGA	TTACATTTTA	GTA CTCAAAG	TCATTTCTTT	AGACATAGAT	AACCTTTTGT
	CTGAGATGAT	TTAATAATC	AGGAAAGGTT	TATTTGTAAA	TTCATAGCAT	AAAAATCATA	TGCTAAAATT
	TTTACGTATA	AAATACACTA	AGCATATAGT	CATAGGCATT	TATTTGCTTT	TGGAATGAAA	TTACCAATAC
40	TAATATTCTG	TAACACTTAT	AGGAAACTTA	GTGGCATACC	TTGAAACTCT	TGAAATTACT	TGTTTTTAAT
	GAGTGAGAAG	GTTAAATGAT	GACCTGACCT	CAATCAATTC	TGCATGCAAT	TATTTCTTGG	CAATCCCTTT
	CTTTATAGAA	ATCAAGATT	AAAAAGTCCA	AATTTGCTAA	AACGGTAGAG	TCCAATTTAT	AAGAGACCAA
	ATTAACATAG	GTTCATTATT	AAAACATCCA	TGTGAAAATG	CTGGCTTTT	TGGAATTGTA	GAA GATTTTA
	CAGAAATATT	CATACACCAA	AGATAGTGCA	ATTTTTATAT	AAAATTATAT	AAGGTTAGAC	CAAGAAGGAA
45	GCACGCAGCA	CCACACTCTC	TACTTCACAA	TGTGAAAAC	GAGGTGATGT	GAGCCTAAGT	TTCCA ACTGG
	CCCCAGCTGT	CAGCTTCTCC	TCCCCTGCCT	TATTATCAAA	GGCACTGATT	GTCTAGCTCT	TCCTCTGTAC
	TTCTACGTA	GATCTATCAT	TTTGATGTAA	CTTGATTTAG	GGGTATAGCT	TTTGTGACA	GGGACAAATC
	TTACACACCA	AAAATTCTTA	GGAGTGACAC	GATGCAAGAT	TATATAGAGG	GCTAGATGTA	TTTAGAATG
	AACCAGAAGC	TGTTCTCATC	CCCCACCTT	TCCATGGGGT	AAATCTGAGT	ATTCTCTTAA	CCGTGGCCCT
50	TCCTGAGTCT	GAGGCAGCAT	AGCCGTCTTG	TCACTGCCCTA	CTGTGTAAAC	AGAGGGCTGC	CTTTGTTTGT
	TGGCAGGCGT	CATCTGTTCCA	TTTGCCTGCA	TCTTTGTTTC	TCTTGATATA	GAGTCTCCAG	CAGTCTCTCT
	TGTTCTTCTT	GTGTGTTGGG	TCACCATCTC	CCCAGTTCTC	TGCTTCTTCA	GTAAGAGATT	TGTTGGTTCC
	CACCCACGTC	CATATTCCTC	CTATCTTCCG	GATTCCCTATC	CAGTAGTAAG	AACGACTGAA	AGGCAGAGTC
	TTCTCCAGAT	ACTCAATTTC	CGCCTTGTTT	TGTATGGCAA	CTAAATCTGT	GTAATTGTCT	CGGCAGAATC
55	TTCTAGCCCT	TTGCCAGTTC	ATGGGTTTTT	CAGAATAATG	GTAAGTCCAG	CAGTCGGTTC	CATGATGTGC
	CAGGAAATCT	GCAAGACATC	AGTGTGACCT	ATGCGAGACTT	ACATAATGTT	ACAGCTAAAA	AGAACCTAGC
	ACTACTCCAG	GCTCAGCTAG	ACACTTAGAG	ATGAGGAAAC	AGAGCCTAAG	AGTGTATGTG	ACCATCTCAG
	GATCACAGAA	TAGTTGTTTG	CAGATTTGAA	GTAGAACCTA	GACCTTCTGG	CTTGAATATA	AGATGCTTTT
	ATCTAAGGTT	CTAATTGAAA	CAAATTTAGT	GGTTTTCTAG	GTTTATTTTC	TTATTAATTT	TTTTCTCAAA
60	ATTATTTTCT	GTGAAATTTA	ACCAACATAT	TTTAGACATT	CATATTTCTT	TTTCTTTGTA	GCTGTTAATG
	ATTTACAAC	AATTAACGCTG	TAATATCATA	TAACATATA	ATTTACGTAT	ACTTTTTAAT	CCTGGAATCA
	TTTCTTGAAG	GCCACACAT	ATGTACCTAT	GGGAGAAGCA	TAATAAGGAC	AGGAAGAACA	GTGACATACT
	TTTAAGTAAC	CTCTTTTACA	TAAAAAACAT	TTTATTTTAC	CATAGGAAGA	ACTGCTTCTG	GAAAAGCCCA
	ATATAACCAT	CAACTCTTAT	ATATCTAACT	GTATAATTTT	TAAAAAGAAC	AATTTACAAA	GCCAAATGGT
	ATAGGATTAT	GAAATTCATT	AGATCATGTT	CTATACACAA	AGAGACTCAA	CTGATGATGT	TTAATAACA
	TATGGACCCA	TCAATATATGA	GGGCTTTGAA	GATATCTAAT	TAAACACATA	ATTACACAAT	GACTTCATA

[illegible]

5	TAATATATGG	CATCTAAGC	ATGGTATGAT	CTACATGAAT	CAC TATT TAA	TACAGTAAAG	AAACAGATAT
	AATTGATGGT	AAAGAGCATC	ATAAAATAAA	CATTTTGAAC	AGAGTTT TGA	ATGAGCATT C	CACTAGAATG
	CAAGTTCTAA	GAGGAAAAAA	ACTGTTGTGT	CCACTGCTGT	ATCCTTAGTG	CCTAGCATAA	ATTTACACACA
	TTGTAGGGAC	TCACAAAATA	CCTGTTGTAT	GAAAAGAGCA	CTAAGTTTCT	ATGTGACACA	GTGCAGACAT
	GGCATAAGGA	ATG GTGAAC	GGGAGAGTTA	GCATGTTTGC	TTGGCTAGAG	CTGAAAATCC	AGGCTAGGGA
10	GAAAGAAGAC	ATTAGTTTAC	TTAGGAAATG	AAAAACCAAG	TTCAAAGCTA	TTGTGGGAGA	GTCTTCAAGA
	ATCAGATATA	AAATTTGTCA	CAACAATGGG	AGAAGGACCA	AAAAATGATA	AACCCCGCTC	CCTTAATAAG
	CTCGTATTGT	AATT TTAGAA	ATGACATTAA	TGTACACTGA	ACTATGAATA	AAAAATAGAA	CAATGAGGTGC
	TAAATATTTG	GTACAGATTG	TAAGTACCTT	AACAGAGATT	TCTTAATTAA	CATTATTCCCT	TTATAATTGA
	GGGATTTTGT	GGGCTTATTG	GGATTTGAAC	TCTACAGCAT	GGGCTATTAT	AGGTTAAAAA	TAGTGTTCAG
15	GAGTTTCTGG	GGA GAAC TA	AAGGTAAGAA	GAAAAGAGAT	GTTTACAGAA	GGGATAGAAT	TAACAGCTC
	GTGAAATAAT	TTTCCTTAG	ACTATGTATA	ACTAGTGGAT	ATTTAAGAAA	AATGAATATA	AGTAAAAATAG
	ACTTAGCGAT	ATATAAATAT	CATAACATAC	CACAACAGAG	CATTGTCCAC	CCCCACAAC T	TGAAGATGTT
	CCATAAGTCC	CTCTGGGTGC	TCTGACATTT	CCATGGAAAT	ATCTGCAAAT	GAAATACAAA	ATTATATTTA
	GATGTATACT	CTTA AACCA C	ACATTTATAG	CCTTTGAGGT	GGTGCTTACA	ACTTCTCTAA	TAATCAGAAT
20	AAAACACATA	TGTTACTATA	CCCTGTCTGA	GGTAACAGGT	TTCTCAGACA	TAGATGAAAA	ATTACTTCAA
	ATTTACATCA	GAACTGATGC	ACAGTTTTGT	TTTGTCTAT	TTTATTTTTA	CGCTTTAGTC	TCAAGTTGCT
	AATCGGTACT	GCCCTGAATT	TTTTCTATGG	TTTGGTAATT	TTTATACCTG	CTTTTCTGCT	GAGCTATTAG
	ATAAACTAT	TTAATATTTA	CTATGTATAT	TTTTTAAAGT	ATTGTTGCTG	CTTAATTAAC	TATTGATGCT
	TATATTTAAT	GTATAGCCT	CACTCTTGAT	CATAATGGGT	CAATGCCTCA	AATACCTAAA	AAAAAAAAAA
25	ATTAGATAGC	CAGACACCAG	GAAAGAAAAAG	TATTTCTTTT	TTTAATAAAA	AGAAATACCT	TTTTGAGCAA
	CTGAAATGAC	AAAGTCACAA	ATTTCTTGCA	CACCTTAAAA	TATACTTAAT	GTAAATGACG	AGTTAATGGG
	TGCAGACAC	CAACATGGCA	CATGTATACA	TGTTGACAA	ACCTGTATGT	TGTGCACATG	TACCCTAGAA
	CTTAAAGTAT	AATTTTAAAA	AAATTCTATC	TTCCAAAGCA	TATCACTTCT	CAGGTAGACA	CAGTGTTTAT
	TGCAAAAGAT	CTGATTTCAA	TAGTATTTCT	TCAAGAGTCT	CCCCAGAGAC	AAAGTCAAGA	AGAGGAAATC
30	AGCATATCTG	AGAAGAAAGA	TTTCAGGATC	ACTTTTTTTG	AGGGTCTGAG	AAAATGTTTA	GTTTCTATAT
	TATTTAAAAC	CAGAA TTGAA	ATGGGGTGAT	TCCTATCCTT	GCCACCTGCC	TCTACAACCC	CAAGAGTTTC
	TATCTGAGCA	TCTAACGTC	TTTTAGGCTG	AAAGGCTCAC	CATGGCTTTG	CTTGGTCTCT	CTCTAGTTCT
	TCTGCAGCCC	ATTCAGCCTC	TTGACTTAGC	ACAAGGGTCT	CAGGTCTCTG	CCCAAAGGGA	GTGTGCTGTG
	CTGCAGAGTAG	ACTGCACTGA	ATGTCAACAG	AAAGCCTTGC	TTTCTTTTCA	TTCTCTAACC	CAGTCTCACA
35	TCCTCCTGCT	CCCTCCCTTT	TCCCTCCCTT	TCCTCCTGCA	CTTCTCTTTC	CTCTTTCCCT	ACCCCTTTCC
	TAGACTGGCC	TCTATTGCCT	CCCACGTAGA	CAAAAATGAA	CTGCTGATCA	GAAAGTAATG	TGACTAGATT
	CTCTCTTCCT	TCCC TCCTTT	CTATCCTTCC	TTCCATTCTC	CTATGCATCT	TTCCTTACCC	TCCTCTCCT
	TCACTCATTG	TTG TGCTGT	TCTTCTTCCT	CTTCTTTTTC	CTCCTGCTCC	TCTTCTTCTA	CTTGTTCTTG
	TTCTTGTTTT	TGTTTG GTTC	TTGTTCTCCT	CTTCTCCTT	CTCTCTCTCC	TCCTCTCCT	TCTTTTCCAC
40	CACCCTCCCC	TATCTTTTTC	ATAAATGCTA	AACTAACTCT	TGGCTACCTG	TGGTAAATGG	CCCTTGGAAG
	TTGCAAATAC	TACAATCAA	AACTGCATTT	CAGACATATT	TATGATGTTT	GCAAAACTTC	AGTAGAGCTA
	AGCAGTGGAC	TTGATCTGTT	TCGGTCTCCT	CACCTCCGTC	TTTCTTGTCT	CACCACCTAG	TGGACGTCTCT
	TGTTAGTGGC	ACTTCTGAA	GTTAAACCCCT	GAAGAGAGCC	CATGCTCTCT	AGCTTTTCAC	CGTGTAGGTT
	TGGGAGCCTA	CAAGTACCTT	TAATATTCTT	GGACTATAAA	ATGAGATGGT	TTTATAAGAC	TGCATGTGAA
45	ATTAGGACCC	ATAIGATGAA	GGACAATAAA	AAGGAAGACC	CACTGATGTG	AGTCAATGAG	TCAAATGCAA
	ATCAGATTTG	CATITTTAGG	AAAATAATAA	TAACAACAAC	AAAAACTCTG	AAGCTCAGCG	CCCCATATTT
	ATTATATTGT	TTA TCTTTA	TAACAGCTCT	CTGCTATAGA	TATGATTATT	ATCCCCATTC	TAAAGAGTCT
	CAAAGAGGTT	AAGAAACAAA	TTCAAAAAC T	AGCGAAAGAC	AAGAAATAAC	TAAGATCAGA	GCAGAACCAT
	AGGAGGTAG	GACACGAAAA	AGCCTTCAAA	AAATCAATAA	ATCCAGGAGC	TGCATTTTGA	AAAGATTAAC
50	AAAAGTAGAT	GACCATCTAG	TAGACTAATA	AGAAAGAAAG	ATCAATAGAC	ACAATAAAAA	ATGGTAAAGG
	GGATATTACC	ACTGATCCGC	TAGAAATACA	AACTACCATC	AGAGATTACT	ATAAACATCT	TTACACAAAT
	AAACTAGAAA	ATCAGAAGA	AATGGATAAA	TTCTTGACAA	CATACACCCT	CCCAAGACTA	AACCAGGAAG
	AAGTCAAATC	CCTGAATAGA	CTAATAACAA	GTTCTGAAAT	TAAGGCAGCA	ATTAATAGCC	TACCAACTAA
	AAAAAGCCCA	GGATCAGATG	GATTACACAGC	CAAAATCTAC	CAGAGGTACA	AAGAGGTGCT	GGTACCATTC
55	CTTCTGAAAC	TATTCAGAG	AATAGAAAAA	GAGGAACTCC	TCCCTCACTC	ATTTTATGAG	GCCAGCATCA
	TCCTGATACT	AAATCTGGC	AGAGACACAA	CAAAAAAAGA	AAATTTCAGG	CCAATATGCC	TGATGAACAT
	CATTGCGAAA	ATACTCAATA	AAATACGGCA	AACTGAAATC	AGCAGCACAT	CAAAAAGCTT	ATCAACCACA
	ATCAAGTTGG	CTTCTATCCT	GGAATGC AAG	GCTGGTTCAA	CATACACAAA	TCAAATAACA	GAATCCATTA
	CGTAAACAGA	ACCAATCACA	AAAACCACGT	GATTATCTCA	ATAGATGCAG		



5	CTTACAAGGA	ATGIGAAGGA	CCTATTCAAG	GAGAACTACA	AACCACTGCT	CAAGGAAATA	AGAGAGGACA
	CAATGAATG	GAAAAACATT	CCATGCTCAT	GGGTAGGAAG	AATCAATATC	ATGAAAATGA	CCATACTGCC
	CAAGGTAATT	TATAGATTCA	GTGCTATCCC	CATCAAGCTA	CTACTGACTT	TTTTACAGA	ATTAGAAAAA
	AACTACTTTA	AATTTCATAT	GGAACCAAAA	AAGAGCTTGT	ATAGCCAAGA	CAATCCTAAG	CAAAAAGAAC
	AAAGCTGGAG	GCAATCATGCT	ACCTGACTTC	AACTATACT	ACAAGGCTAT	AGTAACCAAA	ACAGCATGGT
10	GCTGGTACAA	AAACAGATAT	ATGGACCAAC	GGAACAGAAC	AGAGGCATCA	GAAAAAACAC	CACACATCTA
	CAACCATCTG	ATCTTTGACA	AAGCTGACAA	AAAGAGCAAA	TGGGAAAGG	ATTCCTCAT	TATAAATGA
	TGTTGGGAAA	ACTGCTAGC	CATATGCAGA	AAACTGAAAC	TGGATCCCTT	CTTACACCT	TATATAAAAA
	TTAACTCAAG	ATGCATTAAG	GAATTAATG	GAAGACCTAA	AACCATAAAA	ATTCTAGGAG	AAAACTAGG
	CAATACCATT	CAGGACGTAG	GTATGGGCAA	AGACTTCATG	ACTAAACAC	CAAAAGCAAC	AGCAACAAAA
15	GCCAAAATTG	ACAATATGGA	TCTAATTAAG	CTAAAGAGCT	TCTGCACAGT	AGAAAAAAAC	AAACTATCAT
	CAAAGTGAAC	AGGAACCTA	CAGAATGGGA	GAAAAATTTT	GCAATCTATT	CACCTGACAA	AGGGCTAATA
	TCCAAAATCT	ACAAGAAACT	TAAACAAATT	TACAAGAAAA	AACAAACAAC	ACCATCAAAA	AGTGAGTGAA
	GGATATGAAC	AGAAGCTTCT	CAAAAGAAGA	AGTTTATGCA	GTCAACAAC	ATATGAAAAA	AAGCTCATCA
	TCACTGGTCA	TTAGAGAAAT	GCAAACTAAA	ACCACAATGA	GATGCCATCT	CATGCCAGTT	AGAATGGCGA
20	TTATTAAAAA	GTACAGGAAAC	AAACAGATGCT	GGAGAGGATG	TGGAGAAATA	AGAATGCTTT	TTACAGTGTT
	GGTGGAAGTG	TAAATTAGTT	CAATCATTGT	GGAAGACAAT	GTGGCGATT	CTCAAGGATC	TATAACTAGA
	AAAACCATTT	GACCTCAGCA	TCCCATTA	GGGTATATAC	CCTAAGGATT	ATAAATCATT	CTACGATAAA
	GACACATGCA	CATATATGTT	TATTGAGGCA	CTATTCACAA	CAGCAAGAG	TTGGAACCAA	CCCAATGCC
	CACCAATGAT	AAATGAGATA	AAGATGATGT	GGCAGATATA	CATCATGGAA	TACTATACAG	CCATAAAAAA
25	GGATGAGTTC	ATGCTCTTTG	CAGGGACATG	GATGAAGCTG	GAAACCGTCA	TTCTCAGCAA	ACTAACACTG
	GAACAGAAAA	CCAACATTA	CCCATTCTCA	CTCATAAGTG	GGAGTTGAAC	AATGAGAACA	CATGGACACA
	GGGAGGGGAA	CATCAGACAC	TGGGCGATGT	CAGGGGATGT	GGGCTAGGG	GAGGAACAGC	ATTAGAGAAA
	ATACCTAATG	TAGATGACAG	GTTGATGAAT	GCAGCAAAAC	ACCATGGCAC	ATGTATACCT	ATGTAACAAA
	CCTGCACGTT	CTGCTCATGT	ATCCCAGAAA	TTAAAGTATA	ATTTAAAAAA	AGTTTAAAAA	AAGAAAAGTTG
30	CCTTAGTCAC	ATAACTAGTA	AGAGACATGG	TTGGGAATTT	GAACAGAGGC	CAATCAGTTC	CAATCCATG
	CTCTTGATCA	TTAACTTGAA	CTTATGGCAG	GAACCTGGAA	GACATGGTAA	AATGGGGAAA	AACGTGGAGC
	CAGGGAGACT	TGTGAAAGTG	CCAGTGCTCC	CACTATACCC	TGAAAGAAGT	ATCTAGACTT	ACTTTTTTCT
	AAGTCTCTCT	CTCAATTTCT	CTCAATCTCT	CTCTCTCTTT	CTCTAAGAGA	TGGGAATGCT	GCTCTGTAC
	TCAGGCTAGA	GTGAGTGGT	CGCATCATAG	CTCATTCGAC	TCAAGGAATC	CTAGGGTCTA	GTGCCCCCTC
35	TCCTCAGCC	TCCCATGTAG	CTAAGACTAC	AGGCACATGC	CCCAACCTC	GACTAATTTT	TTATTTTTTT
	ATTTTTGTAG	AGACAGGATC	TCACTATGTT	GCTCAGGCTG	TAATCTGTCT	TTGAAGCTTG	TCCAATCAGG
	CTTTCAGCCA	CACCAATTCC	CTGAGACTGC	TCTCACCAAG	GTCCTACACT	TCACTAACAC	AAACAGCCTA
	TTCTCCATCC	TCACTTACT	TCACCAGGGA	GCTCTGTT	TTCTCTCTAC	TTCACTGGCT	ATTTCTCTG
	TATCATGTGT	TGATCTCCC	TCATCTCCCC	AACCTCCAAA	CCCTTGGAGT	ACTCCAGAGA	TCACCGCTTT
40	GCTCTTCTGT	GTCTAACCTC	ACTAECTTGG	TGGTCCAATT	CACACTCTTG	ACTTTGAATA	CCATTTAAAT
	GCGAACGAAT	TCTAATTTCT	GTACAACCAG	AACCATTTCT	CTGTAGCCAA	ATGCCTACTC	AACATCTCCA
	TCCCAACAA	AAATAGTTG	TTCAATAAGC	CTCTCATATT	TTACATATCC	CAAACTGAAC	TTCTGAATTT
	CTCTCCAAT	CTGTAGGCT	CTTCCCACAG	CCCTTCCATC	TCACTGGATT	ATAACTCCAT	CCCTCCAGTT
	ACTCAGACCA	AAACTTTTGG	AGTTAACTGA	GACACCTCTC	TTTTTTTTCA	CAAGTCATAT	CCAATGTGTC
45	AACAAATTTT	GGTAGTGGA	ATATTGCGGG	ATTTTTTAAG	AAATCAGAGA	GACCGATGGG	GTTCAGGAGG
	ATATTTATTA	TTTAAGTGCA	CTGGCCAAGT	CAGATTAACA	TCCAAAGGAC	TGAGCCCTGA	ACAAAGAGTT
	AAGTTACCTT	TTAACTCATTT	TGTGGGGTGG	GAGAGAGGGG	TATCTGTGCA	GGGGGAAGCA	TACTACAGAA
	GTGAGAAATA	AAGACAGTTA	TTCAATTAAT	TGAGACATGC	ATTACATCAT	TTCTTACTTT	TCAAGAAAGAA
	ACATGTTTTG	CGACTGAGT	TTATCTGTCT	AGTGACCTTG	CAGCTGCACA	GCTAGAGAAA	CAGGGTCTTC
50	ACAAATGCTG	GGAAGGAGT	AGAGGTAAAGT	CTCAGTACCC	ACAGAAAAAC	CGGAGTTTAA	TTTTTAAAGG
	GCTCCAGCTC	TTTCTCTTTC	TCAGGGGGAG	TTGGGTTTTG	TTACATACAA	ATGAGTTTCC	GCTTACACAT
	TATTTAATTT	CTTTCAATTC	CTGTTCCAAA	AGAAGCCAGA	TACAAAAAGG	TACATGTTGT	CTGATTCCAT
	TTATATGAAA	CATATAGAAG	AGGTAAATCC	ATAGAGACAG	AAAGTAGATT	AGAGGTTCCC	AGGGGCTGAG
	GAAGAAATGG	GGACTAACTG	CTTATAGGGT	ACAGAGTTT	CTTCTGATAA	AAATATTTTG	GAAGTAGATA
55	GACATTTTGT	TAGGCCATTC	TTGCATTGTT	ATAAAGAATT	ACCTGAGACT	TGGTAATTTA	TAAAGAAAAAG
	ATGTTTAATT	GGCTTACAT	TCTGCAAGCT	TTACGGGAAG	CATGGTGCCG	ATATCTGCTC	AGCTTCTGGT
	AAGGCTCAG	GAGCTTACAC	ATCATGGCAG	AAGGTGAAAG	GGGAGCAGGC	ATATCAGATA	GCAAAAGCAG
	GAGCAAGAGA	GAGATGTGGG	GAGGTGACAG	TCACTTTTAA	ACAGCCAGAT	CTGTGTAGAA	CTCATTCACT
	ATCATGAAGA	CAGTACCAAG	AGGATGGTAC	TAAATCATTC	ATGAGAAACC	CCACCTCAT	GATCAAAATCA
60							

[illegible]

Variable	Mean	SD	Min	Max
Age	35.5	10.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	9	16
Income	3.5	1.5	1	6
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical health	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Emotional health	0.5	0.5	0	1
Behavioral health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Occupational health	0.5	0.5	0	1
Financial health	0.5	0.5	0	1
Family health	0.5	0.5	0	1
Community health	0.5	0.5	0	1
National health	0.5	0.5	0	1
Global health	0.5	0.5	0	1
World health	0.5	0.5	0	1
Universal health	0.5	0.5	0	1
Human health	0.5	0.5	0	1
Planetary health	0.5	0.5	0	1
Ecosystem health	0.5	0.5	0	1
Biodiversity health	0.5	0.5	0	1
Climate health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Economic health	0.5	0.5	0	1
Political health	0.5	0.5	0	1
Cultural health	0.5	0.5	0	1
Religious health	0.5	0.5	0	1
Philosophical health	0.5	0.5	0	1
Artistic health	0.5	0.5	0	1
Scientific health	0.5	0.5	0	1
Technological health	0.5	0.5	0	1
Industrial health	0.5	0.5	0	1
Commercial health	0.5	0.5	0	1
Service health	0.5	0.5	0	1
Manufacturing health	0.5	0.5	0	1
Construction health	0.5	0.5	0	1
Transportation health	0.5	0.5	0	1
Communication health	0.5	0.5	0	1
Information health	0.5	0.5	0	1
Energy health	0.5	0.5	0	1
Water health	0.5	0.5	0	1
Food health	0.5	0.5	0	1
Health health	0.5	0.5	0	1
Life health	0.5	0.5	0	1
Existence health	0.5	0.5	0	1
Being health	0.5	0.5	0	1
Consciousness health	0.5	0.5	0	1
Spirituality health	0.5	0.5	0	1
Religion health	0.5	0.5	0	1
Philosophy health	0.5	0.5	0	1
Art health	0.5	0.5	0	1
Science health	0.5	0.5	0	1
Technology health	0.5	0.5	0	1
Industry health	0.5	0.5	0	1
Commerce health	0.5	0.5	0	1
Service health	0.5	0.5	0	1
Manufacturing health	0.5	0.5	0	1
Construction health	0.5	0.5	0	1
Transportation health	0.5	0.5	0	1
Communication health	0.5	0.5	0	1
Information health	0.5	0.5	0	1
Energy health	0.5	0.5	0	1
Water health	0.5	0.5	0	1
Food health	0.5	0.5	0	1
Health health	0.5	0.5	0	1
Life health	0.5	0.5	0	1
Existence health	0.5	0.5	0	1
Being health	0.5	0.5	0	1
Consciousness health	0.5	0.5	0	1
Spirituality health	0.5	0.5	0	1
Religion health	0.5	0.5	0	1
Philosophy health	0.5	0.5	0	1
Art health	0.5	0.5	0	1
Science health</				

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	Male	0.75	0	1
Marital Status	Married	0.65	0	1
Education	High School	0.45	0	1
Occupation	Unemployed	0.35	0	1
Income	\$15,000	12,000	0	40,000
Health Status	Good	0.85	0	1
Smoking Status	Non-smoker	0.70	0	1
Alcohol Consumption	Occasional	0.55	0	1
Stress Level	Low	0.40	0	1
Sleep Quality	Good	0.75	0	1
Energy Level	High	0.60	0	1
Mood Stability	Stable	0.80	0	1
Life Satisfaction	High	0.70	0	1
Resilience	High	0.65	0	1
Optimism	High	0.75	0	1
Gratitude	High	0.80	0	1
Forgiveness	High	0.70	0	1
Empathy	High	0.85	0	1
Compassion	High	0.75	0	1
Patience	High	0.80	0	1
Kindness	High	0.70	0	1
Generosity	High	0.65	0	1
Humility	High	0.75	0	1
Modesty	High	0.80	0	1
Shyness	Low	0.30	0	1
Introversion	Low	0.25	0	1
Extroversion	High	0.70	0	1
Social Skills	High	0.85	0	1
Communication Skills	High	0.75	0	1
Teamwork Skills	High	0.80	0	1
Leadership Skills	High	0.70	0	1
Problem Solving Skills	High	0.85	0	1
Decision Making Skills	High	0.75	0	1
Time Management Skills	High	0.80	0	1
Organization Skills	High	0.70	0	1
Planning Skills	High	0.85	0	1
Execution Skills	High	0.75	0	1
Adaptability Skills	High	0.80	0	1
Flexibility Skills	High	0.70	0	1
Resilience Skills	High	0.85	0	1
Stress Management Skills	High	0.75	0	1
Emotional Regulation Skills	High	0.80	0	1
Self-awareness Skills	High	0.70	0	1
Empathy Skills	High	0.85	0	1
Compassion Skills	High	0.75	0	1
Patience Skills	High	0.80	0	1
Kindness Skills	High	0.70	0	1
Generosity Skills	High	0.85	0	1
Humility Skills	High	0.75	0	1
Modesty Skills	High	0.80	0	1
Shyness Skills	Low	0.30	0	1
Introversion Skills	Low	0.25	0	1
Extroversion Skills	High	0.70	0	1
Social Skills Skills	High	0.85	0	1
Communication Skills Skills	High	0.75	0	1
Teamwork Skills Skills	High	0.80	0	1
Leadership Skills Skills	High	0.70	0	1
Problem Solving Skills Skills	High	0.85	0	1
Decision Making Skills Skills	High	0.75	0	1
Time Management Skills Skills	High	0.80	0	1
Organization Skills Skills	High	0.70	0	1
Planning Skills Skills	High	0.85	0	1
Execution Skills Skills	High	0.75	0	1
Adaptability Skills Skills	High	0.80	0	1
Flexibility Skills Skills	High	0.70	0	1
Resilience Skills Skills	High	0.85	0	1
Stress Management Skills Skills	High	0.75	0	1
Emotional Regulation Skills Skills	High	0.80	0	1
Self-awareness Skills Skills	High	0.70	0	1
Empathy Skills Skills	High	0.85	0	1
Compassion Skills Skills	High	0.75	0	1
Patience Skills Skills	High	0.80	0	1
Kindness Skills Skills	High	0.70	0	1
Generosity Skills Skills	High	0.85	0	1
Humility Skills Skills	High	0.75	0	1
Modesty Skills Skills	High	0.80	0	1
Shyness Skills Skills	Low	0.30	0	1
Introversion Skills Skills	Low	0.25	0	1
Extroversion Skills Skills	High	0.70	0	1
Social Skills Skills	High	0.85	0	1
Communication Skills Skills	High	0.75	0	1
Teamwork Skills Skills	High	0.80	0	1
Leadership Skills Skills	High	0.70	0	1
Problem Solving Skills Skills	High	0.85	0	1

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[illegible]

[illegible]

[illegible]

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Klasifikasi	
Spesies	100%
Genus	100%
Familia	100%
Ordo	100%
Kelas	100%
Filum	100%
Kingdom	100%
Morfologi	
Ukuran	100%
Warna	100%
Struktur	100%
Reproduksi	100%
Ekologi	100%
Perilaku	100%
Interaksi	100%
Persebaran	100%
Manfaat	100%
Risiko	100%
Kelestarian	100%
Referensi	100%

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Variable	Mean	SD	Min	Max
Age	32.1	12.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.5	8	16
Income	35.0	15.0	10	60
Occupation	25.0	15.0	0	100
Health status	75.0	25.0	0	100
Life satisfaction	60.0	20.0	0	100
Stress level	45.0	15.0	0	100
Work-life balance	55.0	18.0	0	100
Family support	65.0	22.0	0	100
Community involvement	50.0	20.0	0	100
Personal growth	60.0	25.0	0	100
Financial stability	55.0	18.0	0	100
Emotional well-being	65.0	20.0	0	100
Physical health	70.0	22.0	0	100
Mental health	60.0	20.0	0	100
Social relationships	55.0	18.0	0	100
Work environment	65.0	20.0	0	100
Leadership skills	50.0	20.0	0	100
Teamwork	60.0	22.0	0	100
Communication	55.0	18.0	0	100
Problem-solving	65.0	20.0	0	100
Decision-making	50.0	20.0	0	100
Time management	60.0	22.0	0	100
Organization	55.0	18.0	0	100
Productivity	65.0	20.0	0	100
Quality of work	50.0	20.0	0	100
Job satisfaction	60.0	22.0	0	100
Work-life balance	55.0	18.0	0	100
Family support	65.0	20.0	0	100
Community involvement	50.0	20.0	0	100
Personal growth	60.0	25.0	0	100
Financial stability	55.0	18.0	0	100
Emotional well-being	65.0	20.0	0	100
Physical health	70.0	22.0	0	100
Mental health	60.0	20.0	0	100
Social relationships	55.0	18.0	0	100
Work environment	65.0	20.0	0	100
Leadership skills	50.0	20.0	0	100
Teamwork	60.0	22.0	0	100
Communication	55.0	18.0	0	100
Problem-solving	65.0	20.0	0	100
Decision-making	50.0	20.0	0	100
Time management	60.0	22.0	0	100
Organization	55.0	18.0	0	100
Productivity	65.0	20.0	0	100
Quality of work	50.0	20.0	0	100
Job satisfaction	60.0	22.0	0	100
Work-life balance	55.0	18.0	0	100
Family support	65.0	20.0	0	100
Community involvement	50.0	20.0	0	100
Personal growth	60.0	25.0	0	100
Financial stability	55.0	18.0	0	100
Emotional well-being	65.0	20.0	0	100
Physical health	70.0	22.0	0	100
Mental health	60.0	20.0	0	100
Social relationships	55.0	18.0	0	100
Work environment	65.0	20.0	0	100
Leadership skills	50.0	20.0	0	100
Teamwork	60.0	22.0	0	100
Communication	55.0	18.0	0	100
Problem-solving	65.0	20.0	0	100
Decision-making	50.0	20.0	0	100
Time management	60.0	22.0	0	100
Organization	55.0	18.0	0	100
Productivity	65.0	20.0	0	100
Quality of work	50.0	20.0	0	100
Job satisfaction	60.0	22.0	0	100
Work-life balance	55.0	18.0	0	100
Family support	65.0	20.0	0	100
Community involvement	50.0	20.0	0	100
Personal growth	60.0	25.0	0	100
Financial stability	55.0	18.0	0	100
Emotional well-being	65.0	20.0	0	100
Physical health	70.0	22.0	0	100
Mental health	60.0	20.0	0	100
Social relationships	55.0	18.0	0	100
Work environment	65.0	20.0	0	100

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1. General information	
1.1. Name of the project	1.2. Date
1.3. Version	1.4. Author
1.5. Contact person	1.6. E-mail
1.7. Address	1.8. Phone
1.9. Fax	1.10. Mobile
1.11. Internet	1.12. Other
1.13. Other	1.14. Other
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40	AAAGAACATG	TAAGTAAATA	ATTGTTGCAA	AAAAAGTGGT	TTTAAGGAAG	TCATTAAAAG	TGGCTTTTTG
	GGGTTTTTTA	GTTTTATCTT	ATTTCCCTCT	TATAAAGAAA	GAAGTTTTAA	GAATTTGTGT	TGAGACAGAC
	ACAGGGATCC	TGAATATAGT	ATGTCATGTT	GCATTGACCA	ATATTCAATT	ACCATTATGA	TTAGATGTCA
	GAACCTCCTT	TTATAAAGGA	AAGTTAATCC	TTATTTAGTC	CATCTCTACA	TGCCAGAGGT	AGCCTTGAGG
	CACAAAAGCT	TGCCATAGAAT	TTATGGGTCA	CAGACAGTTT	TAATATTGCT	ATTTGTTGGG	CGAATGAAAA
45	TCACTAGTTA	ATTAATACCT	CTCTTTGCTG	ATAGGATGCT	AAAAATGTTA	CGCACCTGGC	CTAATGTTAC
	CCTTTTTTAG	TTCTATTTT	GCAAGATCAT	GGAAGTCAGA	AAATAATATT	TATACATGCT	TGCATCTCTT
	GAAGCACA	ATAATTAATG	GATGTTCACT	AAACAATGAA	TGAATATGTG	ATTCAGTAAA	TTTATGATCT
	CTAATAGTAT	GAAATTAAGT	AAATTTGGCT	CTTGAGCTTT	GATTTGTTTT	TTCTCTCATT	TTTATTTATC
	CGTAATCAGA	ATAGTGAATC	TGTGTATTCT	GGGTGTTTAC	ACCTAGTTTC	AGACCTTCTC	CAGGCTCTTT
50	TCAAGGAGGC	CTATCTCTT	CAAAAGCAGT	TAATGGAACT	GCTGGACATG	GTTTGCATGG	ACCCTTTAGT
	AGATGACAAT	GATGATATTT	TGAATATGGT	AATAGGTGAG	TGAAGAAAAC	TTTCTGCTTA	GTATATGGTG
	ACTATAAATC	ATGATCAAT	TAAAAATTGTC	TCTAATGATT	CATGTTATTT	TCTTACTAAT	TATGCATTA
	AATTGATTTA	AATCTTACCA	AATAAATTTT	TAATCTTGAA	ATTTGGAATT	TGTAAAAATT	ATTTTGGGTA
	CCTTAACCTA	G					

Table 1. (continued)	
1.0	0.00
1.5	0.00
2.0	0.00
2.5	0.00
3.0	0.00
3.5	0.00
4.0	0.00
4.5	0.00
5.0	0.00
5.5	0.00
6.0	0.00
6.5	0.00
7.0	0.00
7.5	0.00
8.0	0.00
8.5	0.00
9.0	0.00
9.5	0.00
10.0	0.00
10.5	0.00
11.0	0.00
11.5	0.00
12.0	0.00
12.5	0.00
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13.5	0.00
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14.5	0.00
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15.5	0.00
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16.5	0.00
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68.5	0.00
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69.5	0.00
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70.5	0.00
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71.5	0.00
72.0	0.00
72.5	0.00
73.0	0.00
73.5	0.00
74.0	0.00
74.5	0.00
75.0	0.00
75.5	0.00
76.0	0.00

[illegible]

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 AGAAAGTCTA AACACAGTA TAGTCTATAG TGGCAAGAGA GAGTATGGGG GCTGCTTAGC CAGGGTGGCT
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 AGACAGCTCC CTTC AACCTC TTTTATAAGG GCACCTATGT CATTCAATGAG GGCAGAGCCC TCATGACTTA
 ATCACTTCCC CAAAGGCCCC ACCTCTTAAT AGTATCACAT TGGGTGTAG GTGTCTGGGA GCACACCAAT
 CTTCAGGCCA TATCATCTCA CTTGGAAAAA AGTCAAAATA AAACCAGTAG ATTTAATTAA TATTACACTA
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 15 CTAGGTGGCT TAAACAATA GAATTTTATT CTCTCACATT TCTAGAGGCA GAAAGTTCACA GTGTGTCAAT
 AGGGCCATGT TCTCTGGAAG GCTTTAGGGG AGAATATATT TCATATCTTT CTCTTAGCTT CTCGGTGTCA
 CTGGCAATCC TTACCTTACT TTGGCTTTCT GTGTCTTCAC ATCATCTTTT TATAAGAACA CCAGTGATAG
 TGATTAAGGG CATACCTTAC TTTAATATGA CCTCATCTTA ACTAATTATG TCTTCAATAA CCCTATTTCC
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 20 ATAACAACCC CTAATAATCGA TATTATTCT CAATTAAAGTC TTGAAATTGG TTCAAAAAAG AGAATATTCT
 ATTAGAGTTT TTA/TGTATA GTTTTAAACAT ATAGTTCTTT AGCCCCCAAT TTTTTTTTTT TTTTTTTTTT
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00400 " 6 2 9 4 5 6 0

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 (SEQ. ID NO: 3009)
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 CAGCTTCTCG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT
 TGCCACAGC AGACTAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA
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 15 CAACGCGCTG ATACCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA
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 GGACTGGTGG CTCATCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG
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 25 CTCATGGATT ACATCGGTAT TAACCTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG
 TGAGCAAGAA ATTTAAAAAT TGTTCACAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT
 GACCTCGGTC CCAATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC
 CGGAGCAGCC ATAAGGACAG CATGAACCTGA CCACCCTTAG AAGCACTCT-3' (FRAG. NO: 2481)
 (SEQ. ID NO: 2481)
 30 5'-GATCAAAATT TTACCTATT ATGCATTGA TATATAAATA AGTATATAAA TGCACACACA GACACAGCAA
 TGATGGTGAA CAGTCTTCAT ACAATTATAT GGATGAATCT CATAAAATGC TGAGTTAAAG AAATCAGACC
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[illegible]

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Coulam et al. (2005)	
Study design	Retrospective cohort study
Study period	1996-2000
Study location	United States
Study population	Patients with a diagnosis of Crohn's disease
Study variables	<ul style="list-style-type: none"> Independent variables: Age, sex, race, ethnicity, education, income, insurance status, comorbidities, and use of other medications. Dependent variables: Hospitalization rates, surgery rates, and mortality rates.
Study results	<ul style="list-style-type: none"> Patients with Crohn's disease had higher hospitalization rates compared to the general population. Patients with Crohn's disease had higher surgery rates compared to the general population. Patients with Crohn's disease had higher mortality rates compared to the general population.
Study limitations	<ul style="list-style-type: none"> Retrospective design. Potential for confounding. Incomplete data.
Study conclusions	Patients with Crohn's disease have a higher burden of disease compared to the general population, with higher rates of hospitalization, surgery, and mortality.

Table 1. Continued	
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1.5	0.00
2.0	0.00
2.5	0.00
3.0	0.00
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76.0	0.00

[illegible]

1

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	ACCATGTGCC	TTTAAACAAG	GTTACTTGAA	CCCTCCAAC	TCAGTTTCTT	CATCTATATA	AGAGGAATAA
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	TGTAGATTAG	AGTCAGAAGA	GCAATATACA	AAAGACAAAA	GCTGAGAAAT	TATAGTAGTT	TATGGTCTGT
	GATAAGTGCT	CATGAAGGAT	CTCAGGAGAA	ATGATCACAG	TGAGAAGAA	TGAGAAAAGA	GTGATATGAG
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[illegible]

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[illegible]

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TTAATT AAGGACAGAG CAG TTAGCT ATA T TACCTG TGAC TACAGG AGA ACTGTG TAGT ATTTAA AATGAGGTGG GAGG CAGTCA TGAT GAGCAC GAG A AATGT CTT A GATGT TTG TACTCT CTGA ATGACT GGA T GACTCT TTA GATTTT TGT A ATTGTT GTGT T TCACT AGC TCTATT CAAC AAAATG TTAA AAGAGC AGC TCTTCC TCATAAACTT ATTTATAAGT AAATGAGTTC CCTT TCCAT ACAGAAAAAA CCT AAGGGGA TGGCAACAG ACAC GAAGCC TCACTGACCT ATAC TTTTAG TGCACTCATG CATCAGGTTC GTTCAAGGTC CTGCTACTCC AGGCAAGACA CTAC TTTAAA ACA T AGGGAT AAA AAAAAAC CCAT TCTCA ATTGTCAGAT TCCC CCAAAA CTATTATAAA	CTAGAAACAC AGTAAAGATC CTTGTTTAGC GATAGATGGT TTTATTGGTA GAAGACTCCA GACTCTAAGC ATCCAGGGGA AAGCAGAGTT ACCTATGTAG TCATTGAACA AGGACACATA AACAAATCAT CAGCGAAAAG CCACATGTGA GACTGAATAG GTGCCTGCAG GATAATATAG GAGGTTTTGC GAGGTAGGAG GATAGTAGTC ATGGATCATA TGAATAAATG TTGAGAGGCT GTCAGGTGTG CAGGAGTTTG GGCATGGTGG AGGCGGAGGT TCAATAAATA AGCCAGGGGA GTACATTTAG AGAGGAAAAGC TCAACTTCTG TTTGAGTGGA AACCTGCAAG CTTGTCTTTC TACATTACCT GGATGGGTGA TGATTTGCCA TATTTCTTGG CACTTAGAGT GGTTGAAGTT AGAAAAGTTCA ACCTGTATAC ACTTTCCATA TTCCAACCTC ACCAAGGACT CATAATGATA CCTTGCCGAG TTTTGTGTGC AAAGTGATTT GAATGCTGTC GTATGAACAG TCCCTACTCT TTTATCTAAT GAGATTGTGG TAGGGACTGG GTTTTATGAT ATGCAATTTT ACATTGCTTC AGCTTAGGAA AATATAATGG AAACTTACCA TTACATGTAT CCAAATTAAT AATTACAAAG ACAAAAAAGG GGTGTATTGA	AGTCACGAAA TGAGAGACCC CTAATCTTTT TTAAAACAAG TTGACAATTA ATCTTCTCTG TAAGACTTAA AAAGAAACAAT CAGAAGGGAT TATCTTGGAC AATATTTTGA AAATCCTAGA TTAAACAAGT GCACTGGAAG GCTGCGACCT CAAATACAAA CATACTAAGC TCTCTTATAG ACTAGGGTGA TAAACTAAGT GTAGAAATAA TATGAGAGTA GGTGCTGTGA TATTAGACAT GTAGGTCAGG AGACCAGCCT TCATGACTG TGCAGTGAGC AATAAGAAAC GTAGATGAGA ATGGTTATAA CAGGAGATGA GGCAGTCAAA GTGTTGAGAC CACAGACAAAT TATGGGAAAT AGCATAGAGC AAGAATGGAT AGAAGAGGAT TGTCAGTTAG TTTTAAATGT AATAACTGTA AGATTCTCTG TTAACTGGTC GGAATCAAAC ATGGCTGTTG AACCAGCCTC ACTGACTAAT GCAACTACTG TTCTTTTCC GATAAACTGA TGGCCCAACA TAGGTTTCTG TACTTCCCAG AATGTGTTAC CTCTCTATTA AACCTAGTAA CCCCATTTTT TAAGATACAG CCTAGGTGAG AAAAAAGGGA GAAAAATCCT CATTTGTAGG GGGGAGATAG GTATACATTT TTTACCTGGG TCTGAAAAGG TGAAAAAAT TTAATACTAG	CTTGGTGATT AAGAGCAGAA TATTTTATT CTTTTATTAA TGGGAATATC TCTGATGGGA AAGATAAGTA ACGTGCAAAA CTGGTGTTGA CTTACCTTAA GGCTTTCTGT TCTCACAGAA GATTTTCAGC GAAAGCTGCT GAAGGATACC TGCCCTTGGG ACAGAGGAAA GTCATAATAA GAGGTGTGAT TAGGGGCTAT ATAAAAAGTG AAAAAAAGAA ATTGAGATAA CCCAGTGAG CCTGTGATCC GGGCAACATG TGGTCCAAG CAAGATCTCG GTAAGGGAAA TACTCAAAGT GAGGAATAGA AGCATCATAG TAATATAAGG AGAAGACCAA TCTTGAGAGA GTAATATAGT TAGCTAATGT GGATGGATGG ACTGGTAGCA ACAGGAAAGT GATCACTGAT AAATTATTTT GGGTTCTTAG TAGGCAACAG AATAGTTTTC TACCTTACCT TGGGGAATTG AGGAAATACC GGGAAATGT ATAGGCACCA TTTATATTGT GCAGGCTCTC AGTCCCCTGG TTTGTTCATT CTTCTTCTCT ACAGTATTTA GTGTAGCACA CAGAAGAAGA AACCAAGAGT ATCTGAGGCA AATGTCCTAA ATTCACTTTA ATATGTAAAG ACCATCTTAC AATACAATGT AAATATAAGC ACAGAAATCA TAAATACTAG	AGAGACCAAT GGGCGAGAAA ACTCTATTAG GAATTGTAC CAATTCCAAG AGCAGCTTGG GAAATTATCC GTACGGAAAT AAAAACGGT ATTGAATGAG GAAGAACATC TTGACATTCC AATGGTACGT TACCTTTGCA GAGAAGCTAG TGCAAGCTTT ACACTGTTAT GGCAACCAGA TTCAGTGGCT CACTCTACTT ATAAAATTA AGGAGATTGA ATTTCAGGTT CAGGACTTTG GGAAAAACCT CACTTGGGGG CCACTGCAAA AGGAAATTA AGGTGAAGAT AAGTGGCAAA AAGGCAAGAG ACAGAAAAGT TTAGAGTAGA CTTTTCTGTG TGAGATCAGG GCACTTAAGT ATGGATGGAT GAAATAAAAA AAGACATTAG ATTGGACATG CCGTTCAGGA GATTTACTGT TGGAAAGACA AGTGACTAAC TTCCAGCCCG CTGTATACTT CTCAACTGAA CATGCAAGCA GAAATATCAT GTCCAAATGT GACTTCATTT AATTATTCCA CATGGCACA TAAAAAAGTAC TTCAACAAAC TATTATTTCA AACTGATATT CAAGACATG TTCCGCGAAA ATAAACAGCT ACAATGTAA AAACTAAAAG TGGATTCTAA CAAACGAAAT ATATATGAAG AGGAGAGTCT TGTAGCAATA GGCAGCAAA	TCCCAAACT CCAAAAGCCA TCACTACAA ACCATGGTCT AAGACAAGGA CAAGATTACC AGGTAAAGAT GGTAAAAAGT TAGAGAAACG AAGCTTCTAA ATTCTAAGTA AGAGAGGGA ACTGTGAAAA TGTTGAAAA GTGTGCAAG GCCTGTTCAA ATGCTGAGAT TTTTATTCCA AAAAGATAAT CAGACAAGAG TGGGGGTAGA TAATGCTTCC GAATCAGGCA AGTGGAGCCC GAAGGCCAAG GTCTCTACAA CTCGAGATGG CCGTGATGG TCTGATCATT AAGGAGGCAA ATAAGTAACA AAGAAGGTTG GACCATTGGA TTGAGGAGAT AAAGGAAACA GATAGTATTT ATGTTCTCAA GGAAGGATGG CAGCATGGGA AAGAGTCTCT TTCTAGTGA CAGAAAAACA TCCCAAACT ATTCTCAGAG ATGTTAAGAC TGTTCTGAA AGCAAACTTA AATGAGAGAT AAATTAATCT GGTGCTTGA GATTGTATTT CAGACACTGT TTTATGTAGC GGTTGCGAT AAGGGACAAA ATTTATTGAG TTTAATCCTC CAGAACCGAT ATTTTAAACC AGAGAAGGGT TTCCTATTTA AAAAAAAAA ATGTTAATAA TATTTAATAG ATCTTAGGAA AGTGAATGGG TGCTGCCAG GGCAGCAAA
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5	CAATGAAACA	GCA^AAAAAG	ACCAGAACTA	TACCTAATTA	TGATGAAGAT	TTAAGGTATG	ATAAACATGA
	CATAATTCAA	ATCAGCAGAA	ATTGGCATAG	ATAGGGTTAA	GACAAATAGC	TAATCATTAG	AGGGGAGGAA
	GGAAAGGAGG	GAGGATAAAA	TTAGGTTCTT	GCCTTCATCT	TACATTAAAA	TAAATCCGAC	ATGTATTACA
	TTTAAATTTT	TTTA^AAAAA	GAAACACAAA	AATACTTGAA	GAAATATAAA	GTGTGTTAT	AGTCTTTTGA
	TGGGAATTTT	TTTTITTTTC	AGAGACAGGG	TCTTGCTCTG	TCACCTAGCC	TAGAGTGCAA	TGGCATGATC
10	ATGGCTCACT	GCAGCCTTGA	ACTCCTGGGC	TCAAGTGATC	CTCCCAGCTC	AGCCCCCAG	GTAGCAGGAA
	CTACAGGCAT	GCGA^ACACCC	ATCCAACTTA	TTTTTTATTT	TTTGTAGAGA	CAGGGGCTTT	GCTTTGTTTC
	CCAGGCTTAT	CTCC^AACTTC	TGCCTTCAAG	CACCTCAGCC	TCCCAAGAGG	CTGGGCTGAT	GGGACATTTT
	TTAACATAGT	GCCA^CATTAC	CATAAATGAA	AAGCTTGTAA	AATACTAATT	TTTAAAACTA	ATATATATCA
	GAAATTTTTA	TAAA^CAAAGT	TAAAAAGCAA	ACACAAAAAA	TTTGTAGCAC	TTATGACAAA	TATATGTATA
15	TATATGAATA	CAA^AAGAGC	CTTTACAAAA	CAGTAAGAAA	ACAATGAATA	CTCCCAATGG	AGTATTCAAA
	ACTAAACTGC	TAA^AAGCAAT	TCAAAAACAAA	AAACATAAAC	TATGCATATA	TGTATGTGAA	AAAGTTTAAC
	CTTATCAAAG	AAGT^AAACTC	TCAAAGAAAT	AAACATCAAA	TAAAGAAATA	GCCTTTTCCC	ACAAAATAAC
	AAAATCTGTA	AGA^TACTGTA	GCTGCGAATG	TTTCAGAAAA	TAAAAAAAAT	CATACACCTA	GTTCGGCATG
	TAATTAATAT	AGA^T^CAGAAC	ACTTTAAAAA	TATTTATAGG	CCAGGCACGG	TGGCTCATGC	CTATAATCCC
20	AGCACTTTGG	GAGG^CCAAGG	CGGGTGGATC	ACCTGAAGTC	AGGAGTTTGA	GACCATCCTG	ACCAACATGG
	TGAAACCCCTG	TCTCTACTAA	AAATACAAAA	ACTAGCCAGG	CATGTTGGCG	TATGTTGGTA	ATCCTGGCTA
	CTCGGGAGGC	TGAGGCAGGA	GAATTGCTTG	AACCCAGGAG	GTGGAGTTTG	CAGTGAGCTG	ACATTGTGCC
	ACTGTACTCC	AGCTTGGGCA	ACAAGAGCAA	AACTCTGTCT	CAAAAAATAA	TAATAAATAA	AAATAAAAAA
	TTTATATACT	CTGACCCATC	AATTTGTCCA	GCATAATTAG	GCATGTGTAC	AAGGGTTTAC	ACACAAGAAT
25	GCCTATTGCA	ATA^TGCTTT	TAATGCTAAA	AAAAATTGGG	GAAAAATGCTT	TAAAAATATA	GATTAAGACT
	GTACATTGTG	GTAC^AGTCAT	ATAATCAATA	GTATACAGCT	ATTATTTATT	TTCAGCCACT	GTCCAAATAA
	TAGCCTGGCC	TAAC^ACACAT	CTGTTAGGAT	ACGCAAGCAC	CGTAGGAGGA	TTCAGCTATA	GTCTCAAGTG
	TTTCACACCA	CTGCTCCTTT	GCTAATAACC	TTCAATGGCT	TTTAAAGAAG	TAAAAAACAA	AGGCAAAATT
	CCTTAGTCAG	CCCT^AAGAC	TCTCTGTTAC	TTAGCTCAAA	CTACCCTTTT	CAACAACACT	GCCCTAACCA
30	GGATGAGTTT	TTT^CCCCCC	TGGAGTACAT	TCAGCCTTTT	CTTATCAAAAC	CTTCCTTTAA	ATAAGTATCT
	TCTCCAGGAC	CAC^TCACTT	TCTTCCCCAA	TTTAGCATTT	CTATATCTCT	CAGGCCCTACC	TCTATAAAGC
	CTGTCCTAAC	CAC^T^CAAACC	CTAGCTTTTT	CTCTGAACTG	CTGAAATAT	TTTTCTCTCA	TTGGCCATTT
	AGGTAAAAAG	GTT^TTTACTG	TTTATTACCT	ACTCAATAAA	AATTTTCTTT	TTTTGAGACA	AGGTCTTACT
	CTGTCCGCTA	GAA^TGGGGGG	AAGTGGTGTG	ATCACAACTC	ACTGCAGCTT	CTACCTCCCA	GCTCAACAGT
35	CCTCCCACCT	CAG^CTAGTG	AGTAGCTGTG	ACTACAGGCA	TGTGCCACCA	TACCCCACTA	CTTTTCACTT
	TTTATTTTTT	GTGA^ZATGGA	ATCTCACTAT	GTTACCCAGG	CTGGTCTGCT	GATCTCAATT	GATCTCCTCA
	CTGTGGCCTC	CCA^AATGCT	GGGATTACAG	GCATGAGCCA	CAATATCTGG	CCCCAGTAAG	CTTTTAAGGC
	CATTAACATG	AGG^ACAGTG	TCTTTTACAC	TATTTTATCA	GCTAGGGCTT	TGCATGGAGT	AGGAGTTTAG
	TAAATGCGGT	TGA^TGGGTTA	ATCAATGTGT	GAAAAATATC	AGAGCCACCA	AAAAACAGATA	TTATGTCTAT
40	TCTCATCAAC	AAT^CAAAATT	GAGTAAACAG	CAATTTTCTA	ATACAGGAAA	CCACAAAACA	TTGAATGGTG
	ACATTAATAA	ATT^CCCCCAG	CAGGAGCCAA	CCAATTTTTT	CATCTGATC	CAAGTTAGCA	AACTGCAAAA
	GATAGGAAGC	ACT^AATGAGT	GGAAATTTGA	GTAGAAGCAT	TTCTTATGAA	GGCTGTCTTG	ACTGGATCAC
	ATTTTTATTG	CTGT^TGGAGG	TGCCAAATGT	GTGTGTTTAT	GCTAATCCTC	CACCTCAGGC	AAACACACGT
	CAAGGATCCT	ACC^AAGTGT	ACCGTCAAGT	GTCGTGTGGC	AGCTCAAGGC	CCCAGCGTTG	TTCCCTTGCA
45	CTAGGGAATA	GAC^ATATTCC	AGGTACAAGT	ACTCCCACCT	TGATGCTACA	GAGGAGTTGC	TGAACTTTGT
	GTCATTAATC	TCT^TTCGTT	AGATCCCAAC	CCTGTTTAAA	TCCCACCTATC	TGCCTACTCT	GGGTCTTCAC
	CAATTTACTA	GAT^CTAGTT	GGAGAAAATC	TACAAAGCCT	TGCTCCCTTT	AGATTTAAAC	AGGTCTCCGT
	TTAAATTTAG	AAT^TGCTAAC	TTCAAGCGGG	CCCTTATGCG	ACAGTATGCC	TGTCAGTCAT	ACTACATTTT
	CTCAATTTCA	TTCA^TGTGAC	TGCTCCATAC	CTTCCCTCT	CTCTTCATAC	TACTATTATC	TCTTCCCCCC
50	TCCCTCATTT	TTAACTGATG	ATCTTGTTTC	CTATTTCTCT	GAGAAAAATG	AAGCCATCAA	AAGAGAGTTT
	CCACAAACTC	CTA^TGCCTT	ATCTAGCCCT	GTACCATATA	CTTTGCATTT	CCTCTCATT	CCATGGATGT
	ACTGCCTATC	TGT^CTTTCTA	TCTAAGGCTA	ACCCCTCCAC	TTCAGTTTGT	AATATTATCA	GCTCTTACCA
	ACTCAAGGCC	ATT^GCTCTAG	CAATTCTCTC	ATTCTCTCTC	ATTTTCTTCC	ATCAAGTTTT	CCTTTTCTTC
	AATTAACAGA	GTA^GCTCTTA	AAGGGAATAA	AAAGTCTTCT	TTTTCAATGC	TTCATCATCA	TGGCCATCAG
55	AGAAATGCAA	ATC^AAACCA	CAATGAGATA	TCATCTCACA	CCAGTTAGAA	TGGCAATCAT	TAAAAAGTCA
	GGAAACAACA	GGT^GCTGAG	AGGATGTGGA	GAAATAGGAA	CACTTTTACA	CTGTTGGTGG	GACTGTAAAC
	TAGTTCAACC	ATT^CTGGAAG	ACAGTGTGGC	GATTCCTCAG	GGATCTAGAA	TTAGAAATAC	CATTTGACCC
	AGCCATCCCA	TTAC^TGGGTA	TATACCCAAA	GGATTATAAA	CAATGCTGCT	ATAAAGACAC	ATGCACACGT
	ATGTTTATT						

1. <i>Staphylococcus aureus</i> (n = 10) 2. <i>Staphylococcus aureus</i> (n = 10) 3. <i>Staphylococcus aureus</i> (n = 10) 4. <i>Staphylococcus aureus</i> (n = 10) 5. <i>Staphylococcus aureus</i> (n = 10) 6. <i>Staphylococcus aureus</i> (n = 10) 7. <i>Staphylococcus aureus</i> (n = 10) 8. <i>Staphylococcus aureus</i> (n = 10) 9. <i>Staphylococcus aureus</i> (n = 10) 10. <i>Staphylococcus aureus</i> (n = 10)	
1	100
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99	100
100	100

	TCGACGTGGCA CCCGAGTAGC AGGTTTCACC AAAGTGCTGG ACCATGTTGT TGGGATTACA ACATTGTCAA TCTGTCTCCT CTCAGGCTCC ACTTAAGACA CCATTTCCAG CTGTGCAGGA AGCTGAACTC AACATAAATC CTGAAATATT ACTCTGTAAT TTTTTTATCC CAGGAAAAAA GGAGAACTTT GTGGTGCTTG ATGGGTGCAG GGCCAGCACT TGGTCCACTC GTTGGGCTGA TCAAGAGAGC TCTTATCCTT TTAGTTCAAT AGGGTACATG TCAACTCGTC CCCTGGTGTG TGTGTATGTT TTATGTGTGA TTCCTTCAAC GCTGGCGCGC TCAGCTCCTC AGATGGGGTT CCCAAAGTGC AAAAAAAAAA ATGCCAGTTT ATGCCAAATT CTCTCAGCCA AAGCCCAACA TAAAACACAG GTTATTTTAT AAAATTGACA GAGGCTAGCA TGGCGTGATC GTAGCTGGGA ACCATGTTGG GCATTACAGG AGAGGCTTCA ATTCCAGGTC GACTTAAAAG TGATGGATAT GGCACATGTT CTTCTTTAAA TCATCAGTCA TAGATTGCTA AGAACCAGG TTCATTAATT TGCCTCTTAA CATGTGAGTC TCTATTTTAG TATGTTATTA GGGGAGGCTC TCTTTAGCCT CTGTCTCAAT GTTTTACTTC	TGA`CTCAGC TGGGACTACA ATGTTGGTCA GAT`ACAGAC GCAT GCTGGT GGAGTGAGCC ATCCAGTGGC TATCTGTTTC TATCTGGGAT TTAAGTGGTC TCTCACTGTT AAT`GGACAA ACCAAAAAAT AAGGATACAC TGTA`CTTTAT AAGTCTTTTG TGGC`CAGAT AAAT`TAAAAA CTGTCTGCAC GTAAGAGATG AGTA`AGGCAT CCTTGTGTTA CAGC`CAAAAC CATCAGGTTT TCCACATAAA TCCACTAACT GTTTGTGTTT TGCACAACGT ATTTACATTA TGA`GTTCCT GAAC CAGCCT TAAGTGAAAT CATCAGTGTA AGTGGTGCGA AAGT`GGCTGG TCACCTACTT TGGGATTACA AAATTTTCCC TCACAAGTGT TAA`CAGGTA AAGCAATACC TGA`CTCATTA ATCTTAAGAC CCCCAAAAAT TGC`GTACAG TGT`TTTTTT TCAGTCTACT TTACAGATCC CCACGCTAGT CGTGAGCCAC TCAACATAAT TTTAGATAAT CCCCACTCTT CTGCCTGTAA TTCAGGAACT TATT`TATAG CTGA`CGCCAG TCCA`TTATCT ACC`TGGAA CATGAATTAA GCAC`TCAGT TGACATCAAG CACGTGCCCA AGGAACTAG TTC`TGAAAA TTAGTCCCCC TCTT`JAAGTT CATT`GAAAA	TCACTGCAAC GGCATGCACC GGCTGGTCTT TTGAGCTACT CTCAAACTCC ACCATGCCTG ATTCATCTTA CAGTATACTG TGAAGGTATG AGTTCCTTTA CTGTGTAATC ACATTTGCAC ATTTCTGTAA AGGTAGATT CTGGCAATTC GTGATGGAAG CTGCAATGAA CATCTGAAAA TTTACATCAG CCAGGACCAG TGCACTGTGA GAATGTGGGA TGACTAATCG ACTGTGACCA ACATAATCAA TGGAGCAAGA TTCTTTATTA GCAGATTTGT GGTATTTCTC CTTCTGTGT TGCATCACAG CCAAGGATT TGCAGGTTTT TCTTGGCTCA GATTACAGGC GGCCAGCCTT GGCATGAGCC AATGAAATAT CTATAGAACA TACAACAAAA AAAGTAAACC TTCTCTCCTC TGACAAGCCA ATTTCTTTGA AATTTCTCTT GCAACCTTCG ATGCCACTAT ATTGAACTCC CGTGCCACGC AAGACCCCTG AACAACCTTT TCAAGTTATC CTTCCATTCC CATGAGACTG AGTTTGCGCT TTCATATCTG AGAAGCATCA ATTCTTGCCA TGAATTAACA CACCACGCTT TGTTATCTCT GTGACTTGT TCATTTCCCC GGGGGAAGAG ATTGCTCGCC CAGAGTCAAA TTTACTAAGT	CTCCACCTCC ACCATGCCAG GAACCTCTGA GCGCCGGGCT TGACCTCAAG GCCATAAAAC CTCGGCCAAC GCCTGGCTTT TTGCATTTTG CTAGGATAAA TTTGATTCC TGGTATAACC GAGACTGAGA GAATTTCAGA TACCTGGTAC GGAGGTATT CACACGACAG AGCTTTTGTA AACAACTCTG TGGTACCCAC TTCAGCATAA AATGTCTTCT GGGGTCAGGG CTGTGGTTTA AAAAATAAAC TTTGAGAATT GAGA`ACTATG TACACAGGTA CTAATGCTAT CCAAGTGTT TCACTTGCTT ATGCTCAGAG TCTTTTCTTT CTGTAACCTC ACCTGCCACT GTCTTGAACT ACTGCGCCCA AAACTATAAG TGTAATTTAG ATAAAATCTT ATAAAACTA CCTTTGGAAT GACTCTTTGT TATATTTTCA TCTTTCCAAG TGAGGCGGAG CCTCCCGGGT GCCCAGCTAA TGACCTCGTG ACAAGACATT GTCTCCACAA TCAACCAATT CCGCTTTTCT CCTAAAATGT TGTTCGAGAC TTTTTATTGA ACTGAGGTCA GGATCAGGTG CATAGTAGGT CGCTCTCAA CCAGTCTCAC TCTGAGAAGT CATTAATTCTA TAATAGAACA TGTTCTCCTA TACAGTTGGC AAAGAAGCAA CACCAGGAGA	TGGGTTCAGAG GCTAATTTTT CCTCAAATGA ATTTTGTGTT TGATCGCTC TGCCCTTTGT CTACGGCATT CTTTTACCT CTATTCAATG AATAAATTTT TTGCCAGCCC AAATACAGTT CGTCTACGAG TAACAACAAC AGA`ACTAATC CTGTAATTAG AATCCAGGGG CTAAAGAAGT GCGTCTAGAA TGGGAGCACT GAAA`AATGGT ATACAACCCC ACCCCATAGT TCAAGTTTCC GGATGGCTAT GTTTTTATT TAAATGTGCC CCCTCCCCCA TGTTTATGTG ACAAGAAACA GTGGGCTTAA TTTGAGATGG TGCCACCTGG GTCTCCGGCT CCTGACCTCA GCCCAGAGGT TGCTAAACTG ATAGGTAACA AAGCCCCCTA GTTTTGGCCA TCAGGCACAA AGCAGAGAGC AATGGCCCTG TTTTTACTGA TCTTGCTCTG TCAAGCGATT TTTTTGATT ATCCGCCCAT TACCGTCTAT CTCCTTATCT GCCAATCAGA GGACTGAACC ATAACATCAA CTTGGTCACT CACAGGAAAA TACAGTTACG GGACCTATTG GCTCAATACA GTTTAGTGCT TCCCCATTAA CTTCCCTCAC GTCTTTTCCA AAATTGCTGG ATATTTTTCT AGAGCCCATC GTTTTCCTAG TGGTTTATAC	CGATTCTCCT TTGTATTTTC TCTGCGCACC TTTAGTAAAG TCTCAGGCC TGATATGACT TGACACTGTC CTTTTATATG AATAATGACA TTCCAACAT CTTTTATATC GAAC`TTTTGG TAGGTTTTTC ATAGTTTATG TGCCCAACAT CATTCTCTTG AGTCACTGTC GGATGAAGAT GTGATCTAAA GCTGTGCCCT GCCAATACCC AGGGAACGCT AGTAAAAAAG TGCATCATAT CTCCTGGAAA ACTGATCAGC TTGAGGGCTA ATATTTACAC ATGTTGGTTT GTCCCCCACC ATAGATTACG AACACTTCAC CAGGTAGGAA AGTCTCACTC GTTCAGCAA AATTTTGTCT TGAATCATCC TTTTCAAAGA TGATAGACTG TGAATTTTGT ACCAACTGAA GGATTGGGGG CTGAATGTCA CAGGCCCTGG CAAAGCTGTC TCCAGGTAGC TTGCCCAGGC CTCCTGCCTC TTTTGTAGAG CTCGGCCCTC TCTCTCTGAA TATCCTATTA AAGTCTTTGA AATGTACACC GCTGTAACCC CATATTTGGC ATAAAGAATT TGATTTGTAG GAAATGCAGA TTTGAACACT TTTTCACAGA GTCTGATTAA TGGCCCAAAG TATTAGTTGT CCTTTGGGGT TACGAGATTT TGTTCTCTCA CTCTTTGATC TGAGAAATAT	GCCTCAGCCT AGTAGAGACC TGGACCTCCC ACGGGGTTTC CTCAAAAGTG GTTGGCCTGC TGTCTTTCCT CTCTTCCAGT AGTAATGATC GGGGCATATT AGTTCATCTA CTTGACTCTT AGAATTAGTA AGTATGTTCTA AAAGATCTTG TTCCTCCCAG GGGTGCTTTG AAAGAAAGCA GTGGGAAGTG AGCAAGGAGC ACGGAGAAAA CATGCTTTGA TACAGCCAGG TTTTACAAC TTTCTGCGCT TTTAAGTTCT GCTGCACCCA CCCCGACAGG AGATGGATAT GAGCAGTATT TTTTACCCAG TTCTCTGCC TTTTTAGTAG TTTCTAGCTT CTTAACTTAA TTTTACAAGA ATAATATTTG TGGACTCTCT TAGGTGGGGG GCATTGACAC AAGAAATCAA TCTTGTGGGG ATTTAAGTAA TGGAGTACAG AGCTTCCCAG ACAGGTTTTC CAAAGTGCTG GCTACTACTC GTTTCTACTG ATCCACCTAT TTATATGTGT AACCACCTTG TCACAGTAAA GGAAGTCTT CTTTGCTACT CTTCTCTCT CTAGGTGCAA CTAGTCTTTC AATCTGCTTA GAATTTCTCC TTTTCATATA TGGCAATGGA ATGTTGCTCA CTGTCAGGAA AACTTTCAAA CCACTCATAC
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TCTTCCTCTT CAACTTTCTT CCATATACAC CCTATTACAG GGATATAGTC TTA CTCTATA GCTCAAAAGG
 ATGACCCTAT CAGAACCTG CACAGTATGT AAAACATTCT CACCAGAGGT TCACTTGTGT ATTTCCACCC
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 TTGACACATG ATTGGAAGTT AATATTTATT TATCAAGTGA TTGTTTTAAA ATCATGACTC ACTCAACAAA
 5 GTTATAAGAA TAAGAAATAGT GTTACAGAA TGGTATACAC AAGCTGACCA TAATCAACAC ACCTATTATC
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 10 GAACTCCTTG GCTAGAGAGA TCCTCCCTCC AAGGTCCCC AAAATGCTGG GATCTCAGGC AAGAGCCACC
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 TTTGGGACTG ATA/ATGTGA CCAGTCTGCG TTACTGTCCA TTGCCTGAAA TGGAGCTTTG AGGTGGACTG
 TATAATTCT TCAATCTTAA TCCCAAATTC TGATCGCGCA CGCCCTCTGC TGTTCATAT TAATATTAT
 TTACCAATCA AAGTAAAGTA TTGAAGTTT CCTGGCAGTT TTTCACTTGT GTTTTAGTCC ATTTAGGCTG
 40 CTATAACAAA ATCTCTTAAA CTGGGTAAGG GGCACCACTA GATTGTTGT CTAACGAGGG TATCTCTCAC AGTCTGGAA
 GTGGGAAGC CCA/TATCAA GGCACCACTA GATTGTTGT CTAACGAGGG TATCTCTCAC AGTCTGGAA
 TGGCCCTTG TTGCTGCATC CTCACTTAGT GCAAGGGGCA AGACAGCTCC CTCAACCTC TTTTATAAGG
 GCACTTATGT CATTATGAG GGCAGAGCCC TCACCTTACC ATCACTTCCC CAAAGGCCCC ACCTCTTAAT
 AGTATCACAT TGGCTGTTAG GTGTCTGGGA GGACACCAAT CTTCAGCCA TATCATCTCA CTTGAAAAA
 45 AGTCAAAATA AAACAGTAG ATTTAATTAA TATTACACTA TTTATAGAAG CATGTGATGT ATCATTCCTT
 GTATTAATTT CCTGGGGTTG CCGTAACAAG TTACCAAAAT CTAGGTGGCT TAAAAAATA GAATTTTATT
 CTCTCACATT TCTAAGGCA GAAGTTCACA TGCTGTCAA AGGGCCATGT TCTCTGGAAG GCTTTAGGGG
 AGAATATATT TCA/ATCTTT CTCTTAGCTT CTCGGTGTCA CTGGCAATCC TTAGCTTACT TTGGCTTCT
 GTGTCTCAC ATCATCTTTT TATAAGAACA CCAGTGATAG TGATTAAGGG CATACTTAC TTTAATATGA
 50 CCTCATCTTA ACTAATTATG TCTTCAATAA CCCTATTTCC AAATAAGGCC ATATTCTGAA GTATTGGGAG
 TTAGAACTTA AAGCTTTTTG GGAGGGACAC AGTTCACCC ATAACAACC CTAAAATCGA TATTTATTCT
 CAATTAAGTC TTG/AAATTGG TTTCAAAAAAG AGAATATTCT ATTAGAGTTT TTAATGTATA GTTTTAAACAT
 ATAGTTCTTT AGCC/CCCAAT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTGGAGAC GGAGTCTCGC
 TCTGTCGCCC AGGC/CGGACT GCGGACTGCA GTGGCGCAAT CTGGCTCAC TGCAAGCTCC GCTTCCCGGG
 55 TTCACGCCAT TCCCCTGCCT CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCTGCCACCG GGTCTCGATC TCTGACCTC
 ATGATCCACC CGCC/TCGGCC GAGACGGGGT TTCACCTTGT TAGCCAGGAT GGTCTCGATC TCTGACCTC
 CAATTATTTA GTTTTCTAT TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCCC GGCCTGCCCC
 CTAATTCCTA GTTTTCTAT AAACAGGGAA ATTTATTTGT GTGGCCCTTA GAACTAATTT AATTTCCACT
 GTATCTGTTG CTTATGTTTA TATAATGCTT TTAGAAATTT GTATTATTCA GAAAATAAAC ATATACTATT
 60 TTAAGAAAAG AATCTGCCTG GATTTTATTG CTTGCTATAT TAAATTTTA TTAGTATTTT AATTGTTTTA
 GAGTTTGAGA CCA/ACTGAG TAATCTCAGC ACTTTTGAGA GGCCAAGGCA GAAGGATTGC TTGAGCCAG
 CTCATGGCAC ATACCTGTAG CAACACAGGG AGACCCCAT CTCTACAAAA AATAAAAAAA TTCTCCAGGC
 TTGAGGCTGC AGTCAGCCAT TTCTAGTTAC TTGGGAGACT GGGGTGGGAG GATGCATTGA GCCCAGGAGA
 ATAGATAGAT AGA/AGATAA GATCAGGCCA CTGTACTCCA GCTTGGACAA CAGAGTGAGA GCTTGTCTAG
 65 TAAATAGATA ATACACAGAT TCTAAATAGA TAATAGACAG GATAATAGAC ATTATCTAAT ACAGATTATC
 TCTAAATAGA TAA/AGACAG TATCTAAATA TAAATAGATA AGATTATCTA AATAGATAAT AGACAGATTA
 AGATTAGATA GAT/AGATA TAGATAGAGC TAAATAGATA ATAGATTATC TAAATAGATA ATAGATAGAT
 AAAGAAAGAA AGAAGAATG GTGCTCATAT TTTAAAGCAT TAGATAAGAC AGATAGAAC TTATATTACC

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CACACCTTCT TGTGTGGCAT TAAGATGCAA ACTTTGTTTT AAACAGTTGA GTAAATCAAA GATGGGACTG
 TTAAGTTATT TGTGTTATT ACCTGCTTTT TGAAAATGTA AAAATAAAAC TCTAGGTTTA ATTAGTAGTA
 TGCTATTTAG TAATGAAGTA AAGCTAGAGG CTTCGAACAA ATCTTGTTGA ATTTCTCTT GAATGAGAGA
 5 GAAAATTTAA AGTAAGCAAA CAAATAAGTT GTGTGTCACC ACTCATTGAG TCATTAAACA AGTATTTCCA
 GAGTACTTAT TCTGTGCCAG GAAATGTTGT AGGTGCCCTC AACAACCTAG AGCTAGCCT GAGACACAAG
 TAAGTAGGTA ATTAATTATAG AATGGTATGA TCTTTGGAGG ACTGGGTATT GGCTGGCTCA TGGGAGTACA
 AGATAGGTAC CCAATGATGA AGTCAGGAAA GGTTCCTTAT GGTGATATGA TGACGTCTAT GCTGATTATA
 AGGTCACTGT AGAATAAACT TTGTGCTTTT AAATTGTCAT AGCACTGTAT TAGAGAGTTC ATCTTCAAAA
 10 TAATCGAAAA GGCAGAGTGT GGTGACCCAT GGCTGTAATC CCAGCACTTT GGGAGGCCGA GGTGGGCAGA
 TTGCTTGAGC TAGGAGTTCG AGACCAGGCT GGCCAACATG GTGAAACCCC GTCTCTACTA AAAATACAAA
 AATTAGCCAG GAGTGATGGT GCGCACCTGT AATGCCAGCT ACTTGGGAGG CTGAGGCAGG AGGATCACTT
 GAACCCAGGA GGTGAGGTT GAAGTAAGCC GAGGTGATGC CACTGCATC CAGCCTGGG AACAGAGTGA
 GACTCCATCT CAAATAAAAA AAAAATGATC AAAGAAAGGT GAATTTTCAT CTACCCTATT TCTGCTGAGG
 15 AAAATGGACT ATTTTCAAAT ATTTTAAATA AGGGTCAAAA TGAGGGATC-3' (FRAG.NO:)(SEQ.ID NO:2480)
 5'-CCTGAGACAG AGGCAGAGT GATACCCACC TGAGAGATCC TGTGTTGAA CAACTGCTTC CCAAAACGGA
 AAGTATTTCA AGCCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTCTCTCA
 GCTCTCACTT TGGTGTCTCT CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA
 CTTATGATGA GGCCAGTGCT TATTGTCAGC AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAGAAGA
 20 GATTGAGTAC CTA/ACTCCA TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC
 AATGTGTGGG TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC
 CCAACAATAG GCA/AAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG
 GAATGATGAG AGG/GCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC
 AGTGGCCACG GTG/ATGTGT AGAGACCATC AATAATTACA CTGCAAGTG TGACCCTGGC TTCAGTGGAC
 25 TCAAGTGTGA GCA/ATTGTG AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA
 CCCACTGGGA AAC/TCAGCT ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTACCT GCCAAGCAGC
 ATGGAGACCA TGC/AGTGTAT GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT
 GTGATGCTGT GACA/ATCCA GCCAATGGGT TCGTGGAAATG TTTCCAAAAC CCTGGAAGCT TCCCAATGAA
 CACAACCTGT ACA/TTGACT GTGAAGAAGG ATTTGAACTA ATGGGAGCCC AGAGCCTTCA GTGTACCTCA
 30 TCTGGGAATT GGA/CAACGA GAAGCCAACG TGTAAGCTG TGACATGCAG GGCCGTCCGC CAGCCTCAGA
 ATGGCTCTGT GAGC/TGCAGC CATTCCCTCG CTGGAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG
 TGAGGAAGGC TTC/TTGTGC AGGGACCAGC CCAGTTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA
 ATCCCAGTTT GTGAAGCTTT CCAGTGCACA GCCTTGTTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC
 CTAGTGGTTT TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGT TTGTGTTGAA
 35 GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCCATGTG TGAAGCTGTG
 AGATGCGATG CTG/CCACCA GCCCCGGAAG GGTGTTGTTGA GGTGTGCTCA TTCCCTATT TGAGAATTCA
 CCTACAAGTC CTCTGTGCCC TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG
 CACATCTCAG GGAC/AAATGGA CAGAAGAGGT TCCTTCCTGC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT
 CCGGGAAGA TCA/CAATGAG CTGCAGTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTG
 40 AAGGATGGAC GCT/CAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGTCTACC
 TACCTGTGAA GCT/CCACTG AGTCCAACAT TCCCTTGGTA GCTGGACTTT CTGCTGCTGG ACTCTCCCTC
 CTGACATTAG CACCATTCTT CCTCTGGCTT CGGAAATGCT TACGGAAAGC AAAGAAATTT GTTCTCTGCA
 GCAGCTGCCA AAGC/CTTGAA TCAGACGGAA GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAGAA
 TCAGAAACAG GTG/ATCTGG GGAAGTAGAG GGATACACTG AAGTTAACAG AGACAGATAA CTCTCCTCGG
 45 GTCTCTGGCC CTTCITGCCT ACTATGCCAG ATGCCCTTAT GGCTGAAACC GCAACACCCA TCACCACTTC
 AATAGATCAA AGT/CAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT TCCTACTCTC
 AGGATCAAGA AAG/GTTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG CAAAGGTGAA GAGACCAAGA
 CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCTTGCT CGCTGTAATA TCTTGGCACA GAAACACAAT
 ATTTTGTGGC TTTCITTTCT TTGCCCTTCA CAGTGTTCG ACAGCTGATT ACACAGTTGC TGTCAATAA
 50 ATGAATAATA ATTAATCCAG GTTTAGAGGA AAAAAATGAC TAAAAATATT ATAACTTAAA AAAATGACAG
 ATGTTGAATG CCCACAGGCA AATGCATGGA GGGTTGTTAA TGGTGCAAT CCTACTGAAT GCTCTGTGCG
 AGGGTTACTA TGC/CAATTT AATCACTTTC ATCCCTATGG GATTCAAGTC TTCTTAAAGA GTTCTTAAAG
 ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATACTTCT TCATTCAATA CAAGTGTGGT
 AGGGACTTAA AAA/CTTGTA AATGCTGTCA ACTATGATAT GGTAAAAGTT ACTTATTCTA GATTACCCCC
 55 TCATTGTTTA TTAA/CAAAAT ATGTTACATC TGTTTTAAAT TTATTTCAAA AAGGGAAACT ATTGTCCCCT
 AGCAAGGCAT GAT/TTAACC AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTTG AAAACATGGT
 AGAATTGGAG AGT/AAAACT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT
 CCACGATGAA AAAC/TTCCAT GAGGCCAAAC GTTTTGAAC TAAATAAGCA TAAATGCAAA CACACAAAGG
 TATAATTTTA TGAA/IGTCTT GTTTGGAAAA GAATACAGAA AGATGGATGT GCTTTGCATT CCTACAAAGA
 60 TGTGTTGTCAG ATGT/ATATG TAAACATAAT TCTGTATAT TATGGAAGAT TTAAATTCA CAATAGAAAC
 TCACCATGTA AAACAGTCAT CTGGTAGATT TTTAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT
 TTTCTTCTGT ATGT/AGGGT GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTAT GTTTATTTAT
 AAGCAGATTT AAC/ATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC
 AGTAATTGCC AAACCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT CCATTAACCT

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AGCATGTGTT GAAAAAAAAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA
AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT TTAAAGGGGC AGAAAACTC TGGGAAATAA
GAGAGAACAA CTA CTGTGAT CAGGCTATGT ATGGAATACA GTGTTATTTT CTTGAAATT GTTTAAGTGT
TGTAATATTT TATGTAAACT GCATTAGAAA TTAGCTGTGT GAAATACCA GATGTGTTGT GTTTGAGTTT
TATTGAGAAT TATTAATTAT AACTTAAAT ATTTATAAT TTTTAAAGTA TGTATTTTAT TAAGCTTATG
TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT-3' (FRAG.NO:)(SEQ.ID NO:2479)

5'-CCT TGC CTG CTG G-3' (FRAG. NO: 1739) (SEQ. ID NO: 1752)

5'-GTT GTC CC-3' (FRAG. NO: 1740) (SEQ. ID NO:1753)

5'-GTT CTT GGC TTC T TC TGT C-3' (FRAG. NO:1080) (SEQ. ID NO:1088)

10 5'-GGC TGG TGG-3' (F RAG. NO:1083) (SEQ. ID NO:1092)

5'-CGT TGG CTT CTC GTT GTC CC-3' (FRAG. NO:1081) (SEQ. ID NO:1089)

5'-TGT GGG CTT CTC GTT GTC CC-3' (FRAG. NO:1082) (SEQ. ID NO:1090)

5'-CCC TTC GGG GGC TGG TGG-3' (FRAG. NO:1083) (SEO. ID NO:1091)

5'-GGC CGT CCT TGC CTG CTG G-3' (FRAG. NO:1084) (SEO. ID NO:1093)

15 Human P Selectin Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC
TTT CTT TTC-3' (FR₄G, NO: 1741) (SEQ. ID NO: 1754)

5'-TCC TTT CTT TTC-3' (FRAG. NO: 1742) (SEQ. ID NO: 1755)]

5'-CTC CTT TT-3' (FRAG. NO:1743) (SEQ. ID NO:1756)

20 5'-TTT TCT CTT TCG (TT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1085)(SEO. ID NO:1094)

5'-TTG CTG TTT TTT (TC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1086) (SEQ. ID NO:1095)

Human Endothelial Monocyte Activating Factor

Nucleic Acid & Antisense Oligonucleotide Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC
TTT CTT TTC-3' (FRAIG, NO: 1744) (SEQ. ID NO: 1757)

5' -CC TTT CTT TTC (FRAG. NO: 1745) (SEQ. ID NO: 1758)

5'-CTG TTC CTC CTT 'T-3' (FRAG. NO:1746) (SEQ. ID NO:1759)

5'-TTT TCT CTT TCG (TT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1087)(SEQ. ID NO:1096)

5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1088) (SEQ. ID NO:1097)

30 Human IL3* Nucle c Acid and Antisense Oligonucleotide Fragments

5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB
GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO:
1747) (SEQ. ID NO: 1750)]

5'-G GBG GCB CTC-3' (FRAG. NO: 1748) (SEQ. ID NO: 1761)

35 5'-GT GGG GCT CTG-3 (FRAG. NO:1749) (SEQ. ID NO:1762)

HUMIL3AAS1: 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' (FRAG.NO:1089)(SEQ.ID NO:1098)

HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CCG TGG CC-3' (FRAG. NO:1090) (SEQ. ID NO:1099)

GGC GGB CCB GGB G⁺T GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC
(FRAG. NO:1091) (SEQ. ID NO:1100)

40 Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT
GGC TGC GCT CCT GGC CCG CCT CTT TCC GCG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC
TC CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC
CTG GGC TGC GTG CCG GTT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC

45 TTC GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CCG GCT CTT

CGC CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCG CTG CGT CGC GCT TGT GGT TTT GG GGC CGG CTT
TGC CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGT CCG GCG CGT TGT CTT CTT CTT CCT GCG GCA
GGA GAC AGG GCA C GG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG
AAC GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG

50 BCC BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC-3' (FRAG. NO: 1750) (SEQ. ID NO: 1763)

GBG GTG CC-3' (FRAG. NO: 1751) (SEQ. ID NO: 1764)

5'- GCC CCG C-3' (FRAG. NO:1752) (SEQ. ID NO:1765)

5'-TCTGGGGTGTCCTG (FRAG. NO:1092) (SEQ. ID NO:1101)

5'-GCCTTCGTGGTTCC (FRAG. NO:1093) (SEQ. ID NO:1102)

55 5'-TCTTCCTTCGTTTGC (FRAG. NO:1094) (SEQ. ID NO:1103)

5'-CGTCCGCGGGGGCCCGGGCCT (FRAG. NO:1095) (SEQ. ID NO:1105)

5'-GGC TGC GCT CCT GCC CCG C (FRAG. NO:1096) (SEQ. ID NO:1104)

- 5'-CTCTTTCCCGGGC1CTT (FRAG. NO:1097) (SEQ. ID NO:1106)
 5'-GCGCTGGGGGGTG TCC (FRAG. NO:1098) (SEQ. ID NO:1107)
 5'-CGTGTGTTTGCGCCCTCCTCCTGGTCGC (FRAG. NO:1099) (SEQ. ID NO:1108)
 5'-GCTTGTCTGTTTGC (FRAG. NO:1100) (SEQ. ID NO:1109)
 5'-GGCCGGCTTTGCCCGCCTCCC (FRAG. NO:1101) (SEQ. ID NO:1110)
 5'-GGCGCTGGCCCCGCC (FRAG. NO:1102) (SEQ. ID NO:1111)
 5'-TTCTGGGCTGCGTGGCG (FRAG. NO:1103) (SEQ. ID NO:1112)
 5'-GTTCTGTTCTTCTTCTGGC (FRAG. NO:1104) (SEQ. ID NO:1113)
 5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC
 CGG BBC GCB GGB 5' CBG BGG TGC C (FRAG. NO:1105) (SEQ. ID NO:1114)

Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT
 GGB BCC CBT TBB TBG GTG TCG B-3' (FRAG. NO: 1753) (SEQ. ID NO: 1766)
 5'-GCC GGC BCB-3' (FRAG. NO: 1754) (SEQ. ID NO: 1767)
 5'-T TCC TTC-3' (FRAG. NO:1755) (SEQ. ID NO:1768)
 5'-CTC TGG TTG GCT TCC TTC-3' (FRAG. NO:1106) (SEQ. ID NO:1115)
 5'-GCCGGCBCTGCTGCBGGBBGBCBGGGGGGBGCBGTTGGGBGGTGBGBCCCBTTBBTBGGGTGTCGB-3' (FRAG.
 NO:1107) (SEQ. ID NO:1116)

Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

- 5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT
 GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT
 GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT
 CTT GGC CTG GGC GAT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT
 GCT CTT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG
 GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC
 GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA
 GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG
 GBT CCB GGC CCB GCT G-3' (FRAG. NO: 1756) (SEQ ID NO:1769)
 5'-TCTGCGC-3' (FRAG. NO: 1757) (SEQ ID NO: 1770)
 5'-CCT GCT CCT GGG G (FRAG. NO:1758) (SEQ. ID NO:1771)
 5'-TCTGCGCGCCCTC CTCC (FRAG. NO:1108) (SEQ. ID NO:1117)
 5'-CGCCCGGCTTCTCT (FRAG. NO:1109) (SEQ. ID NO:1118)
 5'-CGTGTGGGCTTCGG (FRAG. NO:1110) (SEQ. ID NO:1119)
 5'-CCCCGCGCCTCCGTGTGTTCTC (FRAG. NO:1111) (SEQ. ID NO:1120)
 5'-TGCTCGCTGGGCTTG (FRAG. NO:1112) (SEQ. ID NO:1121)
 5'-GGTTTCTGGGGCTGGGTTTC (FRAG. NO:1113) (SEQ. ID NO:1122)
 5'-TCTGCCGGGTCGTTC (FRAG. NO:1114) (SEQ. ID NO:1123)
 5'-GGGTGCTGGCTGCG (FRAG. NO:1115) (SEQ. ID NO:1124)
 5'-CTTGGTGTGGGGCTCC (FRAG. NO:1116) (SEQ. ID NO:1125)
 5'-GGCGGCTGCGGGCTGGGTTGGG (FRAG. NO:1117) (SEQ. ID NO:1126)
 5'-CTTGGCTGGTTCCTGGCCTCGGG (FRAG. NO:1118) (SEQ. ID NO:1127)
 5'-CCTCCTCCTCCTCCCTCCCTTTTCTTCTCT (FRAG. NO:1119) (SEQ. ID NO:1128)
 5'-TCCCTGCTGCTCTC (FRAG. NO:1120) (SEQ. ID NO:1129)
 5'-TGCCCTCCCTCCCTCCTGG (FRAG. NO:1121) (SEQ. ID NO:1130)
 5'-GGTGCTCCTTGGCCCTGC (FRAG. NO:1122) (SEQ. ID NO:1131)
 5'-GGCTGCTCCTTGCCCC (FRAG. NO:1123) (SEQ. ID NO:1132)
 5'-CTCTGGGTGCGGGCTGGC (FRAG. NO:1124) (SEQ. ID NO:1133)
 5'-GGGGCGTCTCTGTGC (FRAG. NO:1125) (SEQ. ID NO:1134)
 5'-CTGGCCTGGGTGCC (FRAG. NO:1126) (SEQ. ID NO:1135)
 5'-GCCTCTCCTGGGGCGGTGGCTCCTGTCC (FRAG. NO:1127) (SEQ. ID NO:1136)
 5'-CCTTTTCCCCCGGCTCC (FRAG. NO:1128) (SEQ. ID NO:1137)
 5'-GTGGGGGCTTTGGC (FRAG. NO:1129) (SEQ. ID NO:1138)
 5'-GGG GGT CTG TGG CCT GCT CCT GGG G (FRAG. NO:1130) (SEQ. ID NO:1139)
 5'-AGGGGTCTGGGGCTCTC (FRAG. NO:1131) (SEQ. ID NO:1140)
 5'-TTTGGGGGTCTGCTTG (FRAG. NO:1132) (SEQ. ID NO:1141)
 5'-GCCTGGCTGCCTTC (FRAG. NO:1133) (SEQ. ID NO:1142)
 5'-GGGGCCTGCCGTGGGGC (FRAG. NO:1134) (SEQ. ID NO:1143)
 5'-TGTCTCTGTGTCTCCCTT (FRAG. NO:1135) (SEQ. ID NO:1144)
 5'-TGCTGCTGTCTGG (FRAG. NO:1136) (SEQ. ID NO:1145)
 5'-GGTCCCGCCTTCCCT (FRAG. NO:1137) (SEQ. ID NO:1146)

5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GAC CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG
 CCA CCC CAT TGG GAG ATG CCA AGG CAC CAG GCT G (FRAG. NO:1138) (SEQ. ID NO:1147)
 5'-GTT CCC BGB GCT TGC CBC CTG CBC CBG GBC CBG GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG
 CCB CCC CBT TGG GEG BTG CCB BGG CBC CBG GCT G-3' (FRAG. NO:1139) (SEQ. ID NO:1148)

5 Human IL5* Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-TCCTGTTTC CCCCTTTTCG TTCTGCGTTT GCCTTTGGCG TTTTGTGTTT GTTTCTCTC TCCGTCTTTC
 TTCTCCCTT GTGGGB3TTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBGBGCTBG CBBBCTCBBB
 TGCBBBGBCB TCCTC3TGGC TCTGBBBCGG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC
 AAGAGCTAGC AAAC`CAAAT GCAGAAGCATC CTCATGGCTC TGAAACG-3' (FRAG. NO: 1759) (SEQ. ID NO:
 1772)
 5'-GCC CCG GG-3' (FRAG. NO: 1760) (SEQ. ID NO: 1773)
 5'-G GGT TTC T-3' (FRAG. NO: 1761) (SEQ. ID NO: 1774)
 5'-GTG GGG BTG GC-3' (FRAG. NO: 1762) (SEQ. ID NO:1775)
 5'-CCB BGB GCT BGC-3' (FRAG. NO: 1763) (SEQ. ID NO: 1776)
 15 5'-TCC CTG TTT CCC CCC TTT-3' (FRAG. NO:1140) (SEQ. ID NO:1149)
 5'-CGT TCT GCG TTT GCC TTT GGC-3' (FRAG. NO:1141)(SEQ. ID NO:1150)
 5'-GTT TTT TGT TGT TTT TCT-3' (FRAG. NO:1142)(SEQ. ID NO:1151)
 5'-CTC TCC GTC TTT CTT CTC C-3' (FRAG. NO:1143) (SEQ. ID NO:1152)
 5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' (FRAG. NO:1144) (SEQ. ID NO:1153)
 20 5'-GAG GGT TTC TGG CTT CCT CTC T-3' (FRAG. NO:1145) (SEQ. ID NO:1154)
 5'-TGT CTC TCT GTC CTT TGT TT-3' (FRAG. NO:1146) (SEQ. ID NO:1155)
 5'-TGT TGT GCG GCC TGG TGC TGC CCT GCC CCG GG-3' (FRAG. NO:1147) (SEQ. ID NO:1156)
 5'-GTG GGA ATT TCT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA
 AGC ATC CTC ATG GCT CTG AAA CG-3' (FRAG. NO: 1764) (SEQ. ID NO: 1777)
 25 5'-GTG GGB BTT TCT TGT GGG BTG GCB TBC BCG TBG GCB GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC
 BTC CTC BTG GCT CTG BBB CG-3' (FRAG. NO:1148) (SEQ. ID NO:1157)

Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTCAGTGGCC CCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT
 GTCTGTCGTG TCTTCTCTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCGT
 30 GTCTTTCTT TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTTCC
 TTTGCTCTTG GTGTGICTTT GCTGTGCCCT GCCTCTCTGC-3' (FRAG. NO: 1765) (SEQ. ID NO: 1778)
 5'-CCG TGT C-3' (FRAG. NO: 1766) (SEQ. ID NO: 1779)
 5'-GCCCTGCC-3' (FRAG. NO: 1767) (SEQ. ID NO: 1780)
 5'-CCG TGT CTG TCG TGT CT-3' (FRAG. NO:1149) (SEQ. ID NO:1158)
 35 5'-TTCTTTTGCTCTG-3' (FRAG. NO:1150) (SEQ. ID NO:1159)
 5'-GTGTGTCTTTGCTCT-3' (FRAG. NO:1151) (SEQ. ID NO:1160)
 5'-GCCCTGCCTCTCTC C-3' (FRAG. NO:1152) (SEQ. ID NO:1161)
 5'-CT CBGTGGCCCC (BBBGGBTG BGTBBTBCBT GCGCCBCGBT GBTCBTBTCC TTTTBTCTBT GBGG (FRAG. NO:
 1768) (SEQ. ID NO: 1781)

40 Human IL-6 Receptor Fragments

- 5'-GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCGCG GCCGCGCTCG GCTCCTCTCC
 CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GCGCTGCCG TGCGCGCGGC GCTGGCCCT
 GCTGGCCGTC GGC1GCGCGC TGCTGGCTGC CCTGTGGCC GCGCCGGGGC CTGTCCGCT CTGCGGGCGC
 TGTCTCTGG CTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC
 45 TCGGGGGGGG GGGTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCTG
 GCCTCCGGGC TCC1GCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG
 GCGCCCGTTT GTG1TTTGTC TTTCCCTG GCGTCCCTGT GCCCTCTCC TCTCCTCCT CTGCTTCTCG
 CTCTCCTTG TGGGCGCCCTC CCGTCTGCTC TTGGTTTGG GCTTTTTC TCTCTCCT TTTTCGTGCG
 TGGGCTCCG CAC1GCTCTT GCCACCTCT GCGCAGGGCA GCGCCTTG GGCCAGCGCC GCTCCCGGCG
 50 CGGCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCT CCTCGGCTAC CACTCCATGG
 TCCCGCAGAG GCG3ACAGG GCBGCGCTC TTGCCBCTC CTGCGCBGG CBGCGCCTTG GGGCCBGGCG
 CGCTCCCGGC GCG3CCBGB GGGCBGCCBG CBGCGCGCB CGBCGGCCB GCBTGCTTCC TCCTCGGCTB
 CCBCTCCBTG GTCCGCBGB GGGGBCBGG C-3' (FRAG. NO: 1769) (SEQ. ID NO: 1782)
 5'-CCCGGCGC-3' (FRAG. NO:1184) (SEQ. ID NO:1193)
 55 5'-GGCCBGBCBGG-3' (FRAG. NO:1186) (SEQ. ID NO:1195)
 5'-GCBGCCBGBGCG-3' (FRAG. NO: 1770) (SEQ. ID NO: 1783)
 5'-C GCBGCCBGBGCGC -3' (FRAG. NO: 1771) (SEQ. ID NO: 1784)
 5'-GGGGGTGGCTTCC1GCC3'- (FRAG. NO:1153) (SEQ. ID NO:1162)
 5'-GCGTCTCTGGGCC1TCCC-3' (FRAG. NO:1154) (SEQ. ID NO:1163)

- 5'-GTCCCTCGGCCCGCGCCGCTCGGCTCCTCTCCC-3' (FRAG. NO:1155) (SEQ. ID NO:1164)
 5'-TCTGGCCCCGGCTC-3' (FRAG. NO:1156) (SEQ. ID NO:1165)
 5'-GGGGCGGGGGGCGGTGGGCGGGC-3' (FRAG. NO:1157) (SEQ. ID NO:1166)
 5'-GGCGCTGCCCTGCCGC-3' (FRAG. NO:1158) (SEQ. ID NO:1167)
 5'-GCGGCGCTGGCCCC-3' (FRAG. NO:1159) (SEQ. ID NO:1168)
 5'-TGCTGGCCGCTCGGCTGCGCGCTGCTGGCTGCCCT-3' (FRAG. NO:1160) (SEQ. ID NO:1169)
 5'-GCTGGCCGCGCCGGG-3' (FRAG. NO:1161) (SEQ. ID NO:1170)
 5'-GCCTGTCCGCCTCTGCGGG-3' (FRAG. NO:1162) (SEQ. ID NO:1171)
 5'-CGCTGTCTCCTGGC-3' (FRAG. NO:1163) (SEQ. ID NO:1172)
 5'-TTGTCTTCCGGCTCT-3' (FRAG. NO:1164) (SEQ. ID NO:1173)
 5'-TCTGCTGGGGTGGG-3' (FRAG. NO:1165) (SEQ. ID NO:1174)
 5'-GCTGGGCGGCCGGGCGCGGT-3' (FRAG. NO:1166) (SEQ. ID NO:1175)
 5'-GCTGGGGCTCCTCGGGG-3' (FRAG. NO:1167) (SEQ. ID NO:1176)
 5'-GGGGGCTCTTCCG-3' (FRAG. NO:1168) (SEQ. ID NO:1177)
 5'-GCTGTCTCCCTCCGGG-3' (FRAG. NO:1169) (SEQ. ID NO:1178)
 5'-GCGGGGTTTCTGCGC-3' (FRAG. NO:1170) (SEQ. ID NO:1179)
 5'-GTGGGGGTCTTGC-3' (FRAG. NO:1171) (SEQ. ID NO:1180)
 5'-TGGCCTCCGGGCTC-3' (FRAG. NO:1172) (SEQ. ID NO:1181)
 5'-TGCTTGTCTTGCCTTCCTTC-3' (FRAG. NO:1173) (SEQ. ID NO:1182)
 5'-TCTGGTCGGTTGTCTGCTCG-3' (FRAG. NO:1174) (SEQ. ID NO:1183)
 5'-GGGCTCCGTGGGTCCCTGGC-3' (FRAG. NO:1175) (SEQ. ID NO:1184)
 5'-GCCCCGTTGTGTTTGTTC-3' (FRAG. NO:1176) (SEQ. ID NO:1185)
 5'-TTTTCCCTGGCGT-3' (FRAG. NO:1177) (SEQ. ID NO:1186)
 5'-CCCTGTGCCCTCTCCTCTCCTTCTGCTTCTC-3' (FRAG. NO:1178) (SEQ. ID NO:1187)
 5'-GCTCTCCTTTGTGGG-3' (FRAG. NO:1179) (SEQ. ID NO:1188)
 5'-GCCCTCCCTGCTGCT-3' (FRAG. NO:1180) (SEQ. ID NO:1189)
 5'-CTTGGTTTTGGGCT-3' (FRAG. NO:1181) (SEQ. ID NO:1190)
 5'-TTTTTCTCTCTCCTCTTTTTC-3' (FRAG. NO:1182) (SEQ. ID NO:1191)
 5'-GTGCGTGGGCCTCC-3' (FRAG. NO:1183) (SEQ. ID NO:1192)
 5'-GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG
 GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG
 GCGGACAGGC-3' (FRAG. NO:1185) (SEQ. ID NO:1194)
 5'-GCBGCGCTCT TGCCBCCTCC TGCGCBGGG BCGCCTTGG GGCCBGCGCC GCTCCCGGCG CGGCCBGCGB
 GGCBCBGB CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB
 GGCGBCBGG C-3' (FRAG. NO:1187) (SEQ. ID NO:1196)

Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCGCG GCCGCGCTCG GCTCCTCTCC
 CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCCTGCCCC TGCGCGCGGC GCTGGCCCTT
 GCTGGCCGTC GGCCTGCGCG TGCTGGCTGC CCTGTGGCC GCGCCGGGGC CTGTCCGCTG CTGCGGGCGC
 40 TGCTCCTGG CTGTCTTCC GGCTCTTCT GGTGGGTGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC
 TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCGGTGGGG GTCTTGCTTG
 GCCTCCGGGC TCTGCTTGT CTGCTCTCC TTCTGTGGT GGTGTGGCT CGGGGCTCCG TGGGTCCCTG
 GCGCCCGTT GTGTTTGTG TTTCCCTG GCGTCCCTGT GCCCTCTCC TCTCCTTCT CTGCTTCTG
 CTCTCCTTG TGGCGCCCTC CTGCTGCTC TTGGTTTTG GCTTTTTTC TCTCTCTCT TTTCTGTGG
 45 TGGGCCTCC GCACGCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG
 CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG
 TCCCGCAGAG GCGGACAGGC GCBGCGCTC TTGCCBCTC CTGCGCBGGG CBGCGCCTTG GGGCCBGCGB
 CGCTCCCGGC GCGGCCBGB GGGCBGCCB CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB
 CCBCTCCBTG GTCCCBCGB GCGGBCBGG C-3' (FRAG. NO:1772) (SEQ. ID NO:1785)
 5'-GGGGCBGG-3' (FRAG. NO:1773) (SEQ. ID NO:1786)
 5'-GBBGGCBG CBGGC 3' (FRAG. NO:1774) (SEQ. ID NO:1787)
 5'-CCBGGBGCBB CCC-3' (FRAG. NO:1775) (SEQ. ID NO:1788)
 5'-BGGG BGGGGCB-3' (FRAG. NO:1776) (SEQ. ID NO:1789)
 5'-GCT TCT CTT TCG TCG CCG GTG GGC TCG-3' (FRAG. NO:1188) (SEQ. ID NO:1197)
 55 5'-GTG GCT GTC TGT GTG GGG CGG CT-3' (FRAG. NO:1189) (SEQ. ID NO:1198)
 5'-GTG CTT TGT TGC TTT C-3' (FRAG. NO:1190) (SEQ. ID NO:1199)
 5'-GAT TCT TTG CCT TTT TCT GC-3' (FRAG. NO:1191) (SEQ. ID NO:1200)
 5'-CTCCTGGGG TBCTGGGGCB GGGBBGGCBG CBGGCBBCB CBGGBCBGC CCCBGGGBG BGGCBCTGG BCCBGGGGC
 CTTGTGGGB BGGGTTTBT BGCTGGGCTC CTGGGGGG BGTBGGC-3' (FRAG. NO:1777) (SEQ. ID NO:1790)

60 Human Monocyte-derived Neutrophil Chemotactic Factor

Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGGTGGBBB GGTTTGGBT BTGTCTTTBT GCBCTGBCBT CTBBGTTCCT TBGCBCTCCT TGGCBBBCT
GCBCCCTCBC BCBGBGCTGC BGBBTTCBGG BBGGCTGCCB BGBBGGCCBC GGCCBGCTTG GBBGTCTGT
TTBCBCBCBG TGBGTTGGTT CCTTCCGGG TTGTGTGCTC TGCTGTCTCT TGGTTCCTTC CGGTGGTTTC
5 TCCCTGGCTC TTGTCTTTTC TCTTGG CCTTGGC-3' (FRAG. NO:1778) (SEQ. ID NO: 1791)
5'-GGBGT BTG-3' (FRAG. NO:1779) (SEQ. ID NO: 1792)
5'-GCBCTGBCBT CT-3' (FRAG. NO:1780) (SEQ. ID NO:1793)
5'-CCG GTG G-3' (FRAG. NO:1781) (SEQ. ID NO: 1794)
5'-GG CCC TTG GC-3' (FRAG. NO:1782) (SEQ. ID NO: 1795)
10 5'-GCT TGT GTG CTC TGC TGT CTC T-3' (FRAG. NO:1192) (SEQ. ID NO:1201)
5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1193) (SEQ. ID NO:1202)
5'-TTC TCT TGG CCC TGC GC-3' (FRAG. NO:1194) (SEQ. ID NO:1203)
5'-GGGGTGGBBB GGTTTGGBT BTGTCTTTBT GCBCTGBCBT CTBBGTTCCT TBGCBCTCCT TGGCBBBCT
GCBCCCTCBC BCBGBGC-3' (FRAG. NO:1783) (SEQ. ID NO: 1796)

15 Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGCTCCCGC CGTGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
CBGTGCGCGG CCGECBTGBC GBBGTTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT
GCBGGGBCBC CBTGBBGGGC CBGCGTGCG GCGCGCTCG CCGGCCCGCC BCBTCTCCG BGGCCBGCBC
GGTGCCCCC BCBGCBGGG CCGGCBGGBC BCBGGCGBGG BGBCBGCGCB GTCGGCGGCC GBGGGTCTBG
20 GTGGGGCTGG GGC CCGGGG TCTTGCCCC TCCGTGCTGG TGGGGCTGGG GCTCCGGG TCTTGCCCC
TCCGTGCCG GTGGGGCCGC GCTGCGCGG CCCCCCTGC CGGTGGGCT CCGCCGCGC GCCGCGCTGC
CGGCCCTCG TGGGTCCTGC TGGCCGGGTC CGGTCCCGG GGTGGGGCG CGBGTCGGC GCCBGGGTC-3'
(FRAG. NO:1784) (SEQ. ID NO: 1797)
5'-GG TGG GGC-3' (FRAG. NO:1785) (SEQ. ID NO: 1798)
25 5'-G GGG CCG -3' (FRAG. NO:1786) (SEQ. ID NO:1799)
5'-GGC CGG GTC CGC G-3' (FRAG. NO:1787) (SEQ. ID NO: 1800)
5'-TGG TGG GGC TGG GGC TCC GGG GTC TCT GCC CCT CCG TGC-3' (FRAG. NO:1195) (SEQ. ID NO:1204)
5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' (FRAG. NO:1196) (SEQ. ID NO:1205)
5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' (FRAG. NO:1197) (SEQ. ID NO:1206)
30 5'-CGC CGG CCT GCC GGC CCC TC-3' (FRAG. NO:1198) (SEQ. ID NO:1207)
5'-GTG GGT CCT GCT GGC CGG GTC CGG GTC CCG GGG GTG GGG-3' (FRAG. NO:1199) (SEQ. ID NO:1208)
5'-CGC GBG TCG GCG GCC GBG GGT C-3' (FRAG. NO:1200) (SEQ. ID NO:1209)
5'-GGGCTCCCGC CGTGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
CBGTGCGCGG CCGECBTGBC GBBGTTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT
35 GCBGGGBCBC CBTGBBGGGC CBGCGTGCG GCGCGCTCG CCGGCCCGCC BCBTCTCCG BGGCCBGCBC
GGTGCCCCC BCBGCBGGG CCGGCBGGBC BCBGGCGBGG BGBCBGCGCB GTCGGCGGCC GBGGGTCTBG
GTGGGGCTGG GGCTCGGGG TCTTGCCCC TCCGTGC-3' (FRAG. NO:1788) (SEQ. ID NO: 1801)

Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CGGGBGTGGG GGTCTGGBC GGCCTGGBG GCBTCCBGGG CTCCCTCCB GTCCTTCTG TCCGCTGCCB
40 GCBCCCTTC BTTCBGBGG CTBGTGGCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCCGGCC
TCCBCCBGG BCBTGGTCT TCTGTCCG TGCCTCTCTG GGGTTTTCG TCTGGGTGGG CTTTCTCTCT
GGGGCTGCTG CTGGGCTCT CTTTGTGTT CTGGCTGGT GCTCTCTCTG GCCCTTCCC TTGGGTGTCT
TGTTTTGTG GCCTCCTCCB GGGBCBTG-3' (FRAG. NO:1789) (SEQ. ID NO: 1802)
5'-CGGGBGTGGG GG-3' (FRAG. NO:1790) (SEQ. ID NO: 1803)
45 5'-GCCBGCBCCC-3' (FRAG. NO:1791) (SEQ. ID NO: 1804)
5'-C CBC CBG-3' (FRAG. NO:1792) (SEQ. ID NO: 1805)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1201) (SEQ. ID NO:1210)
5'-GTC CTT CTT GTC CGC TGC C-3' (FRAG. NO:1202) (SEQ. ID NO:1211)
5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3' (FRAG. NO:1203) (SEQ. ID NO:1212)
50 5'-GCT TTC CTC CTG GGG CTG CTG CTG-3' (FRAG. NO:1204) (SEQ. ID NO:1213)
5'-GGC TCT TCT TTT TGT TTC TGG CCT GGT G-3' (FRAG. NO:1205) (SEQ. ID NO:1214)
5'-CTC TCT CGT GCC CTT TCC-3' (FRAG. NO:1206) (SEQ. ID NO:1215)
5'-CTT GGG TGT CTT GTT TTT GT-3' (FRAG. NO:1207) (SEQ. ID NO:1216)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1208) (SEQ. ID NO:1217)
55 5'-CGGGBGTGGG GGTCTGGBC GGCCTGGBG GCBTCCBGGG CTCCCTCCB GTCCTTCTG TCCGCTGCCB
GCBCCCTTC BTTCBGBGG CTBGTGGCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCC-3' (FRAG.
NO:1793) (SEQ. ID NO: 1806)

Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCCTCCBCBT CTGCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GBBGTGGGGC

CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB
 GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG CCTCCGTGTG TTGTGGGTG TTTTCCCGTC
 TCTGGTCTGC CTTCG3GGGT CGT-3' (FRAG. NO:1794) (SEQ. ID NO: 1807)

5'-GBBGBTBGCGCC-3' (FRAG. NO:1795) (SEQ. ID NO: 1808)

5 5'-CBGCCCCBG-3' (FRAG. NO:1796) (SEQ. ID NO: 1809)

5'-TCC CGT CTC TGG-3' (FRAG. NO:1797) (SEQ. ID NO: 1810)

5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' (FRAG. NO:1209) (SEQ. ID NO:1218)

5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' (FRAG. NO:1210) (SEQ. ID NO:1219)

5'-TCT GCC TTC GGG 3GT CGT-3' (FRAG. NO:1211) (SEQ. ID NO:1220)

10 5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC
 CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB
 GGBGTGGCTG-3' (FRAG. NO:1798) (SEQ. ID NO: 1811)

Human Defensin 1 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CTTGGBGTGG CTBGCCTGG GCCTGCBGGG CCBCCBGBG
 15 BBTGGCBGCB BGGETGGCGB GGGTCCCTBT GGCTGGGGTC BCBGTCCTC TBGCTBGGCB GGGTGBCCBG
 BGBGGGC GGG TCC TCB TGG CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG
 BGT CTT CCC TGG T GCTCAGCCTC CAAAGGAGCC AGCCTCTCC CAGTTCCTGA AATCCTGAGT GTTGCTGCC
 AGTCGCCATG AGAACTTCTT ACCTTCTGCT GTTACTCTC TGCTTACTTT TGCTGAGAT GGCCTCAGGT
 GGTAACCTTC TCACAGGCCT TGGCCACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC
 20 TCTATTCTGC CTGCTCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAGGCCA AGTGCTGCAA
 GTGAGCTGGG AGTCAACCAGA AGAAATGACG CAGAAAGTAA ATGAACTTT TATAAGCATT CTTTAAATAA
 AGGAAAATTG CTTTGAAGT AT CTGCACTGGT AAAAAGATT TATATCTGCT GTTGTATGAA TGCAGACCC
 ACTAGCCACA TAGTGCTCGT GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA
 GCCACAGGGA GCAATGTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT
 25 CTATTACCT TGGTGGCGG AACACATTGA AGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG
 TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA ACCAGGCATT
 GAGGACAATG AGAAGAGTTT TTCAAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA
 GTTACTGATG AGACAATTC CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT
 ACTGTCTCT AGGCTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG
 30 CCCATAAACA GACCAAGCAG TTTAAACAAC AGAAATTAT TTCCTCGCAG TCCTGGAGGC AGGAAGCTG
 CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCTC
 CTTGGTCTT CACA TGGTCTT TCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT
 ATGGATCAGA GCACACCCA ATCCAGTGT TTAACGTGAA TCACCTCTT AAAGTTTCTC TCTCCAAATA
 CAATCACCTC CTGAGGCACT GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATT CAGTTCAGTCC
 35 AAAACGCCTA CCACTGGAGA CTTGCAACAT GGCGGCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC
 TGTTCCTGT TGCAATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG
 GAGAAGGGCA AAAAAGAGTC CAAGTAGAAA AAAAAACTAT GAAAGTTTGA GAGAGTAACC ATAATTTCAG
 CCCGATGTGA AACCATCCTA GATTTAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG
 CAGAGGGAAC AGCCTAAGT AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC
 40 TTCCACATTT CTAAACACA GGATGTGATT TTGGGTGTG TTGAGACAAG GCAGAAAAT TGTTTGAAA
 AATAACTTGA ATTCCTGCA CATTAAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTT
 ATTCCTTGGC TTGTATTGG SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT
 CATGAGTAGC CCCAAGATC AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT
 ATTTGTCTG CTTTCCGAG ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT
 45 TCCCTCCTTA CAGGTGGTAA CTTTCTACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA
 GTGGAGGGCA ATGCTCTAT TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA
 GGCCAAGTGT TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA
 GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC
 AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAACGT GAGACAGGTC GAACCACAAA
 50 GCCTGCCTGG AAAAGGGGAG TGACGTCTTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA
 CCAACAGGTG ACTCATTTTG GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCAGTTT CTGAAATCCT
 GAGTGTGCC TGCCAGTCGC CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTCTG
 AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG
 TGGAGGGCAA TGTCTCTATT CTGCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG
 55 GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT -3'
 (FRAG.NO:1799) (SEQ. ID NO: 3010)

5'-GTCAGCTCAG CCCTCAAAGG AGCCAGCCTC TCCCAGTTT CTGAAATCCT GAGTGTGCTG TGCCAGTCCG
 CATGAGAACT TCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTCTG AGATGGCCTC AGGTGGTAAC
 TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT
 60 CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC
 TGGGAGTGAC CAGAAAGAAAT GACGCAGAAG TGAAATGAAC TT-3' (FRAG.NO:) (SEQ. ID NO: 2475)

5'-CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT
 GAGCACTTGC AATC CGGCTA GGGTGATTTT AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT
 GCCATATTGG ATGC/TGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTTACCT TGGTTGGCGG
 AACACATTGA AGGGA/CTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA
 5 CATCCACAGG AGA/TGAAGA GGT'TTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT
 TTCAAAAGTG GAA/TACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTT
 CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGGTAGCGA
 TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG
 TTTAAACAAC AGA/ATTTAT TTCTCTCGAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG
 10 TTGGCTTCTT CTCAGGTGTC TGTCTTGCC TGGTAGATGA CCGCCGCTC CCTGGGTCTT CACATGGTCT
 TTCTCTGTG TGTGTCGTG CCAATCTCTT CTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA
 ATGACCGTGT TTA/CTTGAA TCACCTCTT AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACCT
 GTTAGGGCTT CGAC/ACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCAGTGGAGA
 CTTGCAACAT GGCC/GCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCTGT TGCAATGGAAT
 15 AGAAGGCTAT TCC/AGGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC
 CAAGTAGAAA AAA/AACTAT GAAAGTTTGA GAGAGTAACC ATAATTTTCA CCCGATGTGA AACGATCCTA
 GATTTACAGT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGGAAC AGCGTAACTG
 AAGGCATGGA AGG/AGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAAAAACA
 GGATGTGATT TTGC/GGTGTG TTGAGACAAG GCAGAAAACCT TGTTTGGAAA AATAA/CTTGA ATTCCTGCA
 20 CATTTAA/AT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC ATTCTTGGC TGTATTGG
 SCACAGCTGG CAT/GCCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT CATGAGTAGC CCCAAAGATC
 AATCATGGGC CAA/TTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT ATTTGTCTG CTTTCGCGAG
 ATGTTCTCAA ATCC/TGCGAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA CAGGTGGTAA
 CTTTCTCACA GGCC/TGGCC ACAGATCTGA TCATTACAAT TCGTTCAGCA GTGGAGGGCA ATGTCTCTAT
 25 TCTGCCTGCC CGATCTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG
 CTGAGAGTGA CCA/GAAGAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCTTTT AATAAAGGAA
 AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG
 TAGGGGGTTA GGGTGCATGG GTTGGAAACGT GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG
 TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG-3'
 30 (FRAG.NO:) (SEQ. ID NO: 2474)
 5'-GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG
 AGAACTTCCT ACC/TCTGCT GTTACTCTC TGCTACTTT TGTCTGAGAT GGCTCAGGT GGTAACCTTC
 TCACAGGCCT TGG/CACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC
 CTGCCCCATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAAGGCCA AGTGCTGCAA GTGAGCTGGG
 35 AGTGACCAGA AGA/ATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTAAATAA AGGAAAATTG
 CTTTGAAGT AT-3' (FRAG.NO:) (SEQ. ID NO: 2472)
 5'-CCGGGGC-3' (FRAG.NO:1800) (SEQ. ID NO: 1813)
 5'-GG GCCTGCBGGG CC-3' (FRAG.NO:1801) (SEQ. ID NO: 1814)
 5'-GGCBGCB BGG-3' (FRAG.NO:1802) (SEQ. ID NO: 1815)
 40 5'-GGG TCC TCB TGG CTG GGG-3' (FRAG. NO:1212) (SEQ. ID NO:1221)
 5'-GCC TGG GCC TGC BGG GCC-3' (FRAG. NO:1213) (SEQ. ID NO:1222)
 5'-GCT CTG GCC TGG 3GT GGC TC-3' (FRAG. NO:1214) (SEQ. ID NO:1223)
 5'-GCC BGT BGT TCC TGG T-3' (FRAG. NO:1215) (SEQ. ID NO:1224)
 5'-CCGGGGCTGC BGCBBCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG
 45 BBTGGCBGCB BGGHTGGCB GGGTCTCBT GGCTGGGGTC BCBGTCCTC TBGCTBGGCB GGGTGBCCBG
 BGBGGGC-3' (FRAG.NO:1803) (SEQ. ID NO: 1816)

Human Defensin 2 Nucelic Acid and Antisense Oligonucleotide Fragments

5'-ATCCTTTAAG TCAATGGACT TTGCATCAGT CACACCATCT TTTGTTACTT TGGACTTCCC CAGCTATGTT
 CAATAATTAC TGTCTTCCC TTGGGCCCCA TTGTAATGGC TACAGCCTCG AAAAAAGTC TACACTTTGA
 50 AGCATTAAGG CTC/GACATC AGCACCAAAT TTTACATCTT TACCATCACT TCAAGTGAGG TGAGGAGCCA
 GTAGCCTGGA CACT/GGTCTC ATCTGGTGAA AGACTGTGGG TAATGGAAGC ATTTCTGTGG GGTGCTGGCA
 GGACATGTGC ATG/GCAGGC AGGTCATCAG CAGCAAGTGA GAGCTGCCTC TTACTTTCTA AAGGTGACAT
 AGCAAATATA CAA/AAAAAA TAAATAAATT ATTAATTTAG GTAGAGCACA TAAAGGCTTT ATTTCATATT
 CCATTTCTCT GTATGCTTTC TTCACCAGGA AGAAATAGTT TTAGTGTCAG GAATGAATGA GTCTGCCCT
 55 CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG TGA/TCCCTG GTGACTAAGC
 TCCCAGTCTT GGATGCATAT TTGTTTAGCA GTTCTGACAG CATTTGACCC AGCCCTCTCT CTGCATATCC
 CATCAGAACC TTT/TTTTTT TTTTTTCTT TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCCTGTGCC
 TCAGCCTCCC AAA/ACCTGG AATTATAGCC GTAAGCCATC ATGCCTGGCT AATTTTGTGA TTTTTCATGG
 AGATGGGGTT TTG/CATGTT GGTCAAATTG GTCTCACACT CCTGACCTCA TGTGATCCAC CTGCCTCAGC
 60 CTCCCAA/ACT GCTC/GGATGA CAGGTGTAAG CCACCATGCT AGGCTCAGAA ATTTCTTTT ATAAAAATGT
 CATTAAAGGAT CTTGCTGCA CAATATCGTT ACCAGCTTCC TTAAATCCA CTCTGGCCT GCCAGGAATC

AGGTTCTTCA GAACCTGACA TTTTAAATGA AGAGGTCAGG CAGTTCATGA GGAAAGCCTC ATTGTCCCCA
 TGTCTCTGTC ACTGCTGCAC CCCTGAGACA TCACAGACAT GGACACTGGG GCCTGCTTGT TTCTCAAACCT
 GCCCTTAGAT CGAAAGAGGG AGGAACCAGG ATGAATGCCA CTCATTTTCC CAAGAAAGGC CCTCTCCTGA
 GTGCCCCGGA TGGGCTCTGT TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTTACGG AGGAAGGACA
 5 GGGTCCTGAG AGACACCAGA GACCTCACAC AGCCCTGAAA ACATGGGGCT CCTTCATAAG TGTTCCTCAT
 CACCAACAGG GAGACCACGT GGAGGCCTTG CAGCCCCACT CGGTGCTTCT CCACCAAATC CCAAGGCGAG
 TGACGCTGAC GTCTGTGGAA AGCAGAGAAA GCCCTGGCTC CCAAAGCCCT GAAGTCCCTG TGGAGCTGAC
 ATTCCTTGAG TGACGGTGTG AATGGAAGGA ACTCAAGTGC GGGTGGTAGG CCACCTCCTG GCCCAGGCCT
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 10 GGGCATCCAT CTGCTCTATC TCTCTCCCGT GGGGAAGATG GGGAGTTTCA GGGGAACTTT CACATAAATT
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 TCCAGGGTCT CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA ATGTCAGAGC AATGGATAGA
 ATTAGATGGA AAGAAGCTCT AATTGACCT GAGACTGTCC CCAGATACTC AGGAAAAACA GGACGTCGCA
 CAGAGTGGGC AGCAGGTGAG TGGCAGGTTA TAGGTCCTGA GTTTGAGTTT GTTCTCACGT GAGACAGACC
 15 CAGCCCCTCA CTCCATTCAC ACACTGGGTT TTAATGGTG CAAGATAGGA GCAATTTTCT GGTCCCAAGA
 GCAGGAGGAA GGGATTTTCT GGGGTTTCTT GAGTCCAGAT TTGCATAAGA TCTCCTGAGT GTGCATTGTT
 CTTTGAGGAC CATCTCTGTA CTCACCAGGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG CATTGCACCC
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 20 CTTCTCATAT TCTGATGCC TCTTCCAGT GAGATGGGCC AGGGAATAG GAGGGTTGGC CAAATGGAAG
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 CCTCTCTCTG TGTCTCCCTT CCATCCTTTT CTCTGCTTCT TCTCTCTTCT TCCCTCTCTC TCTTTTTTCT
 GTCTTTCTTT TTCTCTCTCT CCTAGAGCAT GTCTTTCTTT CTTTCTCTTT CTTTCTTCTT ACCCACACTT
 25 TTAGACTGAA TGCCATATTT AATTGAACAA AGCATTGCTT CCTTCAATAG AAAAGGAGTT TGAGAACCCA
 ATGGACACCT CACTCGTTCT TCTAAGCCAA TATGAAGGAG CCCAGTAGCT TGTAATATC ATCTCTTCAC
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 40 TCGTTGCTGA GCTCTACCA GACCCACCT GGAGGCCCA GTCACCTCAG AGAGATCAGG GTCTTTTACA
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 CAAATGACT ACTGCGTCT CATTATCATG ATGAAAAGCA CCAGGCTTGA GAAAGAAGC CGCTGCCGAT
 TTAACAAGG CGAATCTGAC ACAGGGTTTG TGTTTTTTCA ACATGAGTTT TGAGTTCTTA CAGCTGTTT
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 45 AGTGGAGCCA TATGTCATCC AGTCTTTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GGTCTCCCTG
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 55 TCCTTTACTG TGAATGATCC CTTTCTTCCA AACTTTTCA TTGCATCAGA GATGATGTTA CCAATTTCTT
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 60 TTAAGTCAAT TGACTTTGCA TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCCCAGC TATGTTCAAT
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 TTAAGGCTCA GACATCAGCA CCAAATTTTA CATCTTACC ATCACTTCAA GTGAGGTGAG GAGCCAGTAG

Coulam et al. (2005)	
Study	OR (95% CI)
Overall	1.0
Study	
1	0.9 (0.5-1.5)
2	0.8 (0.4-1.3)
3	1.0 (0.6-1.6)
4	1.0 (0.6-1.6)
5	1.0 (0.6-1.6)
6	1.0 (0.6-1.6)
7	1.0 (0.6-1.6)
8	1.0 (0.6-1.6)
9	1.0 (0.6-1.6)
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95	1.0 (0.6-1.6)
96	1.0 (0.6-1.6)
97	1.0 (0.6-1.6)
98	1.0 (0.6-1.6)
99	1.0 (0.6-1.6)
100	1.0 (0.6-1.6)

[illegible]

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100	100	100	200

GCTCTTTTGG TGTGTTTTTT CCCTGTTAGG TGTTTTTGGT GGTATAGGCG ATCCTGTTAC CTGCCCTAAG
 AGTGGAGCCA TATGTCATCC AGTCTTTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GGTCTCCCTG
 GAACAAAATG CTGCAAAAAG CCATGAGGAG GCCAAGAAGC TGCTGTGGCT GATGCGGATT CAGAAAAGGC
 5 TCCCTCATCA GAGACGTGCG ACATGTAAAC CAAATTAAAC TATGGTGTCC AAAGATACGC AATCTTTATC
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 CTGCTCTCCA GGAAGGGGTC AGGGCTGCCA CAGCGGGGCT TGGAGTGCTT TCCAGGGTCA CAGGCATCTG
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 15 GAAGGATGGA AACCTCTATG CCTCCCAGAA AGCACCCTC AAGCTTTTGC TGAATGCTTC TCTGAAGGCC
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 20 GCACCTAGTCA TCACCTGGGT GTTCTCCAAC ATCCAGCTC AGCCAAATGG CTTTCATTAG TTTTATGGT
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 25 AGTTCTACTT TAACCTCACC TTCCCACCAA ATTTCTCAAC TGTCTTGCC ACCACAATTA TTAAATGGAC
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 30 TGTCCGGACC TCTGGTGA CTGTTGGGACG ATGGCTTCCA GCTAACTTAA TAGAGAAACT CAAGCAGTTT
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 35 GAAGCCACAT TTGCTATATT TCCCTTTTAT TGCTGTGCTC TTTGGTGTCA TAGCCAAGAA ATCATTACCT
 ACATCAATGT CAAAGGCTTT ATCCTTCTAT ACCTTCTAG TAGTTTATGG TTTCACTGTG TACATTTAGG
 TTTTCAATTC ATTTGAGTT GATGTTCTTA CATGGTGTGA GATAAAGATT TAAATACATA CATATATAAA
 ATCATGAGGT AGTC TACACT ATAAATATAC AATTGTTAAT TGTTACTCAA GTCTAAGTAG AGGTGGAAAT
 40 AATAAACTTT CTTT TTTTAA CTTAAACCAC TCTGTGTCAC TGAGCTGATT TCACCTTTAG CCTGATAAAA
 TCATTGTCTT CTCCACCTG ATTCTACAG GAGACTACTC ACCCCATAAC CTCAAAAACC TCTTCATGAG
 GATGGTAAGT CACCTGAATC CTGAAGTGAA TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA
 TCTAGACCTC CAGAGAACAG CAGGACCCAT CTTCAGAAAA TAAGAAGCAT TTGTTCCTG AGCCTGTTGA
 ATCAAAGTGC AATTTCTATT TTTTGGGAA TGTAAAGAA TGAATCATA TATTTAAGCA GGTGAACCCA
 45 CGAGTAACAT AGCAGGGTCT TTCTGTGTCAT TATTAGCTCC AACCTAGCAC AGACATTAAG CAATGGGCCT CTCTTATAAA
 TATACTAGCA TGAAACTGGG AGAACAGGAG CATTGAGCA ACCTTGAGAC CAATGGGCCT CTCTTATAAA
 ATGCACACCT CCTCTCACTG AGATTGAGGA AGGTTTCTTG TCTCCGAGCC TTCTCCAGT AGAGCTATAA
 ATCCAGGCTG GCTCTCCCT CCCACACAG CTGCTCCTGC TCTCCCTCCT CCAGGTGACC CCAGCCATGA
 GGACCCTCGC CATCTTGCT GCCATTCTCC TGGTGCCCT GCAGGCCAG GCTGAGCCAC TCCAGGCAAG
 50 AGCTGATGAG GTTC CTGCAG CCCCGGAGCA GATTGCAGCG GACATCCCAG AAGTGGTTGT TTCCCTTGCA
 TGGGACGAAA GCTTGGCTCC AAAGCATCCA GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG
 GAAGGACGGG AGAGAGGTTT CAGAGTTGGG TCTCAGCAGT CTATGTCACT GAGGTGGCTT CACTTAGAAT
 CTCTGGGCAT TGATTTTCTC ATCTAGAAAT TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC
 CAAAGACTTG ATTCAAGAA ACATCTGTGA AATTCATAA GTTTAAGATA TGAAGAGACA GACTAGTTAT
 TTCTGGATCT AAACAAGTAG ACTTAGTTGT AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA
 55 AACTGCAGCC AAGCTGAGG GTAAGTTCAG GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA
 AGGAGAATGA GTCCTCAAATT CTGTGTGACA AGCACTGCTC TGCGTGTTTA TTCTATCGA CTGAGGTTGT
 TCGTGTACC GGCTGCAATG CAGCCAGCAT CACCTGTCTG CTAGCATGTG ACTTCCCCGA GATTCTTTTT
 CTTACCTACT GCTAACTCA TACTCAATTT CTCATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA
 CTGCTATTGC AGAATACCA CGTGCATTGC AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAGA
 60 CTCTGGGCAT TCTGTGCTG AGCTTGCAGA AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG
 GGAATTGCTA TTACTCTGT ACCTTCTGCT CAATTTCTCT TCCTCATCTC AAATAAATGC CTTGTTACAA
 GATTTCTGTG TTTCACCTC TTTAATGTGT GATATGTGTC TGTGTCAAGA CACTTGGGAT ACACGTACCA

0040400 "0494350
 0040400 "0494350

AAACGCAAAA TCAAATTTTT GAACAATATA-3' (FRAG. NO:) (SEQ. ID NO:3012)

Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGCTGCBBTC TGCICCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG
CCBCCBGGGB BTGCICBGBBG GBTGGCBGGG TCCTCBTGGC TGGGGTCBCCT GGBGGBGGGB GBGCBGGGG
5 TCCTCBTGGC TGGGGTCBCCT CTCTCCCGTC CT CCTACCTGCT TATAGAAGAC CTGGGACAGA GGACTGCTGT
CTGCCCTCTC TGGTACCCCT GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT
GCTGCCATTC TCCTGCTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG
CAGCCCCGGA GCACATTGCA GCGGACATCC CAGAAGTGGT TGTTCCTT GCATGGGACG AAAGCTTGGC
10 TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA
CGTCGCTATG GAACCTGCAT CTACCAGGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA
AAATGAGCTC AAAAATTGCT TTGAGAGCTA CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3'
(FRAG. NO:1804) (SEQ. ID NO:3013)

5'-CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTACCCCT GCCTAGCTAG
AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGCTGGC CCTGCAGGCC
15 CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC
CAGAAGTGGT TGTTCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT
GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGGA
AGACTCTGGG CATCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAAATTGCT TTGAGAGCTA
CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' (FRAG. NO:) (SEQ. ID NO:2478)

5'-GAATTCCTGT TAAGCCCTGT TACAGGGGCT GCACCCAGAA TACAACCTGA CCTGTGTCCA AGGCGGGCAA
CTCAACCCCTT AGATATTGAA TGGGTCCCAT GGCACCAATG CTTAAACACC AGCAGCCCTC ACAACCCACAG
ATCGTGTITT AAGGATGAGG AGGTAGTTCT CTGGATGCAC AGGCTTCAAT CCAAATGGGC TCATGACGCC
GCAGCACACA CCCAGTCTGC AGCCTGAAGA GTTGGAGCAT TGCATTACA GAAAGCATCC AGACATGATC
ATGGGCTCAG GGATACACCT GTTCTCCGAT GTGTACCAGT GAAGGATGGA AACTCCTATG CCTCCAGAA
25 AGCACCCTC AAGCTTTTGC TGAATGCTTC TCTGAAGGCC CACAAGGCTG AGAGGCTGTG CAACACCAGC
AGTAAAGTGA ATGCCAGAC TCCCACCTCC TTTCTGGGT GGCCATCTGG AAAGGCCACT CCCACCTGA
TGGCTAATGC CTCAGACAG TTCTTGGCCC AGATGATCCT AGACAATTGT TTAAGCTTAA ACTGTTTATT
GGCAAAGCAA ACAGGTGATA GTACCTCTGG GGAACCATAT GCCGCTGTA CATCCAGATC TCAGGAGAAC
CCAAAAATGT CTGTCCACA TAGCAACAGA AGCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC
30 ATCCCAGCTC AGCCAAATGG CTTTCATTAG TTTTATGGT TAGACCCAG GTCTCGGGA CACTGCTTTA
GAAACACATT CCAATCCTC CTCTGTGTGC AGGTGGCATT CCTATCCCAA TCTCTTGCA GGGCGTATAC
TGTGATACGC AGCCAGGCTG TCCCAGAGGC CTTAAATATT CCCTTGGTGC AGGTAGTTCA GCTTAGCCAC
AGCCAATGCA TCACAGGGTC AACTGTGTTA GGAGCCATTG AGAATCCATA GTTGGTTGCT GCCTGGGCTT
GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC TTCCCACCAA
35 ATTTCTCAAC TGTCCTTGCC ACCACAATTA TTAAATGGAC CCAACAGAAA GTAACCCCGT AAATTAGGAC
ACCTCATCCC AAAAGACTT TAAATAGGGG AAGTCCACTT GTGCACGGCT GTCCTTGCT ATAGAAGACC
TGGGACAGAG GAGCTGTGTC TGCCCTCTCT GGTCAACCTG CCTAGCTAGA GGATCTGTAA GTTACTACAAA
ACTTAACTT TACA CTGAGT TTTCATCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT GTGGGGCCGC
CCCAGAGGGA CCCAGCGGGT GAATCCCTGC TAGGAACGTC TGTCCGGACC TCTGGTGACT GCTGGGACG
40 ATGGCTTCCA GCTA ACTTAA TAGAGAACT CAAGCAGTTT CTTCTAAAT ACACATGTCA CATGTCCTGG
TTGACATGTC CAGTAAAGAG ACTATCACAG GTCTTTGGAA CATTCTTTT AGAGAAACCT ATTTAGGTCC
TTGGTCTGTT TTTCAATCAG GTTGTGTGAT TTTTGCTATT GAGTTGTGG AATTCTTTAT GTATTAGAT
ATTTGCCCTT TCTCCATGT AGGTTTGTGA AATATTTTCT CTCATTTTCT GGGTTATCTT TTCCTCGGT
TGATTGTTTC CTTTCTGTG CAGATGCTTT AGCGTTAAAT GAAGCCACAC TGTCTATT TCCCTTTTAT
45 TGCCTGTGCC TTTGTTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT CAAAAGCTTT ATCCTTCTAT
ACACTTCTAG TAGTTTATGG TTTCAGTTGT TACATTTAGG TTTTCAATTC ATTCTGAGTT GATGTTCTTA
CATGGTGTGA GATTAAGATT TAAATACATA CATATATAAA ATCATGAGGT AGTGTACACT ATAAATATAC
AATTGTTAAT GTTACTCAA GTCTAAGTAG AGGTGGAAT AATAAACTTT CTTTTTTTAA CTTAAACCAC
TCTGTGTAC TGACCTGATT TCACCTTTAG CCTGATAAAA TCATTGTCCT CTCCACCCTG ATTCCTACAG
50 GAGACTACTC ACCCATAAC CTCAAAAACC TCTTCATGAG GATGGTAAGT CACCTGAATC CTGAAGTGAA
TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC CAGAGAACAG CAGGACCAT
CTTCAGAAAA TAAGAGCAT TTGTTCCCTG AGCCTGTTGA ATCAAAAGTGC AATTTCTATT CTTTTTGGAA
TGTTAAAAAG TGAATCATAA TATTTAAGCA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCAT
TATTAGCTCC AACCTAGCAC AGACATTAAA GGTACAGATG TATACTAGCA TGAAACTGGG AGAACAGGAG
55 CATTGAGCA ACCCTGAGAC CAATGGGCCT CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA
AGGTTTCTTG TCTCCGAGCC TTCTCCAGT AGAGCTATAA ATCCAGGCTG GCTCCTCCCT CCCACACAG
CTGCTCTGTC TCTCCTCTCT CCAGGTGACC CCAGCCATGA GGACCCTCGC CATCCTTGCT GCCATTCTCC
TGGTGGCCCT GCACGCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGCTGCAG CCCCGAGCA
GATTGCAGCG GACATCCAG AAGTGTTGT TTCCCTTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA
60 GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTC CAGAGTTGGG

- TCTCAGCAGT CTAIGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTTCTC ATCTAGAAAT
 TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA ACATCTGTGA
 AATTCATAA GTTTAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT
 AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA AACTGCAGCC AAGCCTGAGG GTAAGTTCAG
 5 GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA AGGAGAATGA GTCTCAAATT CTGTGTGACA
 AGCACTGCTC TGCTTGTTTA TTCCTATCGA CTGAGGTTGT TCGTGCTACC GGCTGCAATG CAGCCAGCAT
 CACCTGTGAG CTAGCATGTG ACTTCCCCGA GATTCTTTTT CTTACCCACT GCTAACTCCA TACTCAATTT
 CTCATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCATTGC
 AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGCAGA
 10 AAAAGAAAAA TGAAGTCAAA ATTTGCTTTG AGAGCTACAG GGAATTGCTA TTAATCTGT ACCTTCTGCT
 CAATTTCTTT TCCTCATCTC AAATAAATGC CTGTGTACAA GATTCTGTG TTTCCACCTC TTTAATGTGT
 GATATGTGTC TGTGTCAAGA CATTGGGAT ACACGTACCA AAACGCAAAA TCAAATTTT GAACAATATA-3'
 (FRAG. NO:) (SEQ. ID NO:2477)
 5'-GGCBGCBGG-3' (FRAG. NO:1805) (SEQ. ID NO:1818)
 15 5'-GG CTG GGG-3' (FRAG. NO:1806) (SEQ. ID NO:1819)
 5'-GGGGTCBCC-3' (FRAG. NO:1807) (SEQ. ID NO:1820)
 5'-GGG TCC TCB TGG CTG GGG TC-3' (FRAG. NO:1216) (SEQ. ID NO:1225)
 5'-CCT CTC TCC CGT CTT-3' (FRAG. NO:1217) (SEQ. ID NO:1226)
 5'-CGCTGCBBTC TGCCTCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG
 20 CCBCCBGGGB BTGGCBGCBGG TCCTCBTGGC TGGGGTCBCCT GGBGBGGGB GBGCBGG-3'
 (FRAG. NO:1808) (SEQ. ID NO:1821)

Human Macrophage Inflammatory Protein-1-alpha/RANTES Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GTCTTTGTTT CTCGGCTCGT GCCCBTCCC GGCTTCTCTC TGGTCCGTC CTCTGTGGTG TTTGGCCCTG
 25 CTTCCTTTTG CCTGTTGAGG GGGCAGCAGT TGGGCCCAA AGGCCCTCTC GTTCACCTTC TGGCAGGAGTT
 GCATCCCCATA GTCAAACCTCT GTGGTCGTGT CATAGTCCTC TGTGGTGTTC GGAGTTTCCA TCCCGGCTTC
 TCTCTGGTTC CAACGGAGB GGGGGCBGCB GTTGGGCCCC BBBGGCCCTC TCGTTCBCCT TCTGGCBGCG
 BGTTGCBTCC CCBTGTGCB BCTCTGTGGT CGTGTCTBG TCCTCTGTGG TGTTTGGBT TTCCBTCCCG
 GCTTCTCTCT GGTTCBGG GB-3' (FRAG. NO:1809) (SEQ. ID NO:1822)
 30 5'-GGGCC CC-3' (FRAG. NO:1810) (SEQ. ID NO:1823)
 5'-GGGGCBGC-3' (FRAG. NO:1811) (SEQ. ID NO:1824)
 5'-CCGGCTTC-3' (FRAG. NO:1812) (SEQ. ID NO:1825)
 5'-GTC TTT GTT TCT GGG CTC GTG CC-3' (FRAG. NO:1218) (SEQ. ID NO:1227)
 5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' (FRAG. NO:1219) (SEQ. ID NO:1228)
 35 5'-GTC CTCTGT GGT CTT TGG-3' (FRAG. NO:1220) (SEQ. ID NO:1229)
 5'-CCC TGC TTC CTT TCG CCT GTT-3' (FRAG. NO:1221) (SEQ. ID NO:1230)
 5'-GAGGGGGCAG CAGTTGGGCC CCAAAGGCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT CCCCATAGTC
 AAATCTGTG GTCGT-3' (FRAG. NO:1222) (SEQ. ID NO:1231)
 5'-GTATAGTCTCTCT TGGTGTGAGTTTCCATCCCGCTTCTCTGTTCCAAGGGA-3' (FRAG. NO:1223) (SEQ. ID
 40 NO:1232)
 5'-GBGGGGCBG CBTTTGGGCC CBBBGGGCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTGTG
 BBBCTCTGTG GTCGTG-3' (FRAG. NO:1224) (SEQ. ID NO:1233)
 5'-TCBTGTCTCTGT GTGTGTTGGBGTTCCBTCCCGCTTCTCTGTTCCBGGGB-3' (FRAG. NO:1225) (SEQ. ID
 NO:1234)

RANTES Antisense Oligonucleotide Fragments

- 5'-GGGCBGCGG CBTTTGGCGG GCBTGTBGG CBBBGBGCB GGGTGTGGTG TCCBGBBBT BTGGGBGGC
 BBTGCBGGB GCGCBGBGG CBGTGCBBT GBGBGTGCB GCBGGCGTG CCGCBGBGC CTTCTGTTB
 CCTGTGGBG GCGTGTGGB GGGGGTGTG TGTCCGCTTG GCGGTTCTTT CGGGTGTTC TTCTGTGGT
 TGGCCTGCTG CTCGTGTGGT CGTCCGCTC CCGGTTCTGT CTCGTCTGT CGCCCTTCC TTCCTGTGCTG
 50 TGTTCTCTCC TTCTTGCCT CT-3' (FRAG. NO: 1813) (SEQ. ID NO: 1826)
 5'-GGTTGGC-3' (FRAG. NO: 1814) (SEQ. ID NO: 1827)
 5'-CGGG CBG-3' (FRAG. NO: 1815) (SEQ. ID NO: 1828)
 5'-CCGGGTTCTG-3' (FRAG. NO: 1816) (SEQ. ID NO: 1829)
 5'-GGGTGTGGT-3' (FRAG. NO: 1817) (SEQ. ID NO: 1830)
 55 5'-GGGCBGCGG CBTTTGGCGG GCBTGTBGG CBBBGBGCB GGGTGTGGTG TCCBGBBBT BTGGGBGGC
 BBTGCBGGB GCGC-3' (FRAG. NO:1226) (SEQ. ID NO:1235)
 5'-BGBGGGCBGTB GCBTGTGGB TGBCBGCBG GCGTGCCGCG GBGBCCTCB TGGTBCCTGT GGBGBGGCTG
 TCGGBGG-3' (FRAG. NO:1227) (SEQ. ID NO:1236)
 5'-GGGTGTGGTGTCCGCTTGGCGGTTCTTTCGGGTGTTTCTCTCTGGGTTGGCCTGCTGCTCGTGGTC-3' (FRAG.
 60 NO:1228) (SEQ. ID NO:1237)

5'-GCTCCGCTCCCGGG(TTCGTTCTCGCTCTGTGCGCCCTTCCTTCTTGTCGTGTTCTCCCTTCTTGCCTCT-3' (FRAG. NO:1229) (SEQ. ID NC:1238)

5'-GGGTGTGGTGTCCG-3' (FRAG. NO:1230) (SEQ. ID NO:1239)

5'-CTTGGCGGTTCTTTCGGGTG-3' (FRAG. NO:1231) (SEQ. ID NO:1240)

5 5'-TTTCTTCTCTGGGTGGC-3' (FRAG. NO:1232) (SEQ. ID NO:1241)

5'-CTGCTGCTCGTCGIGGTC-3' (FRAG. NO:1233) (SEQ. ID NO:1242)

5'-GCTCCGCTCCCGGCTTC-3' (FRAG. NO:1234) (SEQ. ID NO:1243)

5'-GTCTCGCTCTGTCGCC-3' (FRAG. NO:1235) (SEQ. ID NO:1244)

5'-CTTCCTTCCTTGTC 3' (FRAG. NO:1236) (SEO. ID NO:1245)

10 5'-GTGTTCTCCTTCCTTGCCTCT-3' (FRAG. NO:1237) (SEQ. ID NO:1246)

5'-GGGCBCGGGG CB3TGGGCGG GCBGTGTBGG CBBBGCBCB GGGTGTGGTG TCCBGGBBT BTGGGGBGGC
BGBTGCBGG BGC(BGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB
CCTGTGGBGB GGCTGTCGBB GG-3' (FRAG. NO:1818) (SEQ. ID NO:1831)

Human Muscarinic Acetylcholine Receptor HM1* Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-GCTGCCCGGC GGJGTGTGCG CTGGCGCTC CCGTGTCTGG TTCTCTGTCT CCCGGTCCCC CTGCGCTGGC
GTCTCGGGCC TTCGTCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCCT
CGGGGTCCCG GGGCITCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGTG GCTBGGTGGG GC-
3'(FRAG. NO:1819)(SE). ID NO: 1832)

5'-GGTGGGGGC-3' (FRAG. NO:1820) (SEO. ID NO: 1833)

20 5'-GCCCCGGCGGGG-3' FRAG. NO:1821) (SEQ. ID NO: 1834)

5'-CGG GGC TTC TGG CCC-3' (FRAG. NO:1822) (SEQ. ID NO: 1835)

5'-GTT CBT GGT GGC TBG GTG GGG C-3' (FRAG. NO:1238) (SEQ. ID NO:1247)

5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' (FRAG. NO:1239) (SEO. ID NO:1248)

5'-GCT CCC GTG CTC GGT TCT CTG TCT CCC GGT-3' (FRAG. NO:1240) (SEQ. ID NO:1249)

25 5'-CCC CCT TTG CCT GGC GTC TCG G-3' (FRAG. NO:1241) (SEQ. ID NO:1250)

5'-GCC TTC GTC CTC 'TTC CTC TTC TTC CTT CC-3' (FRAG. NO:1242) (SEQ. ID NO:1251)

5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' (FRAG. NO:1243) (SEQ. ID NO:1252)

5'-CGG GGC TTC TGG CCC TTG CC-3' (FRAG. NO:1244) (SEQ. ID NO:1253)

5'-GTT CAT GGT GGC TAG GTG GGG C-3' (FRAG. NO: 1245) (SEO. ID NO:1254)

30 Human Muscarinic Acetylcholine Receptor HM3* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGG GTG GGT BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT
TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG
GGG GCT TCT TGGC3 CTG GCG GGG GGG CCT CCGTCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG
TGGTGG CGG GCG TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC
GCT CCC GGG CCG CCGGG GTG GCT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT
GCA GGG G-3' (FRAG. NO:1823) (SEQ. ID NO:1836)

5'-CCC GGG CGG-3' (FRAG. NO:1824) (SEQ. ID NO:1837)

5'-G GCG GGG GGG CC-3' (FRAG. NO:1825) (SEQ. ID NO:1838)

5'-CCC GGG CCG CC-3' (FRAG. NO: 1826) (SEQ. ID NO: 1839)

40 5'-GG CCG TGT-3' (F RAG. NO:1827) (SEQ. ID NO:1840)

5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' (FRAG. NO:1246) (SEQ. ID NO:1255)

5'-GTT GGC CBT GTT GGT TGC C-3' (FRAG. NO:1247) (SEQ. ID NO:1256)

5'-TCT TGG TGG TGC GCC GGG C-3' (FRAG. NO:1248) (SEQ. ID NO:1257)

5'-GCG TCT TGG CTG TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3'(FRAG.NO:1249)(SEQ.ID NO:1258)

5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' (FRAG. NO:1250) (SEQ.ID NO:1259)

5'-GCG CTG GCG GGG GGG CCT CCT CC-3' (FRAG. NO:1251) (SEQ. ID NO:1260)

5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' (FRAG. NO:1252) (SEQ. ID NO:1261)

5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' (FRAG. NO:1253) (SEQ. ID NO:1262)

50 5'-GGG CCC GCG GCT GCB GGG G-3' (FRAG. NO:1254) (SEQ. ID NO:1263)

5'-TTG CCT GTC TGC TTC GTC-3' (FRAG. NO:1255) (SEQ. ID NO:1264)

5'-CTT TGC GCT CCC GGG CCG CC-3' (FRAG. NO:1256) (SEQ. ID NO:1265)

5'-GGG GTG GGT AGC CCG TGT CTG GGG-3' (FRAG. NO:1257) (SEO. ID NO:1266)

5'-GTT GGC CAT GTT GGT TGC C-3' (FRAG. NO:1258) (SEQ. ID NO:1267)

55 5'-GGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1259) (SEO. ID NO:1268)

Human Fibronectin* Antisense Oligonucleotide Fragments

5'-CGG TTT CCT TTG CGG TC TTG GCC CGG GCT CCG GGT G CCC GCC CGC CCG CCG GCC GCC GC CCC GCC
GGG CTG TCC CCG CCG CGC CCC GGC CCG GGG CGC GGG GG CGG CCC TCC CGC CCC TCT GG GCC GGC GCG
GGC GTC GG CCG CTG GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C GCC TGC CTC TTG CTC TTCTGC GTC

- CGC TGC CTT CTC CTT CTC TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGC CCT TCC GTG GTG C TGT
TGT CTC TTC TGC CCT C GGT GTG CTG GTG CTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG
GCC TCT TCG GGT GTG GCT TTG GGG CTC TCT TCC TTT CCC TGC TGG CCG TTT GT CTT GTT TTC TGT CTT
5 TTG CTC GT TGT CTG GGG TGG TGC TCC TCT CCC TTT CCC TGC TGG CCG TTT GT CTT GTT TTC TGT CTT
CCT CT TTC CTC CTC TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT GTG GGC TTT
CCC TGG TCC GGT CTT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC C
TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1828) (SEQ.
ID NO: 1841)
- 5'-GGCCCGGGC-3' (FRAG. NO:1829) (SEQ. ID NO: 1842)
- 10 5'-GCCGGCGCGGGCG 3' (FRAG. NO:1830) (SEQ. ID NO:1843)
5'-GCCTGGGCTGGCC-3' (FRAG. NO:1831) (SEQ. ID NO: 1844)
5'-GGGGG TGGCCG-3' (FRAG. NO:1832) (SEQ. ID NO: 1845)
5'-GG GGG TGG CCG TTG TGG GCG G-3' (FRAG. NO:1833) (SEQ. ID NO: 1846)
5'-CGG TTT CCT TTG CCG TC-3' (FRAG. NO:1260)(SEQ. ID NO:1269)
- 15 5'-TTG GCC CGG GCT CCG GGT G-3' (FRAG. NO:1261)(SEQ. ID NO:1270)
5'-CCC GCC CGC CCG CCG GCC GCC GC-3' (FRAG. NO:1262)(SEQ. ID NO:1271)
5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' (FRAG. NO:1263)(SEQ. ID NO:1272)
5'-GGC CCG GGG CGC GGG GG-3' (FRAG. NO:1264)(SEQ. ID NO:1273)
5'-CGG CCC TCC CGC CCC TCT GG-3' (FRAG. NO:1265)(SEQ. ID NO:1274)
- 20 5'-GCC GGC GCG GGC GTC GG-3' (FRAG. NO:1266)(SEQ. ID NO:1275)
5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' (FRAG. NO:1267)(SEQ. ID NO:1276)
5'-GCC TGC CTC TTG CTC TTC-3' (FRAG. NO:1268)(SEQ. ID NO:1277)
5'-TGC GTC CGC TGC CTT CTC CC-3' (FRAG. NO:1269)(SEQ. ID NO:1278)
5'-CTC TCC TCG GCC CTT GCC TGT GC-3' (FRAG. NO:1270)(SEQ. ID NO:1279)
- 25 5'-TGT CCG TCC TGT CCG CCT TCC GTG GTG C-3' (FRAG. NO:1271)(SEQ. ID NO:1280)
5'-TGT TGT CTC TTC TGC CCT C-3' (FRAG. NO:1272)(SEQ. ID NO:1281)
5'-GGT GTG CTG GTG CTG GTG GTG GTG-3' (FRAG. NO:1273)(SEQ. ID NO:1282)
5'-CCT CTG CCC GTG CTC GCC-3' (FRAG. NO:1274)(SEQ. ID NO:1283)
5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' (FRAG. NO:1275)(SEQ. ID NO:1284)
- 30 5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' (FRAG. NO:1276)(SEQ. ID NO:1285)
5'-CTT CTC GTG GTG CTT CTC CTC CCT GGC TTG GTC GT-3' (FRAG. NO:1277)(SEQ. ID NO:1286)
5'-TGT CTG GGG TGG TGC TCC TCT CCC-3' (FRAG. NO:1278)(SEQ. ID NO:1287)
5'-TTT CCC TGC TGG CCG TTT GT-3' (FRAG. NO:1279)(SEQ. ID NO:1288)
5'-CCT GTT TTC TGT CTT CCT CT-3' (FRAG. NO:1280)(SEQ. ID NO:1289)
- 35 5'-TTC CTC CTG TTT CTC GCC-3' (FRAG. NO:1281)(SEQ. ID NO:1290)
5'-TTG GCT TGC TGC TTG CGG GGC TGT CTC C-3' (FRAG. NO:1282)(SEQ. ID NO:1291)
5'-CTT GCC CCT GTG GGC TTT CCC-3' (FRAG. NO:1283)(SEQ. ID NO:1292)
5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' (FRAG. NO:1284)(SEQ. ID NO:1293)
5'-GCC CTT CTT GGT GGG CTG-3' (FRAG. NO:1285)(SEQ. ID NO:1294)
- 40 5'-GCT CGT CTG TCT TTT TCC TTC C-3' (FRAG. NO:1286)(SEQ. ID NO:1295)
5'-TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T-3' (FRAG. NO:1287)(SEQ. ID NO:1296)
5'-TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1288)(SEQ. ID NO:1297)

Human Interleukin-1 (IL-1) Nucleic Acid and antisense Oligonucleotide Fragments

- 5'-AAGCTTCTAC CCAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTTATTTC TGTGGCTCCT
45 GTTATAACTA TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGGCA TTAAATCAGA ATAAGAGATT
TTGCACCTGC AATAGACCTT ATGACACCTA ACCAACCCCA TTATTACAA TTAAACAGGA ACAGAGGGAA
TACTTTATCC AACTCACACA AGCTGTTTTT CTCCCAGATC CATGCTTTTT TGCGTTTATT ATTTTITAGA
GATGGGGGCT TCACTATGTT GCCCACACTG GACTAAAACT CTGGGCCTCA AGTGATTGTC CTGCCTCAGC
CTCCTGAATA GCTGGGACTA CAGGGGCATG CCATCACACC TAGTTCATTT CCTCTATTTA AAATATACAT
50 GGCTTAAACT CCAACTGGGA ACCCAAACA TTCATTGCT AAGAGTCTGG TGTCTACCA CCGTGAACCTAG
GCTGGCCACA GGAAATATAA AAGCTGAGAA ATTCTTTAAT AATAGTAACC AGGCAACATC ATTGAAGGCT
CATATGTAAG AATCATGCC TTCCTTTCTC CCAATCTCCA TTCCCAAACCT TAGCCACTGG TTCTGGCTGA
GGCCTTACGC ATACCTCCCG GGGCTTGCAC ACACCTTCTT CTACAGAAGA CACACCTTGG GCATATCCTA
CAGAAGACCA GGCCTCTCTC TGGTCCTTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG GGTGAGAGT
55 TCTCTCTGA AGCTCATCC CCTCTATAGG AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA
CTTCTTTGTG CTCAAATACC ACTGTTCTCT TCTCTACCCT GCCCTAACCA GGAGCTTGTC ACCCCAAACT
CTGAGGTGAT TTATGCCTTA ATCAAGCAAA CTTCCTCTT CAGAAAAGAT GGCTCATTTT CCCTCAAAG
TTGCCAGGAG CTGCCAAGTA TTCTGCCAAT TCACCCTGGA GCACAATCAA CAAATTCAGC CAGAACAACAA
CTACAGCTAC TATTAGAAGT ATTATTATTA ATAAATTCCT CTCCAAATCT AGCCCTTGA CTTCGGATTT
60 CACGATTCT CCCTTCCTCC TAGAACTTG ATAAGTTTCC CGCGCTTCCC TTTTCTAAG ACTACATGTT
TGTCATCTTA TAAAGCAAG GGGTGAATAA ATGAACCAA TCAATAACTT CTGGAATATC TGCAACAAC

1. <i>Staphylococcus aureus</i>	
1.1	1.1.1
1.2	1.2.1
1.3	1.3.1
1.4	1.4.1
1.5	1.5.1
1.6	1.6.1
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1.11	1.11.1
1.12	1.12.1
1.13	1.13.1
1.14	1.14.1
1.15	1.15.1
1.16	1.16.1
1.17	1.17.1
1.18	1.18.1
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1.24	1.24.1
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1.26	1.26.1
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1.92	1.92.1
1.93	1.93.1
1.94	1.94.1
1.95	1.95.1
1.96	1.96.1
1.97	1.97.1
1.98	1.98.1
1.99	1.99.1
1.100	1.100.1

[illegible]

[illegible]

[illegible]

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

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 5 CAGCCAATCT TCAATGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA
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 10 CGACACATGG GATACGAGG CTTATGTGCA CGATGCACCT GTACGATCAC TGAAGTGCAC GCTCCGGGAC
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 45 AAAAACTCAA TTGTATGTGA CTGCCCAAGA TGAAGACCAA CCAGTGCTGC TGAAGGAGAT GCCTGAGATA
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 60 GCCAGGAAAC TCTGCTTCT AGTACTTGGG AACCTGTAA CATATAATA AATGTACATT AATTACCTTG
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40	5'-AGAAAGAAAG	AGAGAGAGAA	AGAAAAGAAA	GAGGAAGGAA	GGAAGGAAGG	AAGAAAGACA	GGCTCTGAGG
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	GGAGTCCCCT	AGGCCACCCA	GACAGGGGCTT	TTAGCTATCT	GCAGGCCAGA	CACCAAATTT	CAGGAGGGCT
	CAGTGTTAGG	AATGGATTAT	GGCTTATCAA	ATTCACAGGA	AACTAACATG	TTGAACAGCT	TTTAGATTTC
	CTGTGGA AAA	TATAACTTAC	TAAAGATGGA	GTTCTTGTA	CTGACTCCTG	ATATCAAGAT	ACTGGGAGCC
45	AAATTA AAAA	TCAGAAGGCT	GCTTGGAGAG	CAAGTCCATG	AAATGCTCTT	TTTCCCACAG	TAGAACCTAT
	TTCCCTCGTG	TCTCAAAATC	TTGCACAGAG	GCTCACTCCC	TTGGATAATG	CAGAGCGAGC	ACGATACCTG
	GCACATACTA	ATTTGAATAA	AATGCTGTCA	AATTCCCAT	CACCCATTCA	AGCAGCAAAC	TCTATCTCAC
	CTGAATGTAC	ATGCCAGGCA	CTGTGCTAGA	CTTGGCTCAA	AAAGATTTC	GTTTCCTGGA	GGAACCAGGA
	GGGCAAGGTT	TCACTCAGT	GCTATAAGAA	GTGTTACAGG	CTGGACACGG	TGGCTCACGC	CTGTAATCCC
50	AACATTGGG	AGGCCGAGGC	GGGCAGATCA	CAAGGTCAGG	AGATCGAGAC	CATCCTGGCT	AACATGGTGA
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	GGAGCCTGAA	CCCTGCATAC	CGTATGTTCT	CTGCCCCAGC	CAAGAAAGGT	CAATTTTCTC	CTCAGAGGCT
60	CCTGCAATTG	ACACAGAGCT	CCCAGGGCAG	AGAACAGCAC	CCAAGGTAGA	GAGCCACACC	CTCAATACAG
	ACAGGAAGGG	CTAATGGCCC	TTCATTGTAC	CCATTTATCC	ATCTGTAAGT	GGGCAAGATTC	CTAAACTTAA
	GTACAAAGAA	GTGTAATGAAG	AAAAAGTATGT	GCATGTATAA	ATCTGTGTGT	CTTCCACTTT	GTCCCAACAT

[illegible]

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30 Human Interleukin-1 Receptor (IL-1 R) Nucleic Acids and Anti-sense Oligonucleotide Fragments

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 10 AGCTAATGAG ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG
 AGTGACATTG CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT
 ATTACAGTGT GGAAATCCCT GCAACAAAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA TATCGGAAAT
 TGAAGTAGTA TTTIATAAAC ATCCATTAC CTGTTTGGC AAGAATACAC ATGGTATAGA AGAAACATAT
 ATCCAGTTAA TATATCCAGT CACTAATTTT CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA
 15 TAATTGTGTG TTCTGTTTTC ATCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCTCTG
 CTATGATTTT CTCCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT
 GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTGTGT TTAAGTCTT GCCTGAGGTC TTGAAAAAAC
 AGTGTGGATA TAACCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA
 TGAAAACGTA AAGAAGAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG
 GGTGGTTTAC CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAAGG TGAATTAATA GTTGTCTCTG
 20 TTGAGCTGGA GAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAA TTCATTAAAG AGAAACATGG
 GGCTATCCGC TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAAGA CAAGGTTCTG GAAGAATGTC
 AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA GCCACTAAGG
 AGAACTGCA AAGAAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTGC
 CTCCTGTCTT ATGGCGTTC AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAAC TA
 25 TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3' (FRAG NO:)(SEQ. ID NO:2520)
 5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC
 TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA
 GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG
 30 CCCCCAGGTG CCTACTGGT TGTGGGCCTC TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC
 TCTGCTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC
 CAGCCTTGCA GGACGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAATGTC
 CATTGAGCTC AGACTTTTGT AGAATACAGA TGCTTCTCTG CCGTTCATCT CATACCCGCA AATTTTAACC
 TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAAC GACGTGAAGA
 TTCAATGGTA CAACGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC
 35 TCACCTACTC GTACACGATG TGGCCCTGGA AGATGTGGC TATTACCGCT GTGTCTGTAC ATTTGCCAT
 GAAGGCCAGC AATCAACAT CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTC
 CTGTGATCAT TTCCCTCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAAGT
 GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA CATAGAGAGC
 GCCTACCCGG GAGCCGCGT GACCGAGGGG CCACGCCAGG AATATTGAGA AAATAATGAG AACTACATTG
 40 AAGTGCCATT GATTTTGTAT CCGTGCACAA GAGAGGATTT GCACATGGAT TTTAAATGTG TTGTCCATAA
 TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCTCT GGGCATTGTG
 CTGGCCCCAC TTTCATGGC CTTCTTGGTT TTGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA
 CTGGAAGAGC AGAGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA
 TAAATGGAAT GAAATTAATTC AAACACAAAA AAAAAAAAAA AAAAAAA-3' (FRAG. NO:)(SEQ. ID NO:2518)
 45 5'-GCCGAGACCG ACCTGGAGCG CGCGGCGCGG CCGGAGGAG CCGAGCGCGC CGGGCGCGGC GTGGGGGCGC
 CGGCTGCCCC GCGCGCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGCACCGTAG CACTCCTCGC
 TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA
 CGGCCGTCCG TCCAGGTAGA CGCACCTCT GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT
 AAAAGACAAG GCCCTCTCCA AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG
 50 ATTTCTTCTC TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT TTTAGTGTCA TCTGCAATG
 AAATTGATGT TCGTCCCTGT CCTCTTAACC CAAATGAACA CAAAGGCACT ATAACCTGGT ATAAAGATGA
 CAGCAAGACA CCTCTATCTA CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT TTGGTTTGT
 CCTGCTAAGG TGGAGGATTG AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA
 AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACCTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA
 55 ACTACCCGTT GCACGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTT TTAATAATGA AAATAATGAG
 TTACCTAAAT TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA
 AAGATAGGCT CATCTGTATG AATGTGGCTG AAAAGCATAG AGGGAACAT ACTTGTCTATG CATCCTACAC
 ATACTTGGGC AAGCAATATC CTATTACCCG GCAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA
 AGGCCTGTGA TTGTGAGCCC AGCTAATGAG AGTAATGAA TAGACTTGGG ATCCCAGATA CAATTGATCT
 60 GTAATGTCAC CGGCAGTTG AGTGACATTG CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA
 CCCAGTGCTA GGGCAAGACT ATTACAGTGT GGAATTCCT GCAACAAAA GAAGGAGTAC CCTCATCACA
 GTGCTTAATA TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTAC CTGTTTGGC AAGAATACAC

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- 15 **Human Interleukin-8* Fragments Antisense Oligonucleotide Fragments**
5'-GBTGTTTGTT BCBBBGCBT CBBGBBTBGC TTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT
GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC
TTGGBGTCBT GTTT3CBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT GTGCTCTGCT GTCTCTG TTC
CTTCCGGTGG TTCTTCCTG GCTCTGTCC TTTCTTGG CCCTTGGCCC-3' (FRAG. NO:1834) (SEQ. ID NO:1847)
- 20 5'-G CTC CGG-3' (FRAG. NO:1835) (SEQ. ID NO:1848)
5'-CBBGBBTBGC-3' (FRAG. NO:1836) (SEQ. ID NO:1849)
5'-CBCBC BGTBGGTGC-3' (FRAG. NO:1837) (SEQ. ID NO:1850)
5'-BCCBBBGCBT CBBGBBTBGC-3' (FRAG. NO:1838) (SEQ. ID NO:1851)
5'-GCCBBGBGBG CCBGGCCBGC-3' (FRAG. NO:1839) (SEQ. ID NO:1852)
- 25 5'-GTG CTC CGG TGG CTT TTT-3' (FRAG. NO:1289)(SEQ. ID NO:1298)
5'-GCT TGT GTG CTC TGC TGT CTC TG-3' (FRAG. NO:1290)(SEQ. ID NO:1299)
5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1291)(SEQ. ID NO:1300)
5'-TTC TCT TGG CCC TTG GCC C-3' (FRAG. NO:1292)(SEQ. ID NO:1301)
5'-GBTGTTTGTT BCBBBGCBT CBBGBBTBGC TTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT
- 30 GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC
TTGGBGTCBT GTTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT-3' (FRAG. NO:1840) (SEQ. ID NO:1853)

Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

- 5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTAGATC ATCAAAATCC CACATCTGTG
GATCTGTAAT ATTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB
35 CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBGTGB BBTBTBGTB TCBBBBBTCC CBCBTCTGTG
GBTCTGTBBT BTTTBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG
TGGCTCGGTG CTTCGCCCC TGTTGTTGCG GCGCTCGGT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC
CTCTTTCTCT TTGTTGGGG GTTCTGTGG CGGGCTGCT GTCTCGTTCC-3' (FRAG.NO:1841)(SEQ. ID NO:1854)
5'-CBGGGGC-3' (FRAG. NO:1842) (SEQ. ID NO:1855)
40 5'-GCBGGTGGC-3' (FRAG. NO:1843) (SEQ. ID NO:1856)
5'-GCGGCGCTC-3' (FRAG. NO:1844) (SEQ. ID NO:1857)
5'-TGGCTCGGTGCTTCGCCCC (FRAG. NO:1293)(SEQ. ID NO:1302)
5'-TGTTGTTGCGGCGCTC (FRAG. NO:1294)(SEQ. ID NO:1303)
5'-GGTTGGTGTGGCCCTG (FRAG. NO:1295)(SEQ. ID NO:1304)
45 5'-TGGTGCTTCGTTTC (FRAG. NO:1296)(SEQ. ID NO:1305)
5'-CCCTCTTCTCTTCTTC (FRAG. NO:1297)(SEQ. ID NO:1306)
5'-GGGGTCTCTGTGGC (FRAG. NO:1298)(SEQ. ID NO:1307)
5'-GGGCTGCTGTCTCGTTCC (FRAG. NO:1299)(SEQ. ID NO:1308)
5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTAGATC ATCAAAATCC CACATCTGTG
50 GATCTGTAAT ATTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGG-3'
(FRAG. NO:1845) (SEQ. ID NO:1858)
5'-B CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBGTGB BBTBTBGTB TCBBBBBTCC CBCBTCTGTG
GBTCTGBBT BTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG-3' (FRAG.
NO:1846) (SEQ. ID NO:1859)

55 Interleukin-11 (IL-11) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCTCAGGGCA CATGCTCCC CTCCCCAGGC CGCGGCCAG CTGACCCTCG GGGCTCCCCC GGCAGCGGAC
AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA
ACTGTGTTTG CCGCTGCTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC

Table 1. Demographic characteristics of the study population	
Age (years)	65.5 (SD 10.5)
Gender	Male 55 (82.7%), Female 12 (17.3%)
Education (years)	12.5 (SD 2.5)
Marital status	Married 45 (69.2%), Single 15 (22.9%), Divorced 1 (1.6%), Widowed 10 (15.3%)
Occupation	Retired 45 (69.2%), Unemployed 15 (22.9%), Student 1 (1.6%), Homemaker 10 (15.3%)
Income (USD/month)	1,200 (SD 300)
Health status	Good 45 (69.2%), Fair 15 (22.9%), Poor 1 (1.6%), Very poor 10 (15.3%)
Comorbidities	Hypertension 35 (53.8%), Diabetes 25 (38.5%), Arthritis 30 (46.2%), Heart disease 20 (30.8%), Stroke 15 (22.9%), Cancer 10 (15.3%), Asthma 5 (7.7%), Depression 12 (18.5%), Anxiety 8 (12.3%), Other 15 (22.9%)
Medication use	Yes 45 (69.2%), No 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare utilization	Regular 45 (69.2%), Occasional 15 (22.9%), Never 1 (1.6%), Refused 10 (15.3%)
Health insurance	Yes 45 (69.2%), No 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare access	Easy 45 (69.2%), Difficult 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare quality	Good 45 (69.2%), Fair 15 (22.9%), Poor 1 (1.6%), Very poor 10 (15.3%)
Healthcare satisfaction	Yes 45 (69.2%), No 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare utilization frequency	Monthly 45 (69.2%), Quarterly 15 (22.9%), Annually 1 (1.6%), Never 10 (15.3%)
Healthcare utilization cost	Low 45 (69.2%), Medium 15 (22.9%), High 1 (1.6%), Very high 10 (15.3%)
Healthcare utilization impact	Positive 45 (69.2%), Negative 15 (22.9%), Neutral 1 (1.6%), Unknown 10 (15.3%)
Healthcare utilization satisfaction	Yes 45 (69.2%), No 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare utilization frequency	Monthly 45 (69.2%), Quarterly 15 (22.9%), Annually 1 (1.6%), Never 10 (15.3%)
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Healthcare utilization impact	Positive 45 (69.2%), Negative 15 (22.9%), Neutral 1 (1.6%), Unknown 10 (15.3%)
Healthcare utilization satisfaction	Yes 45 (69.2%), No 15 (22.9%), Unknown 1 (1.6%), Refused 10 (15.3%)
Healthcare utilization frequency	Monthly 45 (69.2%),

[illegible]

CACCCAGCCG CCCC GAGCAG GGA CTGTCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
 AGATATCCTG ACA TGGCCA GGCATGGTGG CTCACGCTG TAATCCTGGC ACTTTGGGAG GACGAAGCGA
 GTGGATCACT GAAC TCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCTGTCT CAAAAAAGAA
 AGAATGATGT CCT CACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT
 5 TCTTTCTATA TATG JATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTGACAA TGACTGTCTC
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 TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTT TAGA ATAACAGAAT
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 GGCTGTGCAC-3' (FRAG. NO:) (SEQ. ID NO:2523)
 10 5'-GCTCAGGGCA CA TCCCTCCC CTCCCCAGGC CGCGGCCAG CTGACCCTCG GGGCTCCCC GGCAGCGGAC
 AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCC TGGGGAACCC CTGGCCCTGT GGGGACATGA
 ACTGTGTTTG CCGCTGGTCT CTGGTCTGTC TGAGCCTGTG GCCAGATACA GCTGTGCCCC CTGGGCCACC
 ACCTGGCCCC CT CAGTTT CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT
 CTCCTGGCGG ACAC GCGGCA GCTGGCTGCA CAGCTGAGGG ACAAAATCCC AGCTGACGGG GACCACAACC
 15 TGGATTCCCT GCCCACCCTG GCCATGAGTG CGGGGCACT GGGAGCTCTA CAGTCCCAG GTGTCTGAC
 AAGGCTGCGA GCGGACCTAC TGTCTACCT GCGGCACGTG CAGTGGCTGC GCCGGG CAGG TGGCTCTTCC
 CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCC GACTGGACCG GCTGCTGCGC CGGCTGCAGC
 TCCTGATGTC CCGCTGGCC CTGCCCCAGC CACCCCGGA CCGCCGCGG CCCCCGCTGG CGCCCCCTC
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 20 GTGAGGGGAC TGTCTGTGCT GAAGACTCGG CTGTGACCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG
 CCAGATCTTA TTTATTTATT TATTTAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCC GCCATTATCT
 CCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATT
 CAGAGCAGG GGTGGGAGG AGGTGGACTC CTGGTCCCG GAGGAGGAGG GGACTGGGGT CCCGATTCT
 TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGG TCTTCCCAT CTAGGCCTGG GCAGGAACAT
 25 ATATTATTTA TTAAAGCAAT TACTTTTCAT GTTGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT
 TGTACAAAAA TGTGAGAAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC-3' (FRAG.
 NO:) (SEQ. ID NO:2521)
 5'-CAGCTGCGGC A TCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTCCC CTCGGGGTCT CCCTGGGTCT
 CCCCAGTCC CTC TGTGCT CTCTCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC
 30 CAGGGCTGCC CTTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT
 CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC
 TTCCCTTCCA CTCTCTCTC CTCTGCTC CACCTCTCCA GGCCCTGTCT TTGTCCCTCC GTCCGGCCTT
 TCTCTGCCTT TCCGTCTCC TCCCTCCCA TCTCTCTCTG CTAGTCTGT CCAGCCGAC CCCACCCAC
 AGTCGGGCCC CAGCTCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG
 35 ACCTCACCAG CTTCTCTCCG ACCACCCCCC CTTTCCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC
 CTCTCCGAG CGCCGCGGCG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAGAGG CAGGCAGGGA
 GGGTGAGTCA GGA TGTGTC GGC CGGCCCT CCCCTGCCG CTGCCCCCG CCGCCCGCC CCAGGCCCCC
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 40 GGCTCCCTGC CTTGCTCCCT GGGGAACCC TGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCTGGGG
 AGGTGGAGG GGAAGGGAG GCAGGGAGGA GAGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGTGAGT
 CGCACAGAGA GGAAGCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG
 AGATGGGCGAG AGAGAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG
 GCCAGACAGG GCGGAGAGG AGCAGAGC GAGACCGAGC AGGGGAGGG ACAGGAGGAC TGGTGCCGGG
 45 AGGGAGGTGA CCGCATCGA CCCAGGCCCG AGGGAGCCCG CGGGGACCG GAGACTCCCT GGGATTCCGG
 CAGAGAGGCT CCGAGGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG TAGCGACCCC
 AGCCGGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGGAGAGCCG GGCAGATGCG GCCGACGGAG
 GCGCGGACAG ACCGACGGCT GCGGGGCCG GGGGGCGGGT TGGGGGTGTG CGAGGCGCGG CGGCGCGGG
 AGCGCTGATT GCGTGGCGGG TGGCCGGGTG GCGGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG
 50 ACCCCGCGC CCGGCGCC CCGCGCGCC CCGCGGCCA GCTCTCCCG TCCCGCGCC CGGCGGGGCC
 ATGGCTCTGC CTTCTCCG CAGGTGCGC TGCGGCCCG GCTTCTGCG CCCACCCGG GGGCTCCTGG
 GAGGGCGTCT AAGGGGTCT CCGTGGGAGA GGTCCGTGTC TCCCGGACTC CGTCTGGGC TTTTGGCTCC
 TTCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGGG GAGGGGGCAG GTTCTGGCCT GTGCTCCCC
 CACCATCCG CCGCGGGG CCAGATTCCG GCGTCCGGGG GCGGACGGGA GACGCCGGG CCGCGTCTGC
 55 TCCGACGGG GGGGAGCCA GAGCCAGGGA GGGAGAGGGA AGCCCGCTG GCCCTGCGAG CTGCCCCGG
 CCGTTCCACC TCGGACTTA AGACCTCCAG CTCATCTCT CTAAGGCCG GGAGTCCAG CCCGAGACC
 TCCTCCCGA GAC CAGGAG TCCAGACCCC AGGCCTCTCT CCTCAGACC TAGGAGTCCA GGCCCCAGC
 CTCTCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC
 AGGCCCTCCT CTC CAGACC CGGAGTCCAG CTTGAGCTCT CTGCCTTATC CTGCCCCAG GTGTTTGCCG
 60 CCTGGTCTG GTCTGTGTA GCCTGTGGCC AGATACAGCT GTCGCCCTG GGCCACCACC TGGCCCCCT

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CGAGTTTCCC CAGACCTCG GGCCGAGCTG GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA
CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG
GAACGGAGAG GAGCTGCGG GCAGCCACTT GGAGGGGTTT TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG
5 GAAGAGTTGG GGGCTGCGG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT
TTTCCCTGCC AGAGGGACAA ATTCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA
TGAGTGCAGG GGCCTGCGG GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
GCAGTGAAGG GGGGCGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGCT CTATCCCCAG
CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
GGGCAGGTGG CTCCTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCTG CAGGCCCGAC TGGACC GGCT
10 GCTGCGCCGG CTGAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCTGGGCC
CCAAAATCCT GTGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTGTGAGA
CCCTGACACG CTAACAGCCC GCTCTGAGAC CTGACACCG TAACAGCCCC GCTCTGAGAC CTTGACCTTA
ACAGTCTGCT TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA
CCCCAAAATC CTGCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA
15 AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC
TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATTGAC CTGGCCAGGC GTGGTGGCTC
ACGCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTGGGAGT TCAAGACCAG
CCAGACCAAC ATGCTGAAAC CCTGTCTCTA CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT
GTAATCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG
20 CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACTCCC TCTCTCTCAA AAAAAACAAA
AAAAAAGAAA AAGAAAGAAA AGAAAAACAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA
TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG
CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG
AAAACCCTGA CACTTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC
25 CCAAAGCCCT GAGACCAAG GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA
ATTCCAATT CTAGCTCTGA GACTCCAGCC CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT
CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCTCTT ACTCGAGCCC ACAGACCTCA GATACTGTCT
GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG GCCAAGGCAG
AAGGACCTCT TGACGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC TTAATTATTA
30 TTATTATTAT TATTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT
TCGGCTTGCT GGAACCTCCG CCTCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCTGA GTAGCTGGGA
CTTCAGGTGC ACACCTGCCAC ACCCGGATAA TTTTTTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTG
CCCAGGCTGG TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC
AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG
35 ATTCCAGCCC CGGCAGCTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA ACCGAGATGC ACCGAGTGAC
TCCACAGACT TCACCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCTT GACTCCAGCC TCCATTTCG
GAACCCACA GCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT
GCAGCCCCGA TTCACTGCA GCTCCACAGC ACCCTGCCC TGCAACCCCG CTGCACCCCC TACCTGTGAC
TCACCTCTCT CCTCICCCA CAGATGTCCC GCCTGGCCCT GCCCAGCCA CCCCAGGACC CGCCGCGGCC
40 CCCGCTGGCG CCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCAG CCATCCTGGG GGGGCTGCAC
CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC
ACCACCGTCC TTCCAAGCC AGATCTTATT TATTTATTTA TTTTCACTACT GGGGGCGAAA CAGCCAGGTG
ATCCCCCGC CATIATCTCC CCCTAGTTAG AGACAGTCTT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT
ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG
45 ACTGGGGTCC CGGAATCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCATCT
AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA
AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAATGT
GTCATACATA TCCACTTGAG GGCAGTTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAACT TGGGACAGGG
50 CAGGTGGAGG GGAACCTCC ATTCAGGTGG AGGTCCCAG TGGGCGGGGC AGCGACTGGG AGATGGGTG
GTCACCCAGA CAGCTCTGTG GAGGCAGGGT CTGAGCCTTG CTGGGGCCC CGCACTGCAT AGGGCCGTTT
GTTTGTTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT
GCAACCTCCA CCTCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCCGA TTAGCTGGGA TCACAGGTGT
GCACCACCAT GCCAGCTAA TTATTTATTT CTTTTGTATT TTTAGTAGAG ACAGGGTTTC ACCATGTTGG
CCAGGCTGGT TTCCAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA
55 GGTGTGAGCC ACCAACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTCCAC AAGTCACCT
GTGATCAACA GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA
GCAAACCTGA AACATCTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCACTGTG GATAGAACGC
CAGGAGCCG CCCCAGCAG GAGCTGTCTG TCAGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
AGATATCCTG ACATGGCCA GGCATGGTGG CTCACGCTG TAATCCTGCG ACTTTGGGAG GACGAAGCGA
60 GTGGATCACT GAACCTCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCCTGTCT CAAAAAGAA
AGAATGATGT CCTCATATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT
TCTTTCTATA TATGTATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC

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CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT
TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTTAGA ATAACAGAAT
ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGTGATTG AGCCTGTACG
GGCTGTGCAC-3' (FRAG. NO:_) (SEQ. ID NO:2522)

5 Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT
GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
GTCTGGGTGG GGCIGGGCTG CBGGCTCCGG GCGGTCCBGCCBTGGGTCTG GGGGCTGGG CTGCBGGCTC
CGGGCGGGCG GGTGCGGGCT GCGTGTGGG GGCTGCCCCG CAGGCCCTGC GGTCCBGCCB TGGGTCTGGG
10 GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGGCTGCG TGCTGGGGGC TGCCCCGAG GCCCTGC-3' (FRAG.
NO:1847) (SEQ. ID NO: 1860)
5'-GBGCBGG BBG-3' (FRAG. NO:1848) (SEQ. ID NO: 1861)
5'-GCCBCBGCBCBGC-3' (FRAG. NO:1849) (SEQ. ID NO: 1862)
5'-GGG TGC GGG C-3' (FRAG. NO:1850) (SEQ. ID NO: 1863)
15 5'-GGT CCB GCC BTG 3GT CTG GG-3' (FRAG. NO:1300)(SEQ. ID NO:1309)
5'-GGC TGG GCT GCB GGC TCC GG-3' (FRAG. NO:1301)(SEQ. ID NO:1310)
5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' (FRAG. NO:1302)(SEQ. ID NO:1311)
5'-GGC TGC CCC GCA GGC CCT GC-3' (FRAG. NO:1303)(SEQ. ID NO:1312)
5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT
20 GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
GTCTGGGTGG GGCTCGGCTG CBGGCTCCGG GC-3' (FRAG. NO:1851) (SEQ. ID NO: 1864)

Human Tumor Necrosis Factor α Antisense Oligonucleotide Fragments

- 5'-GCBCCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BCGCCTCCT CGGCCBGTCT CBCGTCCCGG
BTCBTGCTTT CBGTGCTCBT GGTGTCTTT CCBGGGGBGB GBGGGGCTGG TCCTTGCTG TCCTTGCTGG
25 TGCTCBTGGT GTCTTTCCG CCCTGGGGCC CCCGTGTCTT CTTGGGGCCT CTTCCTCTG GGGGCCGTCT
CTCTCCCTCT CTGCGTCTC TCTCTTCTC TCTCTCTCT CCCCTTTCCC GCTCTTCTG TCTCGGTGTC
TGGTTTCTC TCTCGCTGG CTGCTGTCT GGCCTGCGCT CTGGCCTGT GCTGTCTC CTCCGGTTCC
TGCTCTCT GTCTCTCGCC CCTCTGGGG TCTCCTCTG GGTGGTGGT TTGTGCTTG GGCTGGGCTC
CGTGTCTCCB GTGCTCBTGG TGCCGCTGB GGBGCGTCT GCTGGCGCTG GTCTCTGCTGTC CTTGCTGGTG
30 CTCBTGGTGT CTTTCCGCC CTGGGGCCCC CTTGTCTTCT TGGGGCCTCT TCCCTCTGGG GGCCGTCTC
TCTCCCTCTC TTGCGTCTCT CTCTTCTCT CTCTCTCTC CCCTTTCCCG CTCTTTCTGT CTCGGTGTCT
GGTTTCTCT CTCCGCTGGC TGCTGTCTG GCCTGCGCTC TTGGCCTGT CTGTTCTCTC TCCGGTCTCT
GTCCTCTCT TCTGTCGCC CCTCTGGGT CTCCCTCTGG CGTGGTGGT TTGTGCTTG GGCTGGGCTC
CGTGTCTCCB GTGCTCBTGG TGCTCGCTGB GGBGCGTCT GCTGGC-3' (FRAG.NO:1852)(SEQ.ID NO:1865)
35 5'-GGGGCCCCC-3' (FRAG. NO:1853) (SEQ. ID NO:1866)
5'- GGG GGC CG TCT-3' (FRAG. NO:1854) (SEQ. ID NO:1867)
5'-CCBGGGGBGB GBG3GGCTGG-3' (FRAG. NO:1855) (SEQ. ID NO:1868)
5'-GCBCCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BCGCCTCCT CGGCCBGTCT CBCGTCCCGG
BTCBTGCTTT CBGTGCTCBT GGTGTCTTT CCBGGGGBGB GBGGG-3' (FRAG. NO:1304) (SEQ. ID NO:1313)
40 5'-GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT
GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC
C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T
GGC CTG TGC TGT TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C
GTG GTG GTC TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1305)
45 (SEQ. ID NO:1314)
5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC
CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT
C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC
TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC
50 CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB
TGG TGT CC GCT GBC GGB GCG TCT GCT GGC-3' (FRAG.NO:1306)(SEQ.ID NO:1315)
5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' (FRAG. NO:1655) (SEQ. ID NO:1664)
5'-GTG CTC BTG GTG TCC TTT CC-3' (FRAG. NO:1656)(SEQ. ID NO:1665)
5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' (FRAG. NO:1657)(SEQ. ID NO:1666)
55 5'-CCT CTT CCC TCT GGG GGC CG-3' (FRAG. NO:1658)(SEQ. ID NO:1667)
5'-TCT CTC TCC CTC TCT GTC GTC TCT C-3' (FRAG. NO:1659)(SEQ. ID NO:1668)
5'-TCT TTC TCT CTC TCT CTT CCC C-3' (FRAG. NO:1660)(SEQ. ID NO:1669)
5'-TTT CCC GCT CTT TCT GTC TC-3' (FRAG. NO:1661)(SEQ. ID NO:1670)
5'-GGT GTC TGG TTT TCT CTC TCC-3' (FRAG. NO:1662)(SEQ. ID NO:1671)

5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' (FRAG. NO:1663)(SEQ. ID NO:1672)
 5'-GGC CTG TGC TGT ICC TCC-3' (FRAG. NO:1664)(SEQ. ID NO:1673)
 5'-TCC GGT TCC TGT TCT CTC TGT CTG TC-3' (FRAG. NO:1665)(SEQ. ID NO:1674)
 5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' (FRAG. NO:1666)(SEQ. ID NO:1675)
 5'-GTG GTG GTC TTG TTG CTT-3' (FRAG. NO:1667)(SEQ. ID NO:1676)
 5'-GGG CTG GGC TCC GTG TCT C-3' (FRAG. NO:1668)(SEQ. ID NO:1677)
 5'-CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1669)(SEQ. ID NO:1678)
 5'-GCT GBG GGB GCG TCT GCT GGC-3' (FRAG. NO:1670)(SEQ. ID NO:1679)

Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

10 5'-CTCGGTBGB C GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CTGCGCGGCC
 GBGBTCBCCTG CBGGGBBGG TBGGCTTGC BCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC
 CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBGCGGCTG TGTGTBBGG CGBGCTGGGC CCCGTCTGCT
 GCTCCTCGTG CCGCTCGTC CTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCCGG TGGTGGGGCG
 CGCGCGCTCG CGTCGCTCCG GCTCTCTTT CCCGCTCCGT CGGCCCGGG GCCTTGGTCT CCCTCGTCTT
 15 TCBTGGTBCC G-3' (FRAG. NO:1856) (SEQ ID NO: 1869)
 5'-GCB GCBGGBC-3' (FRAG. NO:1857) (SEQ ID NO: 1870)
 5'-CCCGGCTCCG-3' (FRAG. NO:1858) (SEQ ID NO: 1871)
 5'-CGGCCCGGG GCC-3' (FRAG. NO:1859) (SEQ ID NO:1872)
 5'-CB CGCGG-3' (FRAG. NO:1860) (SEQ ID NO: 1873)
 20 5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' (FRAG. NO:1307)(SEQ. ID NO:1316)
 5'-CCT CGT CCT TCA TGG TAC CGT CGG TGT GGT GGC-3' (FRAG. NO:1308)(SEQ. ID NO:1317)
 5'-CTC GGG TGG GCC GGT GGT G-3' (FRAG. NO:1309)(SEQ. ID NO:1318)
 5'-GGG CGC GCG CGC TCG CGT-3' (FRAG. NO:1310)(SEQ. ID NO:1319)
 5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGG CCT TGG TCT C-3' (FRAG. NO:1311)(SEQ. ID NO:1320)
 25 5'-CCT CGT CCT TCB TGG TBC CG-3' (FRAG. NO:1312)(SEQ. ID NO:1321)
 5'-CTCGGTBGB C GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CTGCGCGGCC
 GBGBTCBCCTG CBGGGBBGG TBGGCTTGC BCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC
 CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBGCGGCTG TGTGTBBGG CGBGCTGG-3' (FRAG. NO:1861)
 (SEQ ID NO:1874)

Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

30 5'-BCCGCGGBG CCGCCBGGT GGBCTGGGBG TGGGTTTCTC CCCGCCGTC TCBCCCBCCG CGGTGBGCTC
 BGCGCCTBBG BCTGCTGTT CTGGBGCTCC TTGGCBGGC BCBBBCBGC BCBGBBBBT CBTGBGCBBB
 TBBTCCBTTC TGBB8BBBGG GGBTCBBB8B CCTCCCGTTC CCCGTCGCC TGGCGCGCGC TCGGGGTTC
 TCGTGGGTTT CTCCCGCCG TTCTCCGTC TGTGCTTT GTGGGCTTCT TGTCTTTTG GCTGTCTTT
 35 TCCTGCTTGG CGTCTTTTCC TTCTTTGTG CTCGGTTGTG GGTCCGCTGG TCCTTTGCC TGTGTGTTT
 TGCTGCCCGT TCGCTGGCG CGCGCTGCGG GTTCTCTG TGTCTCTCC CGCGTCTCT CCGTCTGTTG
 CCTTTGTGGG CTCTTGTCT TTTTGGCTGT TCTTTCTCT CTGGCGTCT TTTCTTTCT TTGTGCTCGG
 TTGTGGGTCC GTGC TCCT TGCCTGTGT GTTCTGCTG-3' (FRAG. NO:1862) (SEQ. ID NO:1875)
 5'-CCGCGGBG CCGCBGGT GGB-3' (FRAG. NO:1863) (SEQ. ID NO:1876)
 40 5'-CCGCCBGG-3' (FRAG. NO:1864) (SEQ. ID NO:1877)
 5'-GGCGCGCGC-3' (FRAG. NO:1865) (SEQ. ID NO:1878)
 5'-GTGGGTCCGC-3' (FRAG. NO:1866) (SEQ. ID NO:1879)
 5'-CCCGTTCGCTGGCGC-3' (FRAG. NO:1313)(SEQ. ID NO:1322)
 5'-GCGCTGCGGGTCTC-3' (FRAG. NO:1314)(SEQ. ID NO:1323)
 45 5'-GTGGGTTCTCCCGCGTCTC-3' (FRAG. NO:1315)(SEQ. ID NO:1324)
 5'-CGGTCTGTGCTTGTGGG-3' (FRAG. NO:1316)(SEQ. ID NO:1325)
 5'-CTTCTGTCTTTTGGCT-3' (FRAG. NO:1317)(SEQ. ID NO:1326)
 5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1318)(SEQ. ID NO:1327)
 5'-GTCTTTCTCTTCTT-3' (FRAG. NO:1319)(SEQ. ID NO:1328)
 50 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1320)(SEQ. ID NO:1329)
 5'-CGCTGGTCTTTGCC-3' (FRAG. NO:1321)(SEQ. ID NO:1330)
 5'-CTGTGTGTTTCTG-3' (FRAG. NO:1322)(SEQ. ID NO:1331)
 5'-CCCGTTCGCTGGCGC-3' (FRAG. NO:1323)(SEQ. ID NO:1332)
 5'-GCGCTGCGGGTCTC-3' (FRAG. NO:1324)(SEQ. ID NO:1333)
 55 5'-GTGGGTTTCTCCCGCGTCTC-3' (FRAG. NO:1325)(SEQ. ID NO:1334)
 5'-CGGTCTGCTTGTGGG-3' (FRAG. NO:1326)(SEQ. ID NO:1335)
 5'-CTTCTTCTCTTTTGGCT-3' (FRAG. NO:1327)(SEQ. ID NO:1336)
 5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1328)(SEQ. ID NO:1337)
 5'-GTCTTTCTTCTT-3' (FRAG. NO:1329)(SEQ. ID NO:1338)
 60 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1330)(SEQ. ID NO:1339)

5'-CGCTGGTCCTTTGCC-3' (FRAG. NO:1331)(SEQ. ID NO:1340)

5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1332)(SEQ. ID NO:1341)

Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GCCCTGTCCG GCGGGAAGCC TCTCTCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA
5 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
GCCGCGCC CTGTCGGGCG GGBBGCCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC
BGCGCBCCB GGGCGCGTCC GCBGBBCTT GGBGGCGGCT GCBTGTCTGCT BCCTGCTCGGGCG GGBBGCCTCCG
GTGGCCGCGC CGCGTCCGGT GGCCGCCGCG CCTCTCTCT CTCCCCGTGG CCCTGTCCGG CGGGTCTGTC
CGTCTGTCT CTTTTCTTT TGCTGTCTTG TCTTCCCGTC TCTGCTTT-3' (FRAG. NO: 1867) (SEQ. ID NO: 1880)
- 10 5'-CGGGCG GGBGCC-3' (FRAG. NO: 1868) (SEQ. ID NO: 1881)
5'-CGGGCGGG-3' (FRAG. NO: 1869) (SEQ. ID NO: 1882)
5'-CCGCBGBBC-3' (FRAG. NO: 1870) (SEQ. ID NO: 1883)
5'-GCGTCCGGTGGCCGCCG-3' (FRAG. NO:1333)(SEQ. ID NO:1342)
5'-GCCTCTCTCTCTCCCC-3' (FRAG. NO:1334)(SEQ. ID NO:1343)
- 15 5'-GTGGCCCTGTCCGGCGGG-3' (FRAG. NO:1335)(SEQ. ID NO:1344)
5'-TCCTGCCGTCTGTCTCCTTT-3' (FRAG. NO:1336)(SEQ. ID NO:1345)
5'-TCTTTTGTCTGCTTTT-3' (FRAG. NO:1337)(SEQ. ID NO:1346)
5'-CTTCCGTCTCTGCTTT-3' (FRAG. NO:1338)(SEQ. ID NO:1347)
5'-GCCCTGTCCG GCGGGAAGCC TCTCTCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA
20 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
GCCG-3' (FRAG. NO: 1871) (SEQ. ID NO: 1884)
5'-GCCCTGTCCG GCGGGBBGCC TCTCTCTCT CCCCGBGTCC GCGBCBGGCC GCBGGCBGB BCCBGCGB
BCCBGGGCGC GTCCGCBGB BCTTGBBGGC GGCTGCBTGC TGCTBCCTGC TCCBGBBGGC TCCGGTGGCC GCCG-
3' (FRAG. NO: 1872) (SEQ. ID NO: 1885)

Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GTCTGTCTC CCCTCTCT CCACTGCTT CTCCCGGGG CTCCCCGGC TCCGGTGGC CGGTGTCCCG
GGCTCCGGCG CGCGGGCGG TCCGGTGGC GGTGGGTGGC GCGGGCTGCC GGGTCCGCGC GGCGCCTGGG
CCCTGTGCT GCTTTTGTCT TGTCCGTTT TGGTGTCTC GGCTGTGTT GTGGTTGTT TGTCTCTCT
TGGGTGTGG CCTTGCGGT TGGCTGTGG GCCCTTTGGG GCCTTGGCTT CTGGCTCGTC TGCTCTCCC
30 GTCTCTCCC ACTCTTCT CCGGGGGCT TCCCCGGCT CGGGTGGCG GTGTCCCGG CTCCGGCGCG
GCGCGGCTT CGGTGCGGG TGGGTGGCG GGGCTGCCG GTCCGCGCG CGCCTGGGC CTTGTGCTGC
TTTTGCTTG TTCCGTTCT GCTGCTCCG TCTGTGTTG GTTGTGTTT TTTCTTCTT GGTGTGGGCC
TTGCGGTTT GGC GTGGGC CTTTGGGGC CTTGGCTTCT GGCTCCAT CCACATGATT GCTTAGATT
GTGCTGTATC TCTCAGGATT ATCACTGATT ACACATCAA CAGTGCCAG CCAAAGGAT GCCCTGAGGC
35 AAAGGGTTT CATTTGAGG CAAATTGAG GACBTCCB BTGTTGCTT BGBTTGTGC TGTBTCTCT
BGBTTTCTB CTGETTBCB BTCCBBCCB TGCCBGCCB BBGGBTGCC TGBGGCBGB GGTTCCTC
TTGBGGCB TTTGBGB-3' (FRAG. NO:1873) (SEQ. ID NO: 1886)
5'-GBGGCBGGG-3' (FRAG. NO:1874) (SEQ. ID NO: 1887)
5'-GCCBCCB BBGG-3' (FRAG. NO:1875) (SEQ. ID NO: 1888)
- 40 5'-CGCTGGGCC C-3' (FRAG. NO:1876) (SEQ. ID NO: 1889)
5'-GTCTGTCTCCCCCTCTCTCCC-3' (FRAG. NO:1339)(SEQ. ID NO:1348)
5'-ACTGCTTCTCCCGCGG-3' (FRAG. NO:1340)(SEQ. ID NO:1349)
5'-GCTTCCCCGGCTT-3' (FRAG. NO:1341)(SEQ. ID NO:1350)
5'-GGGTGGCCGGTGTCCCGGGCTCCGGCGCGCGGC-3' (FRAG. NO:1342)(SEQ. ID NO:1351)
45 5'-GGCTTCGGCTGC-3' (FRAG. NO:1343)(SEQ. ID NO:1352)
5'-GGGTGGTGGCGCG-3' (FRAG. NO:1344)(SEQ. ID NO:1353)
5'-GCTCCGGGTCCGCGCGCGCTGGGCC-3' (FRAG. NO:1345)(SEQ. ID NO:1354)
5'-CTTGTGCTGCTTTT-3' (FRAG. NO:1346)(SEQ. ID NO:1355)
5'-TGCTTGTCCGTTT-3' (FRAG. NO:1347)(SEQ. ID NO:1356)
- 50 5'-TGGCTGCTCCGGTCTGTGTTGTTGTTT-3' (FRAG. NO:1348)(SEQ. ID NO:1357)
5'-TTTCTTCTTGGGTGTGG-3' (FRAG. NO:1349)(SEQ. ID NO:1358)
5'-CCTTGGGTTTTGCT-3' (FRAG. NO:1350)(SEQ. ID NO:1359)
5'-CTGTGGGCCCTTTT-3' (FRAG. NO:1351)(SEQ. ID NO:1360)
5'-GGGCTTGGCTTCTGGCTC-3' (FRAG. NO:1352)(SEQ. ID NO:1361)
- 55 5'-CATCCACATG ATGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC CAACAGTGC
CAGCAAAAG GATCCCTGA GGCAAGGGT TTCCATCTT AGGCAATTT GAGGA-3' (FRAG. NO:1353)
(SEQ. ID NO:1362)
5'-CBTCCBCTG BTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBCTBCTG BTTBCTBCTC CBCCBGTGC
CBGCCBBBG GTGCCCTGB GGCBBBGGT TTCCBTCTT BGGCBBT TT GBGB-3' (FRAG. NO:1354)(SEQ. ID NO:1363)

Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments

	5'-GCCACCATGG	AAACCCCTTG	CCTCAGGGCA	TCCTTTTGGC	TGGCACTGGT	TGGATGTGTA	ATCAGTGATA
	ATCCTGAGAG	ATACAGCACA	AATCTAAGCA	ATCATGTGGA	TGATTTTCACC	ACTTTTCGTG	GCACAGAGCT
	CAGCTTCCTG	GTTACCACTC	ATCAACCCAC	TAATTTGGTC	CTACCCAGCA	ATGGCTCAAT	GCACAACTAT
5	TGCCCCACAGC	AGACTAAAT	TACTTCAGTC	TTCAAATACA	TTAACTACTGT	GATATCTTGT	ACTATTTTCA
	TCGTGGGAAT	GGTCGGGAAT	GCAACTCTGC	TCAGGATCAT	TTACCAGAAC	AAATGTATGA	GGAATGGCCC
	CAACGCGCTG	ATAGCCAGTC	TTGCCCTTGG	AGACCTTATC	TATGTGGTCA	TTGATCTCCC	TATCAATGTA
	TGGCTGGGCG	CTGGCCTTTT	GATCACAATG	ACTTTGGCGT	ATTCTTTTGC	AAGCTGTTC	CCTTTTGTGA
	GAAGTCCTCG	GTGGGGATCA	CCGTCTCAA	CCTCTGCGCT	CTTAGTGTG	ACAGGTACAG	AGCAGTTGCC
10	TCCTGGAGTC	GTGTTCAGGG	AATTGGGATT	CCTTTGGTAA	CTGCCATTGA	AATTGCCTCC	ATCTGGATCC
	TGTCCTTTAT	CCTGGCCATT	CCTGAAGCGA	TTGGCTTCGT	CATGGTACCC	TTTGAATATA	GGGGTGGACA
	GCATAAAACC	TGTATGCTCA	ATGCCACATC	AAAATTCATG	GAGTTCTACC	AAGATGTAAA	GGACTGGTGG
	CTCTTCGGGT	TCTATTTCTG	TATGCCCTTG	GTGTGCACTG	CGATCTTCTA	CACCCTCATG	ACTGGTGAGA
	TGTTGAACAG	AAGCAATGGC	AGCTTGAGAA	TTGCCCTCAG	TGAACATCTT	AAGCAGCGTC	GAGAAGTGGC
15	AAAAACAGTT	TTCGCTTGG	TTGTAATTTT	TGCTCTTGC	TGGTTCCTC	TTCAATTAAG	CCGTATATTG
	AAGAAACTG	TGTATTAACGA	GATGGACAAG	AACCGATGTG	AATTACTTAG	TTTCTTACTG	CTCATGGATT
	ACATCGGTAT	TAACTTGGCA	ACCATGAATT	CATGTATAAA	CCCCATAGCT	CTGTATTTTG	TGAGCAAGAA
	ATTTAAAAAT	TGTATCCAGT	CATGCCTCTG	CTGCTGCTGT	TACCAGTCCA	AAAGTCTGAT	GACCTCGGTC
	CCCATGAACG	GAACAAGCAT	CCAGTGGAAG	AACCACGATC	AAAACAACCA	CAACACAGAC	CGGAGCAGCC
20	ATAAGGACAG	CATGAACCTGA	CCACCCTTAG	AAGCACTCCT	GAATTCGGGA	AAAAGTGAAG	GTGTAAAAAGC
	AGCAACAAGTG	CAATGAAGAGA	TATTTCTCTA	AATTTGCCTC	AAGATGGAAA	CCCTTTGCCT	CAGGGCATCC
	TTTGGCTGG	CACCTGGTGG	ATGTGTAATC	AGTGATAATC	CTGAGAGATA	CAGCACAATC	CTAAGCAATC
	ATGTGGATGA	TTTACCACCT	TTTCGTGGCA	CAGAGCTCAG	CTTCTGGTT	ACCACTCATC	AACCCACTAA
	TTTGGTCTTA	CCCAGCAATG	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAGCTTTC
25	AAATACATTA	ACACTGTGAT	ATCTTGTAAT	ATTTTCATCG	TGGGAATGGT	GGGGAATGCA	ACTCTGCTCA
	GGATCATTTA	CCACAACAAA	TGTATGAGGA	ATGGCCCCAA	CGCGCTGATA	GCCAGTCTTG	CCCTTGGAGA
	CCTTATCTAT	GTGCTCATTG	ATCTCCCTAT	CAATGTATTT	AAGCTGCTGG	CTGGGCGCTG	GCCTTTTGAT
	CACAATGACT	TTGCGGTATT	TCTTTGCAAG	CTGTTCCCTT	TTTTGCAGAA	GTCTCGGTG	GGGATCACCG
	TCTCAACCT	CTGCGCTCTT	AGTGTTGACA	GGTACAGAGC	AGTTGCCTCT	TGGAGTCGTG	TTCAGGGAAT
30	TGGGATTCCCT	TTGCTAACTG	CCATTGAAAT	TGTCTCCATC	TGGATCCTGT	CCTTTATCCT	GGCCATTCCT
	GAAGCGATTG	GCTTCGTCAT	GGTACCCTTT	GAATATAGGG	GTGAACAGCA	TAAAACCTGT	ATGCTCAATG
	CCACATCAAA	ATTATATGGAG	TTCTACCAAG	ATGTAAAGGA	CTGGTGGCTC	TTCGGGTTCT	ATTTCTGTAT
	GCCCTTGGTG	TGCACTGCGA	TCTTCTACAC	CCTCATGACT	TGTGAGATGT	TGAACAGAAG	GAATGGCAGC
	TTGAGAATTG	CCCTCAGTGA	ACATCTTAAG	CAGCGTCGAG	AAGTGGCAAA	AACAGTTTTC	TGCTTGGTTG
35	TAATTTTTCG	TCTTTGCTGG	TTCCCTCTTC	ATTTAAGCCG	TATATTGAAG	AAAAGTGTGT	ATAACGAGAT
	GGACAAGAAC	CGAATGTAAT	TACTTAGTTT	CTTACTGCTC	ATGGATTACA	TCGGTATTAA	CTTGGCAACC
	AGCAATTCAT	GTATAAACCC	CATAGCTCTG	TATTTTGTGA	GCAAGAAATT	TAAAAATTGT	TTCCAGTCAT
	GCCCTGCTG	CTGCTGTTAC	CAGTCCAAAA	GTCTGATGAC	CTCGGTCCCC	ATGAACGGAA	AGAGCATCCA
	GTGGAAGAAC	CACGATCAAA	ACAACCACAA	CACAGACCGG	AGCAGCCATA	AGGACAGCAT	GAAGTACCA
40	CCCTTAGAAG	CACCTCTCGG	TACTCCCAT	ATCCTCTCGG	AGAAAAAAT	CACAAGGCAA	CTGTGAGTCC
	GGGAATCTCT	TCTTGATCC	TTCTTCTTA	ATTCCTCTCC	ACACCAAGA	AGAAATGCTT	TCCAAAACCG
	CAAGGGTAGA	CTGCTTTATC	CACCCACAAC	ATCTACGAAT	CGTACTTCTT	TAATTGATCT	AATTTACATA
	TTCTGCGTGT	TGTATTCAGC	ACTAAAAAAT	GGTGGGAGCT	GGGGGAGAAT	GAAGACTGTT	AAATGAAACC
	AGAAGGATAT	TTACTACTTT	TGCATGAAAA	TAGAGCTTTC	AAGTACATGG	CTAGCTTTTA	TGGCAGTTCT
45	GGTGAATGTT	CAATGGGAAC	TGGTCACCAT	GAAACTTTAG	AGATTAACGA	CAAGATTTTC	TACTTTTTTT
	AAGTGATTTT	TTTGCTCTTC	AGCCAAACAC	AATATGGGCT	CAAGTCACTT	TTATTTGAAA	TGTCATTGCG
	TGCCAGTATC	CCGAATTC	GAATTCGGGA	AAAAGTGAAG	GTGTAAAAGC	AGCACAAGTG	CAATAAGAGA
	TATTTCTCTCA	AATTTGCCTC	AAGATGGAAA	CCCTTTGCCT	CAGGGCATCC	TTTTGGCTGG	CACTGGTTGG
	ATGTGTAATC	AGTATAATC	CTGAGAGATA	CAGCACAAT	CTAAGCAATC	ATGTGGATGA	TTTCACTACT
50	TTTCGTGGCA	CAGAGCTCAG	CTTCTTGGTT	ACCACTCATC	AACCACTAA	TTTGGTCTTA	CCCAGCAATG
	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAGCTTTC	AAATACATTA	ACACTGTGAT
	ATCTTGTAAT	ATTTTCATCG	TGGGAATGGT	GGGGAATGCA	ACTCTGCTCA	GGATCATTTA	CCAGAACAAA
	TGTATGAGGA	ATGGCCCCAA	CGCGCTGATA	GCGACTCTTG	CCCTTGGAGA	CCTTATCTAT	GTGGTCATTG
	ATCTCCCTAT	CAATGTATTT	AAGCTGCTGG	CTGGGCGCTG	GCCTTTTGAT	CACAATGACT	TTGGCGTATT
55	TCTTTGCAAG	CTGTTCCTCT	TTTTGCAGAA	GTCCTCGGTG	GGGATCACCG	TCCTCAACCT	CTGCGCTCTT
	AGTGTGAGCA	GGTACAGAGC	AGTTGCCTCC	TGGAGTCGTG	TTCAGGGAAT	TGGGATTCCT	TTGGTAACTG
	CCATTGAAAT	TGCTTCCATC	TGGATCCTGT	CCTTTATCCT	GGCCATTCTT	GAAGCGATTG	GCTTCGTCAT
	GGTACCCTTT	GAAATATAGGG	GTGAACAGCA	TAAAACCTGT	ATGCTCAATG	CCACATCAAA	ATTCATGGAG
	TTCTACCAAG	ATGTAAAGGA	CTGGTGGCTC	TTCGGGTTCT	ATTTCTGTAT	GCCCTTGGTG	TGCACTGCGA
60	TCTTCTACAC	CCTCATGACT	TGTGAGATGT	TGAACAGAAG	GAATGGCAGC	TTGAGAATTG	CCCTCAGTGA
	ACATCTTAAG	CAGCTCGAG	AAGTGGCAAA	AACAGTTTTT	TGCTTGGTTG	TAATTTTTCG	TCTTTGCTGG

004369 04400

TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT
 TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTGGGCAACC ATGAATTCAT GTATAAACCC
 CATAGCTCTG TATTTGTGA GCAAGAAAT TAAAAATGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC
 CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA
 5 ACAACCACAA CACAAGCCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG
 TACTCCATA ATCCTCTCGG AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC
 TTCTTCCTTA ATTCCTCTCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC
 CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTGAGC
 ACTAAAAAAT GGTCTGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTAATACTTT
 10 TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC
 TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC
 AGCCAAACAC AATAAGGCT CAAGTCACTT TTATTTGAAA TGTCATTGG TGCCAGTATC CCGAATTC-3' (FRAG.
 NO:) (SEQ ID NO: 3014)
 5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCTCA AATTTGCCTC
 15 AAGATGGAAG CCCCTGCTC CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
 CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
 CTTCTGGTT ACCACTCATC AACCCTACTAA TTTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC
 CCACAGCAGA CTAATAATTAC TTCAGCTTTC AAATACATTA AACTGTGAT ATCTTGTAAT ATTTTCATCG
 TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
 20 CGCGCTGATA GCCAGTCTTG CCCTTGAGGA CCTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
 AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCTC
 TTTTGCAGAA GTCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC
 AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC
 TGGATCCTGT CCTTATCCTT GGCCATTCTT GAAGCGATTG GCTTCGTCTT GGTACCTTTT GAATATAGGG
 25 GTGAACAGCA TAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
 CTGGTGGCTC TTCCGGTTCT ATTTCTGTAT GCCCTTGGTG TGCATGCGA TCTTCTACAC CCTCATGACT
 TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
 AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
 TATATTGAAG AAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
 30 ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
 GCAAGAAATT TAAATAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
 AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG
 AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCCTCTCC
 35 ACACCCAAGA AGAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT
 CGTACTTCTT TAATTGATCT AATTTACATA TTCTCGTGT TGTATTGAGC ACTAAAAAAT GGTGGGAGCT
 GGGGGAGAAT GAAAGACTGT AAATGAAACC AGAAGGATAT TTAATACTTT TGATGAAAA TAGAGCTTTC
 AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
 AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT
 40 CAAGTCACTT TTATTGAAA TGTCATTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO:) (SEQ ID NO: 2482)
 5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCTCA AATTTGCCTC
 AAGATGGAAG CCCCTGCTC CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
 CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
 45 CTTCTGGTT ACCACTCATC AACCCTACTAA TTTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC
 CCACAGCAGA CTAATAATTAC TTCAGCTTTC AAATACATTA AACTGTGAT ATCTTGTAAT ATTTTCATCG
 TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
 CGCGCTGATA GCCAGTCTTG CCCTTGAGGA CCTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
 AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCTC
 TTTTGCAGAA GTCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC
 50 AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC
 TGGATCCTGT CCTTATCCTT GGCCATTCTT GAAGCGATTG GCTTCGTCTT GGTACCTTTT GAATATAGGG
 GTGAACAGCA TAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
 CTGGTGGCTC TTCCGGTTCT ATTTCTGTAT GCCCTTGGTG TGCATGCGA TCTTCTACAC CCTCATGACT
 TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
 55 AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
 TATATTGAAG AAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
 ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
 GCAAGAAATT TAAATAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
 60 AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG
 AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCCTCTCC
 ACACCCAAGA AGAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT

CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT
 GGGGGAGAAT GAAAGACTGTT AAATGAAACC AGAAGGATAT TTAAGTACTTT TGCATGAAAA TAGAGCTTTC
 AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
 AGATTAACGA CAAAGATTTT TACTTTTTT AAGTGATTTT TTGTCTCTC AGCCAAACAC AATATGGGCT
 5 CAAGTCACTT TTATTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: __) (SEQ ID NO: 2470)
 5'-GCCACCATGG AAACCCCTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA
 ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTTACC ACTTTTCGTG GCACAGAGCT
 CAGCTTCCTG GTTACCACCT ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACAT
 10 TGCCACACAGC AGAATAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA
 TCGTGGGAAT GGTGCGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC
 CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCC TATCAATGTA
 TGGCTGGGCG CTGGCCTTTT GATCACAAATG ACTTTGGCGT ATTCTTTTGC AAGCTGTTC CCTTTTTCGA
 GAAGTCTCG GTGCGGATCA CCGTCTCAA CCTCTGCGCT CTTAGTGTG ACAGGTACAG AGCAGTTGCC
 TCCTGGAGTC GTGTTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC
 15 TGTCTTTAT CCTGSCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA
 GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAG GACTGGTGG
 CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTCTA CACCCTCATG ACTGGTGAGA
 TGTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC
 AAAAAACAGT TTCGCTTGG TTGTAATTTT TGCTCTTTG TGGTTCCTC TTCATTTAAG CCGTATATTG
 20 AAGAAAACTG TGTATTAACGA GATGGACAAG AACCAGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT
 ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA
 ATTTAAAAAT TGTATCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC
 CCCATGAACG GAACAAGCAT CCAGTGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC
 ATAAGGACAG CATGAAGTGA CCACCCTTAG AAGCACTCT-3' (FRAG. NO: __) (SEQ ID NO: 2469)

25 Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments

5'-CTGCTGBGGC TTGGTCTCC GGGCGBTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG
 BTCTGGTCGCT GTCTGBCCBG TCGBCCBGT BBTTCBGBTC BTCBTGGCT CCTBTCTCTT CTGCBBCBG
 CTGBGTGGBG BCBHGBBBBB BGBCTGCCBB GGCCBCGBGG BTTCBTGT TGGBTCTTGC GBCGBCBGT
 30 CCCGCGGGGT GCTGAGTTTCT TCTGTTCTC CCGBGCBCB GTGGTCGCTC CGCTTCTC TGGTCTCTC
 GGTCCGCGG GGTGCTGTCT GTGCTGTG GTGGCTGGG TCTCCGGGCG GTTCTCTC TTTCCGC-3' (FRAG.
 NO:1877) (SEQ ID NO: 1890)
 5'-CTCC GGGCGB-3' (FRAG. NO:1878) (SEQ ID NO: 1891)
 5'-GGCCBCBGG-3' (FRAG. NO:1879) (SEQ ID NO: 1892)
 5'-GGGTCTCCGGGCG 3' (FRAG. NO:1880) (SEQ ID NO: 1893)
 35 5'-GGG TCTCCGGGCG G-3' (FRAG. NO:1881) (SEQ ID NO:1894)
 5'-CGTGGTCGCTCCG(-3' (FRAG. NO:1355)(SEQ. ID NO:1364)
 5'-GTTTCTCTGTTTCTCCG-3' (FRAG. NO:1356)(SEQ. ID NO:1365)
 5'-GTCCCGCGGGGTG(-3' (FRAG. NO:1357)(SEQ. ID NO:1366)
 5'-TCTGGTCGCTGTC(-3' (FRAG. NO:1358)(SEQ. ID NO:1367)
 40 5'-GGCTTGGGTCTCCGGGCG-3' (FRAG. NO:1359)(SEQ. ID NO:1368)
 5'-GTTTCTCTCTTTTCCG-3' (FRAG. NO:1360)(SEQ. ID NO:1369)
 5'-CTGCTGBGGC TTGGTCTCC GGGCGBTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG
 BTCTGGTCGCT GTCTGBCCBG TCGBCCBGT BBTTCBGBTC BTCBTGGCT CCTBTCTCTT CTGCBBCBG
 CTGBGTGGBG BCBHGBBBBB BGBCTGCCBB GGCCBCGBGG BTTCBTGT TGGBTCTTGC GBCGBCBGT
 45 CCCGCGGGGT GCTGAGTTTCT TCTGTTCTC CCGBGCBCB-3' (FRAG. NO:1882) (SEQ ID NO: 1895)

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGGCTBBGBT GBTCCBCBTC BCTBCBCGT TGCCCBCCBC BGBGTCBCC BCBTGBCCG TGTBGGCBGC
 TGCCCBGGG BCBTCTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCG BGGTGTBGT GGBGTGTTT
 GGGGBBGGT CTGCTCCBC CGGBGGBCG TTBCTCBTTT CBBGCTBGG CGGTBBBGCC CTBCTBTCTG
 50 TBCBCBCCC CCTCTGCBG CBGBGTCTG TCGTGGCGCC TGGGCTCBG GGTCCGGG TAAGATGATC
 CACATCACTA CCACGTTGCC CACCACAGAG GTCACCACAA TGACCGTGA GGAGCTGCC CAAAGGACAA
 TTTGCCAGGC TGGTGCACG AACTGATTGG GTTCCGAGGT GTTAGTGGAG ATGTTTGGG AGAGGTCTGA
 GTCCACCGGG AGGACGTTAT CCATTTCGAA GCTAGGCGGT AAAGCCCTAC TATCTGTACA CAACCCCTT
 CTGCAGCAGA GTCTGTCTG GTGCGCTGGG GCTCAGGGT CGTCTGTCTG TGGCGCTCG GGCTCTTCTT
 55 TTGTGGGCTC TTCTGTGGCT GTGGCTGTGG TCTCTGTGTG TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG
 GGGCGTCTCT CTGGTCTCTC CTCGTGGGCC CCC-3' (FRAG. NO:1883) (SEQ. ID NO:1896)
 5'-GGGBGGBCG-3' (FRAG. NO:1884) (SEQ. ID NO:1897)
 5'-GGGTC CG-3' (FRAG. NO:1885) (SEQ. ID NO:1898)
 5'-GGGCC CCC-3' (FRAG. NO:1886) (SEQ. ID NO:1899)
 60 5'-GTCCTGTCTGGGCGCTGGGGCTC-3' (FRAG. NO:1361)(SEQ. ID NO:1370)

5'-TTCTTTTGTGGGCT-3' (FRAG. NO:1362)(SEQ. ID NO:1371)

5'-CTTTGGTGGCTGTGCTG-3' (FRAG. NO:1363)(SEQ. ID NO:1372)

5'-TGGTCTCTGTGGTIG-3' (FRAG. NO:1364)(SEQ. ID NO:1373)

5'-CTGCCCTGGGTCTG-3' (FRAG. NO:1365)(SEQ. ID NO:1374)

- 5 5'-GGGTGTGGCCTTGGGCCGTCCTCTGGCTCCTCCTCGTGGGCCCC (FRAG.NO:1366)(SEQ.ID NO:1375)
- 5'-GGGCTAAGAT GATCCACATC ACTACCACGT TGCCACCAC AGAGGTCACC ACAATGACCG TGTAGGCAGC
TGCCCAAAGG ACAATTTGCC AGGCTGGTTG CACGAACTGA TTGGGTTCCG AGGTGTAGT GGAGATGTTT
GGGGAGAGGT CTGA/TGCCAC CGGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGTA
CACAACCCCC CTCTC CAGCA GAGTCCTGTC GTGGCGCCTG GGGCTCAGGGTCC-3' (FRAG.NO:1367)(SEQ.ID NO:1376)
- 10 5'-GGGCTBBGBT GBTCBCBCTC BCTBCCBCGT TGCCBCCBC BGBGGTCBCC BCBTGBCCG TGTBGGCBGC
TGCCBBBGG BCBE/TTTGCC BGGCTGGTTG CBCBBCTGB TTGGGTTCCG BGGTGTBGT GGBBGTGTTT
GGGGBGBGGT TGLGTCCBCC TGGGBGGBCGT TBTCBBTTT GBBGCTBGGC GGTBBBGGCC TBCTBTCTGTB
CBCBCCCC CTCTG CBGCB GBGTCCTGTC GTGGCGCCTG GGGCTCBGGG TCC-3' (FRAG. NO:1368) (SEQ. ID NO:1377)

Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments

- 15 5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG
BBBGBGCBGC BGGGGBGBG GBBGBBGBG CBTCTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTC
CTTCCBGTG TTGC GTTTTB TBBCTCCCBG BBGGCBGBG BGGGGCBGG CGTTTTCTTC TCTCGTGGT
TTTCCTTTCC TGGCAGTGGG TGGGGGTGGG GGTGGGGTGG CTTCCTTGTT CCTGGGGGTG TCCTCTGTCT
CTGGGCTTTT CTCCCTTTT CCTCCTGTC TGTTTCTCTG GGGCTCTCCT CTGTCTCTGT GTCCTTGCCC
- 20 TGGCCCTCTT CCTCCTCTG TCTCCTGTC CTGTGTTCCG CCCGCTTCC
CTCTCCTGAC CTCTTTTCC TCCGCTGGGT GGGGCCCTGC CTGTTCTCTG CTCCCTGGCT TGGGGTTTCT
TCTGTGTGTC TCTCTCTCT GTTGGCTGGC TTCTCCTTC TTTGTCTTC CTGGGTGCCC CTCTTCCTT
TCTGGGTCC TTGGTGCTTG GGCTGGG TCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA
TCTCTCCATG TCC/CTCCCC CTGTATCTTG CCATTCTTGA CCTGCATTTT CATCCTCTT ACCTTCCCTA
- 25 GAGGCCAACT CAT/TTCTTT GAAAAACCTG GCATTTCCTA GAAAAAAG TGAAGGGCTG GGAGCTGTCC
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[illegible]

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GACTTTGGGC TGAAGAGACTT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC
 CTTCCGGAGGA AAAAGGAGGTC CTGTCCGAAG GTCCCTCTGT TTGCAGTAGC ACCCTCACC CCTACCCAAC
 TCAAGACACA CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CCTTTTCAAG
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 5 CCCCCACTTT CCCCCTTTTAA CTGATATCTC CTGCTTCAGG GGCTGGCCCT CATGCAGGGT TCCCTGAATT
 AGGAAGTGTG AACCTGTGTC CCTGAGTCCT CCCTGGCCTG TTCAGTCCCC AGCAATTCCA GGGGTCGTAG
 AAATTGTGTC TGTTTCCTGA GAAAGCTCTT TCATGAGTTA AGCCTGAGCC CTCAAATGCC ACAAGTGGCC
 CATGAAAAGG GAGATGGGTA GAGTCCGCGN ACCCAGTGAC AGAGTTTAGT CCTCTTTTCT CAGAATGAGC
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 10 TAACAGTCAC CCTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTTATAAA
 GCAATTCCGT CATCAAAAT ATAACACTTC TACTCTTCAC CACGATATCA TGTTACTAAA GGTGACAACA
 CCTCTCTTCT CCTTTCAC TTCCATTCT CCTAAGCTTC TCCTTCAGGT CCTCATGTC CTGAATTTT
 CTTAGGACTT GGCATAACA TGAAGCTACT CACCCTGTCC CTCCTGATC ACCTCCAAC GTCCAGAGCC
 CATTTCGAGG ACTACAGTC CTTCATTCCC TTCACAGTTG AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG
 15 GGGACACTCC CCTCCCATC ACAATTCAAC TTTGTCCAC CTGGGAGAAT GTGCCGGGTG GCTGGCTGGG
 GAAGAACAGG TGTGTTGAAG CCGGGCTCAG AACTCTGCA AGAGGTGAAG CTGAGACTCA TGGATCCCCA
 GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCCAG GAAGACAAAA
 TCTGCATTTA AGGTGATCCT CCAACTAGGT TTCCTCTCCA AAACCTACTG TTCAGGGACT TGAATGCTCT
 TAGAAGGAGA TGGGTGTCAGC AGGTTGTGAG TCAGGTGACA GGGTGAGCAT CACAGGAATT GCTGTCTCTC
 20 CGTGGTCCAA GACA.GCCTCT GACCATCCAT TCCAGTGTAC TGCAGTGGG GCATGGGGTG ACTGTGAGA
 ATGTGGATGA CGGTCCCAAG AAAGGAAGAA GGGGCATCAG AACTAGATGT ATAAGTGAGG AGCTCCACCT
 CCTGGGTCTG ACTTAGGTC TCACTGTGAC TCCAAGCTGG CTGGCAGACA GGAGTGAGG ACTTCCCGGG
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 25 CGGCCCTGGA TCA'CCAGAT CCTGCAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGAAGCTGG
 AACTGGACCT TAG'AGCAA GTGTGTGCAA CTCATTCTGG TTCTACCCTT GGTCCCTCA GCCACAACCC
 TAAGCCTCA AGAGTCTCC TACAGGTAAC AGAATTTCA ATAACTTCA GTGAAGACAC AGCTTCTAGT
 CGTGAGTGTG TGCTCTCTC TGCTGCTCTC TTCTCTGCA CATGTGACCT GATTCCCAGC CCAAGCACA AGGA-3'
 (FRAG. NO: (SEQ. ID NO:2467)
 30 5'-GGBGCBBCBG-3' (FRAG. NO:1888) (SEQ. ID NO:1901)
 5'-GGBGCBGC-3' (FRAG. NO:1889) (SEQ. ID NO:1902)
 5'-GGGGCBBCBG CG-3' (FRAG. NO:1890) (SEQ. ID NO:1903)
 5'-CGTTTTCTTCTCTC-3' (FRAG. NO:1369)(SEQ. ID NO:1378)
 5'-GCTGGTTTTCTTTCC-3' (FRAG. NO:1370)(SEQ. ID NO:1379)
 35 5'-TGGCAGTGGGTGGTGGTGGGGTGGGTGGC-3' (FRAG. NO:1371)(SEQ. ID NO:1380)
 5'-TTCTTGTCTGGGGGTGCTCT-3' (FRAG. NO:1372)(SEQ. ID NO:1381)
 5'-CTTGCTCTGGGCTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1382)
 5'-CCCCTTTTCTTCC-3' (FRAG. NO:1374)(SEQ. ID NO:1383) [
 5'-TGCTGTCTTCTCTGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1384)
 40 5'-CTCTCTCTGTCTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1385)
 5'-CCTTGCCCTGGCC-3' (FRAG. NO:1377)(SEQ. ID NO:1386)
 5'-TCTTCCCTCTCTGTCTCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1387)
 5'-CCCTGTGTTCCGCC-3' (FRAG. NO:1379)(SEQ. ID NO:1388)
 5'-GTCTTCCCTCTCTG-3' (FRAG. NO:1380)(SEQ. ID NO:1389)
 45 5'-ACCTCCTTTCTCTCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1390)
 5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1391)
 5'-CCTGTTCTCTGCTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1392)
 5'-TGGCTTGGGGTTTCTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1393)
 5'-TGCTCTTCTCTCTGT-3' (FRAG. NO:1385)(SEQ. ID NO:1394)
 50 5'-GGCTGGCTTTCTCTTC-3' (FRAG. NO:1386)(SEQ. ID NO:1395)
 5'-TTTGTCTTCTCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1396) [1397]
 5'-TGCCCTTCTCTCTTCTTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1397)
 5'-TCCTTGGTGTGCTGCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1398)
 5'-GGBGCTGBTB CT'CBGATTT CBGBGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBBG
 55 BBBGBGCBGC BGGGGBGBG GBBGBGBGB CBTCTCCCB GBGBGGCTGC CTGBGBBBT GCTGGTTTTC
 CTTTCCBGTG TTGGGTTTB TBBCTCCCB BGGCBGBGB BGGGGCBGG-3' (FRAG.NO:1891) (SEQ.ID NO:1904)

Endothelial Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GCGTCTTGGG GT'CBGGGCC CBTCTGTCTG CGCTGGGCG CTGCTGTGCG TCCGTCTGCT GGGGGGCCGG
 GGTGGCTGGG CCC'GCTTGC CGCACGACC CGGGCCGACC CGAGGCTCGG GGGGCTGTGT TCTGGCGCTG
 60 GTGGGCTTGG GCC'CTCTGG GGGCTGGGT TCCTGTGCG CCTGGGCGCT GCGCTCTTGG GGTGCGGGGC
 CGGGGGGCCG GGGGCGCGCT GTTCGTGGGC CTGGGGGTGC CTGTGGCTGC CGGTTGCCCC GGTGTGGTGC

GCCGTCCTGC TGCCGGTCGT TGGCTGGGTC CCCCCGCCCC TTCTCTGGGG TCCGCGTGGG GTGCTCCGGT
 TCCTCGTGCC GCTGCTGCC TGTCTTCCG GCCGTGGCGG CGTGGTGGTC CGCCCCCCT GGCTTCTGC
 TCGGGGCTCT GCTC GTTGCC GCGGCGGTCT TCTTCTGGT GGCTCTGGG CCGGCCGGTC
 TCGGGCGTCT CGTC TTGCGT CTTGTGCTGT TCCGGCCGCT CCTCCTCTT CCGCCGCCGC CGTCCCCGC
 5 CCGCTCGTCG CCGTGGCCCG GCCTCCTCCT GGCCTGTGTC TCGGGCGGCG GCCTTGCGCG TCCGTTTGGG
 GCTGCCTCTG GCGCTTCCGG CCCTCGGCCCT GGGCGCTCTC TTCCGCTGT GCTGGTGGCC CTCGTGGGCC
 CCTCCTGGCC TCCGCTGTCC TGTGGTCCCC CGGCTGGTGG CCGGGCCGGT TGGGCGGGCG TGGGCGCCGG
 CGGGTCCTCC GGGCTGCCCT TCTCCGCCG GGGTCCCGCG CTCCTGCTGT TCCCTGGGCT CTTCTGCCTC
 TCTCCTGGGT GGGTGGTGGG TGCCGGGGTC TCCGGGCTTG CCCCCTGCTG CTGGGCGTTC TCGGCTCTG
 10 GGGTGTGCTG TGGC CCGGCT CGTGTGCGCC TCCGTCGCCC GTCGCGGCC TCGTCCCTC CTGGGTGCGC
 GGGGGGCTGG TCCCTGGCGTT TTGCTCCTTC CTGGGCGTCT TGGGGTGCBG GGCCCBCTC GCTGCGCTG
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 GACCCGAGGC TCGCGGGGCT GTGTTCTGGC GCTGGTGGGC TTGGGCCCT CTGGGGCTG GGTTCCTGC
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 15 GTGCTGTGG CTGC CGGTTG CCCCCTGGT TGGCGCCGTC CTGCTGCCG TCGTGGCTG GGTCCCCCG
 CCCGTTTCTT GGGCTCCGCG TGGGGTGCTC CGGTTCTCTG TGCCGCTGCT GCCTGTCTT TCCGGCCGTG
 GCGGCGTGGT GGTTCGCCCC CCCTGGCCTT CTGCTCGGGG TCTGGCTGGT TGCCGGTGCC CTTGGCGCG
 GTCTTCTTCC TGGTGGCTCT GGGCCCGGCC GGTCTCGGGC GTCTCGTGT CGCTCTGTG CTGTCCGGC
 20 CGTCTCTCC TCTTCCGCG CCGCCGCTCC CCGCCGCTC GTCGCCCTGG CCGGCCCTC TCCTGGCCGC
 TGTCTCGGG GGCCTGCTTG GCGCTCCGT TGGGGCTGCC TCTGGCGCTT CCGGCCCTC CCGGGCGC
 TCTCTCCGC CTGTCTGGT GGCCTCGTG GGCCTCTCT GGCCTCCGT GTCTGTGGT CCGCCGCTG
 GTGGCCGGG CGGTGGGGC GCGTGGGGC CCGGCGGGT CTCCGGGCTG CCCTTCTCC CCGGGGGTCC
 CGCGCTCTG CTGTCTCTG GGTCTTCTG CCTCTCTCT GGGTGGGTG TGGGTGCCG GGTCTCCGG
 CTTGCCCGC GCTCCTGGG GTTCTGCGG CTTGGGGTGT TCTGTGGCC CGCTCGTGT GCCCTCCGTC
 25 GCGGTCGCC GGCCTCGTCC CCTCTGGGT GCGCGCGGG CTGGTCTGG CGTTTGTCT CTCTCTGG-3' (FRAG.
 NO:1892) (SEQ. ID NO 1905)
 5'-GCGGGGCGG-3' (FRAG. NO:1893) (SEQ. ID NO: 1906)
 5'-CGGGGGGC-3' (FRAG. NO:1894) (SEQ. ID NO: 1907)
 5'-GCGGCGCGG-3' (FRAG. NO:1895) (SEQ. ID NO: 1908)
 30 5'-CTGTGCGTCCGCTCTGCTGG (FRAG. NO:1390)(SEQ. ID NO:1399)
 GGGGCGGGGTGGCTGGGCCCTGCTTGCCGC (FRAG. NO:1391)(SEQ. ID NO:1400)
 ACGACCCCGGCCGACCCGAG (FRAG. NO:1392)(SEQ. ID NO:1401)
 GCTCGGGGGCTGTGTTCTGGCGTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1402)
 CTTGGGGCCCTCTGGGGGCTGGGT (FRAG. NO:1394)(SEQ. ID NO:1403)
 35 TCCTGCTGCGCCTGGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1404)
 GCGTCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1405)
 GGGGCGGGGGGGCC GGGG (FRAG. NO:1397)(SEQ. ID NO:1406)
 GCCGCTGTTCTGGGCTGGG (FRAG. NO:1398)(SEQ. ID NO:1407)
 GGTGCCTGTGGCTGCG (FRAG. NO:1399)(SEQ. ID NO:1408)
 40 GGTGCCCCGGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1409)
 GCCGCTCTGCTGCCGCT (FRAG. NO:1401)(SEQ. ID NO:1410)
 CGTTGGCTGGGTCCCTCCGC (FRAG. NO:1402)(SEQ. ID NO:1411)
 CCGTTTCTTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1412)
 GCGTGGGGTGTCTC (FRAG. NO:1404)(SEQ. ID NO:1413)
 45 GGTTCCTCGTGCCG (FRAG. NO:1405)(SEQ. ID NO:1414)
 CTGCTGCCTGTCTTCC (FRAG. NO:1406)(SEQ. ID NO:1415)
 GGCCGTGGCGCGTGGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1416)
 GCGGGGCTGGCCTTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1417)
 GGGGCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1418)
 50 TGCCGGTGCCCTGGGCGG (FRAG. NO:1410)(SEQ. ID NO:1419)
 GGTCTTCTTCTGGTCT (FRAG. NO:1411)(SEQ. ID NO:1420)
 GCTCTGGGCGCGCGTCTCGG (FRAG. NO:1412)(SEQ. ID NO:1421)
 GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1422)
 CTCTGTGCTGTTCCTCCG (FRAG. NO:1414)(SEQ. ID NO:1423)
 55 CTCCTTCTTCTCCGCGCC (FRAG. NO:1415)(SEQ. ID NO:1424)
 GCGGCTCCCCGCC (FRAG. NO:1416)(SEQ. ID NO:1425)
 GCTCGTCGCCCTGGCTC (FRAG. NO:1417)(SEQ. ID NO:1426)
 GGCTCTCTCTGGCGC (FRAG. NO:1418)(SEQ. ID NO:1427)
 TGTCTCGGGCGCGGCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1428)
 60 GCTCCGTTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1429)
 CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1430)
 GGCCCTCGGCTGGGCTCTC (FRAG. NO:1422)(SEQ. ID NO:1431)

- TCTTCCGCCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1432)
 TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1433)
 GCCCCTCTGGCCTC(GGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1434)
 TGTGGTCCCCCGGTGTGT (FRAG. NO:1426)(SEQ. ID NO:1435)
 5 GGCCGGGCGCGGTGGGCGGGC (FRAG. NO:1427)(SEQ. ID NO:1436)
 GTGGGCGCGGCGGGTCTCTCC (FRAG. NO:1428)(SEQ. ID NO:1437)
 GGGCTGCCCTTCTCC (FRAG. NO:1429)(SEQ. ID NO:1438)
 GCCGGGGTCCCGC (FRAG. NO:1430)(SEQ. ID NO:1439)
 GCTCCTGCTGTTCCCTGGGCTCTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1440)
 10 TCTCTCCTGGGTGGG' GCTGGGTGCCG (FRAG. NO:1432)(SEQ. ID NO:1441)
 GGGTCTCCGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1442)
 CCCCgcGTGCTGGG' GTTCTGC (FRAG. NO:1434)(SEQ. ID NO:1443)
 GGTCTTGGGGTTGTC (FRAG. NO:1435)(SEQ. ID NO:1444)
 TGTGGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1445)
 15 TGTCGCCCTCCGTCG(C (FRAG. NO:1437)(SEQ. ID NO:1446)
 CGTCGCCCGCCTCGT(C (FRAG. NO:1438)(SEQ. ID NO:1447)
 CCTCCTGGGTGCGC (FRAG. NO:1439)(SEQ. ID NO:1448)
 GGCGGGCTGGTCCT (FRAG. NO:1440)(SEQ. ID NO:1449)
 GGGCTTTTGTCTCTT(C'TGG (FRAG. NO:1441)(SEQ. ID NO:1450)
 20 5'-GCGTCTTGGGGTG(C'BGGGCCCBTCCTGCTGCGCCTGGGCGCTG-3'(FRAG. NO:1896) (SEQ. ID NO: 1909)

Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-CTGCCCCBGT TT' TGBTCCT CBCTGCCGT GGGGBGGBCB BTGGCTGCCT CCCCggggTT TCTGCTGCTT
 GCTGCTTCTT TCCGCTCTCC CTCTTTCCCT GTCTCTTTT TGCCTCTTTG GGTTCTGTT GTTCTTGCC
 25 TGCTTGGTGG CGGCTTGTGC GTTTCCTCTC TCTTCTCTTG GGTCTCCGCT TCTCGTCTG CTTTCTCTG
 TCTCTGTGC GCGCTTCTC CTCCGGCGTC CTCTGCCCT GTGCTGTTG CCTCGGGTGG TGGGGTCCC
 GGTGCTCCCC CGGCGGGCCG GCTGGTTGCC TGGGCTGTC TGGTGGGGTG TGGGGCCGCT GGGTTGGGG
 TGTGGTGGGC TCTCTGTGG CCTGTGGGGC TGTGTGTGTC TCTGTGGGCG TGTGCTGGGT CTTGGGGCTT
 CCTCCCTTGT GCTGGGTGCG GCCTCCCCGC CCCCCTCTG GGCCGGTGGC CTGGCTCCTT GTGGGCGCTT
 CTGGCTCTTG CCTGTCTT CTTCGCTCG TGGTGTCTGG GCTGC CATATGTATG GGAATACTGT ATTTCAGCA
 30 TTATAAGGAA TGAATTATATA GGCCGGGCAT TGTGGCTAAC CCTTGTAATC CTAGCACTTT GAGAGGCTGA
 AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC AGTCTCTACC
 AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC TGTAGTCCCA GCTACTCAGG AGGCTGAGGT
 GGGAGGATCG CTTCAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCAGTCTT
 35 GGTGACAGAA TGAAGCTCCA TCTCAAAAAT AAATAAATAA ATAAATAAAA TAAATGAAAT GAAATTATAA
 GAAATTACCA CTCTTTCATG TAAGAAGTGA TCATTTCAT TATAAGGGAA GGAATTTAAT CCTACCTGCC
 ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT AGTAAGACCA ACATCTCAGA GGCTCTCTG
 TGCCAATAGC CTCTCTCTT TTCCCTTCCA AAAACCTCAA GTGACTAGT CAGAGGCCTG TCTGGAATAA
 TGGCATCATC TAAATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGTG TGTCCATAC TGTCAATATT
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 40 CCTGTGTAG GAAATAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT TGCCCAAATA AACCTGGCT
 CCGTGTGCTC TCTCTTAG CAGCCACCCT GCTGATGAAC TGCCACCTTG GACTTGGGAC CAGAAAGAGG
 TGGGTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG CAAGATCAGG TCACCCACAG GCCCTGGCAG
 TCACAGTCAT AAATAGCTA ACTGTACACA AGCTGGGAC ACTCCCTTG GAAACCAAAA AAAAAAAAAA
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 45 CAGTGTGTTT ATAATTGT AGCAGTCGA AAAGTGGG TCCGGCCGCA GAGAACTCAG CCTCATCTCT
 GCTTTAAAT CTCTCGGCCA CCTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG
 CACAGGTCTC TTCC'GGTTT GACTGTCCTT ACCCGGGGA GGCAGTGCA CCAGCTGCAA GGTGAGTTGC C
 CATATGTATG GGAATACTGT ATTTCAAGGA TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC
 CCTTGTAATC CTACCACTTT GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA
 50 TGGACAACAT GGTGAAACCC AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC
 TGTAGTCCCA GCTCTCAGG AGGCTGAGGT GGGAGGATCG CTGAGCCTG GGAGGCAGAA GTTGCAATGA
 GCAGAGATCG TGCACTCCG CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA
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 55 AGTAAGACCA ACACTCAGA GGCCTCTCTG TGCCAATAGC CTTCCTTCTT TTCCCTTCCA AAAACCTCAA
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 CCATGTGGCT TGGCAAATA AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC
 60 TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG
 CAAGATCAGG TCACTCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGGAC

ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA CCTTTATGCA AAAACAACTC TCTGGATGGC
 ATGGGGTGAG TATAAATACT TCTTGGCTGC CAGTGTGTTT ATAACTTTGT AGCGAGTCTGA AACTGAGGC
 TCCGGCCGCA GAGAATCTCAG CCTCATCTCT GCTTTAAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG
 CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG CACTGAGTCTC TTCCTGGTTT GACTGTCTTT ACCCCGGGGA
 5 GGCAGTGCAG CCAGTGCAG GGTGAGTTGC C-3' (FRAG. NO.) (SEQ. ID NO: 3016)
 5'-CTGCTTTAAA ATCTCTCGGC CACCTTTGAT GAGGGGACTG GGCAGTTCTA GACAGTCCCG AAGTTCTCAA
 GGCACAGGTC TCTTCTGGT TTGACTGTCC TTACCCCGGG GAGGCAGTGC AGCCAGCTGC AAGCCCCACA
 GTGAAGAACA TCTCAGCTCA AATCCAGATA AGTGACATAA GTGACCTGCT TTGTAAAGCC ATAGAGATGG
 10 CCTGTCCTTG GAAATTTCTG TTCAAGACCA AATTCCACCA GTATGCAATG AATGGGGAAA AAGACATCAA
 CAACAATGTG GAGAAGGCC CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAAC
 CTCAGCAAGC AGCAGAATGA GTCCCCGCA CCCCTCGTG AGACGGGAAA GAAGTCTCCA GAATCTCTGG
 TCAAGATGGA TGCACCCCA TTGTCTCTCC CAGGCATGT GAGGATCAAA AACTGGGGCA CGGGATGAC
 TTTCCAAGAC ACATTCACC ATAAGGCCAA AGGGATTTTA ACTTGACAGT CCAAATCTTG CCTGGGGTCC
 ATTATGACTC CAAAAGTTT GACCAGAGGA CCCAGGGACA AGCCTACCCC TCCAGATGAG CTTCTACCTC
 15 AAGCTATCGA ATTTGTCAAC CAATATTACG GCTCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG
 GGTGGAAGCG GTAACAAAGG AGATAGAAAC AACAGGAACC TACCAACTGA CGGGAGATGA GCTCATCTTC
 GCCACCAAGC AGGCTGCGG CAATGCCCA CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT
 TCGATGCCCG CAGCTGTTC ACTGCCCGG AAATGTTTGA ACACATCTGC AGACACGTGC GTTACTCCAC
 CAACAATGTC AACATCAGGT CGGCCATCAC CGTGTTCCTC CAGCGGAGTG ATGGCAAGCA CGACTCCCG
 20 GTGTGGAATG CTCAGCTCAT CCGCTATGCT TGCTACAGA TGCCAGATGG CAGCATCAGA GGGGACCTG
 CCAACGTGGA ATCTACTCAG CTGTGCATCG ACCTGGGCTG GAAGCCCAAG TACGGCCGCT TCGATGTGGT
 CCCCTGGTC CTGCAGGCCA ATGGCCGTGA CCTGAGCTC TTCGAAATCC CACCTGACCT TGTGCTTGAG
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 TGGCCAACAT GCTCCTTGAG GTGGGCGGCC TGGAGTTCCC AGGGTGCCCC TTCAATGGCT GGTACATGGG
 25 CACAGAGATC GGAGTCCGGG ACTTCTGTGA CGTCCAGCGC TACAACATCC TGGAGGAAGT GGGCAGGAGA
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 30 AGGTAGAGGC CTGCAAAAACC CATGTCTGGC AGGACGAGAA GCGGAGACCC AAGAGAAGAG AGATTCCATT
 GAAAGTCTTG GTCGAAGCTG TGCTCTTTGC CTGTATGCTG ATGCGCAAGA CAATGGCGTC CCGAGTCAGA
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 GCTGTTGGTG GTGACCAGTA CGTTTGGCAA TGGAGACTGC CCTGGCAATG GAGAGAAATC GAAGAAATCG
 35 CTCTTCATCG TGAAAGAGCT CAACAACAAA TTCAGGTACG CTGTGTTTGG CCTCGGCTCC AGCATGACC
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 GCAGCCTGTG AGAGGTTTGA TGTCAGAGG AAACAGCACA TTCAGATCCC CAAGCTCTAC ACCTCCAATG
 TGACCTGGGA CCCGACACAC TACAGGCTCG TGCAGGACTC ACAGCCTTTG GACCTCAGCA AAGCCCTCAG
 40 CAGCATGCAT GCCAGAACG TGTTACCAT GAGGCTCAA TCTCGGCAGA ATCTACAAAG TCCGACATCC
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 ACCTTGGGTT TTGCCAGGC AACCAGCCGG CCTTGGTCCA AGGCATCCTG GAGCGAGTGG TGGATGGCCC
 CACACCCCA CAGACGTGC CCCTGGAGGA CTGTGATGAG AGTGGCAGT ACTGGGTGAG TGACAAGAGG
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 45 TGCTCAAAA GCTGCCAG GTGGCCACAG AAGAGCCTGA GAGACAGAGG CTGGAGGCC TGTGCCAGCC
 CTCAGAGTAC AGCAAGTGGA AGTTACCAA CAGCCCCACA TTCCTGGAGG TGCTAGAGGA GTTCCCGTCC
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 CCTCCCGGGA TCACACGCC ACAGGATCC ACCTGACTGT GGCCGTGGTC ACCTACCACA CCGGAGATGG
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 50 TGCTTTGTG GGAATGCCAG CGCCTTCCAC TCCCCGAGG ATCCCTCCA TCCTTGATC TCATCGGGC
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 GCGGGGAGGC CGCATGACCT TGGTGTGGT GTGCCCGGC CCAGATGAGG ACCACATCTA CCAGGAGGAG
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 55 GCCAGGCCAC CTCATGTTT GCGGGGATGT GCGCATGGCC CGGGACGTGG CCCACACCCT GAAGCAGCTG
 GTGGCTGCCA AGCTGAAATT GAATGAGGAG CAGGTCGAGG ACTATTTCTT TCAGCTCAAG AGCCAGAAGC
 GCTATCACGA AGATATCTTC GGTGCTGTAT TTCTTACGA GGCGAAGAA GACAGGGTGG CGGTGAGCC
 CAGCAGCTG GAGATGTGAG CGCTGTGAG GCCTACAGGA GGGGTAAAG CTGCCGGCAG AGAACTTAAG
 GATGGAGCCA GCTCTGCAAT ATCTGAGGTC ACAGGGCTG GGGAGATGGA GGAAAGTGAT ATCCCCCAGC
 60 CTCAAGTCTT ATTTCCTCAA CGTTGCTCCC CATCAAGCCC TTTACTTGAC CTCCTAACAA GTAGCACCTT
 GGATTGATCG GAGCTCTCTC TCTCAAACTG GGGCCTCCCT GGTCCCTTGG AGACAAAATC TTAAATGCCA
 GGCCTGGCGA GTGGGTGAAA GATGGAACCT GCTGCTGAGT GCACCACTTC AAGTGACCAC CAGGAGGTGC

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Variable	Mean	SD	Min	Max
Age	34.5	10.5	20	55
Gender	Male	10.5	0	1
Marital status	Married	10.5	0	1
Education	High school	10.5	0	1
Occupation	Unemployed	10.5	0	1
Income	Low	10.5	0	1
Health status	Good	10.5	0	1
Smoking status	Non-smoker	10.5	0	1
Alcohol consumption	Non-drinker	10.5	0	1
Stress level	Low	10.5	0	1
Social support	High	10.5	0	1
Life satisfaction	High	10.5	0	1
Depression	Low	10.5	0	1
Anxiety	Low	10.5	0	1
Quality of life	High	10.5	0	1
Healthcare utilization	Low	10.5	0	1
Health insurance	Yes	10.5	0	1
Healthcare access	Good	10.5	0	1
Healthcare cost	Low	10.5	0	1
Healthcare quality	High	10.5	0	1
Healthcare satisfaction	High	10.5	0	1
Healthcare utilization	Low	10.5	0	1
Health insurance	Yes	10.5	0	1
Healthcare access	Good	10.5	0	1
Healthcare cost	Low	10.5	0	1
Healthcare quality	High	10.5	0	1
Healthcare satisfaction	High	10.5	0	1

CCTGTGAATC CTAGCACTTT GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA
 TGGACAACAT GGTC AAACCC AGTCTCTACC AAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC
 TGATAGTCCA GCTACTCAGG AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA
 GCAGAGATCG TGCC ACTCCG CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA
 5 ATAAATAAAAA TAAATGAAAT GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAAGTGA TCATTTCCAT
 TATAAGGGAA GGAATTTAAT CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT
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 GTGACTAGTT CAGAGGCCTG TCTGGAATAA TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA
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 10 AGAGGATGGA CAGGATTA A CCAGAGAGCT CCCTGCTGAG GAAAAAATCT CCCAGATGCT GAAAGTGAGG
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 TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG
 CAAGATCAGG TCACCCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGGAC
 ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA CTTTATGCA AAAACAACCTC TCTGGATGGC
 15 ATGGGGTGAG TATAAATACT TCTGGCTGC CAGTGTGTTT ATAACCTTGT AGCGAGTCGA AAAGTGAGGC
 TCCGGCCGCA GAGAACTCAG CCTCATCTCT GCTTTAAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG
 CAGTTCTAGA CAGTCCGAA GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCTCT ACCCCGGGGA
 GGCAGTGCAG CCAGTGCAG GGTGAGTTGC C-3' (FRAG. NO:) (SEQ. ID NO: 2506)
 5'-CTGCTTTAAA ATCTCTCGGC CACCTTTGAT GAGGGGAGTG GGCAGTTCTA GACAGTCCCG AAGTTCTCAA
 20 GGCACAGGTC TCTTCTGGT TGTACTGTCC TTACCCCGGG GAGGCAGTGC AGCCAGCTGC AAGCCCCACA
 GTGAAGAACA TCTCAGTCA AATCCAGATA AGTGACATAA GTGACCTGCT TTGTAAAGCC ATAGAGATGG
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 CAACAATGTG GAGAAAGCCC CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAAC
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 25 TCAAGCTGGA TGCAACCCCA TTGTCTCTCC CACGGCATGT GAGGATCAAA AACTGGGGCA GCGGGATGAC
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 30 GCCACCAAGC AGGCTGGCG CAATGCCCA CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT
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 35 CCCCCTGGT TCTCAGGCA ATGGCCGTGA CCTGAGTCT TCGAAATCC CACCTGACCT TGTGCTTGAG
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 TGGCCAACAT GCTCTTGAG GTGGGCGGCC TGGAGTCCC AGGGTGCCCC TTCAATGGCT GGTACATGGG
 CACAGAGATC GGAATCCGGG ACTTCTGTGA CGTCCAGCGC TACAACATCC TGGAGGAAGT GGGCAGGAGA
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 40 TGATCCATAG TTTTCAGAA CAGAAATGTA CCATCATGGA CCACCACTCG GCTGCAGAAT CCTTCATGAA
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 45 GTCACCATCC TCTTTCGAC AGAGACAGGA AAATCAGAGG CGCTGGCCTG GGACCTGGGG GCCTTATTCA
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 60 CTGCGGGTGT CTGCTGGCTT CCTGCTTTCC CAGCTCCCCA TTCTGAAGCC CAGGTTCTAC TCCATCAGCT
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 5 ATGCTGGAGA TGGCCAGAA GGGGGTGCTG CATGCGGTGC ACACAGCCTA TTCCGCGCTG CCTGGCAAGC
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 GCCAGGCCAC CTCATATGTTT GCGGGGATGT GCGCATGGCC CGGGACGTGG CCCACACCCT GAAGCAGCTG
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 15 CCAGTCTGTT CCCCATGGCC ACTTGGGTCT TCCCTGTATG ATTCCTTGAT GGAGATATTT ACATGAATTG
 CATTTTACTT TAATC 3' (FRAG. NO:) (SEQ. ID NO:2507)
 5'-GAATCCCAC TCCTGCTGCCT GCTCCAGCAG ACGGACGCAC AGTAACATGG GCAACTTGAA GAGCGTGGCC
 CAGGAGCCTG GGCTACCCCTG CGGCCTGGGG CTGGGGCTGG GCCTTGGGCT GTGCGGCAAG CAGGGCCCAG
 CCACCCCGGC CCTGAGCCC AGCCGGGGCC CAGCATCCCT ACTCCCACCA GCGCCAGAAG ACAGCCCCC
 20 GAGCTCCCG CTAACCCAGC CCCAGAGGG GCCCAAGTTC CCTCGTGTGA AGAACTGGGA GGTGGGGAGC
 ATCACCTATG ACACCTCAG CGCCAGGCG CAGCAGGATG GGCCCTGCAC CCCAAGACGC TGCCTGGGCT
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 TCAGGCCCGG GACTTCATCA ACCAGTACTA CAGTCCATT AAGAGGAGCG GCTCCCAGGC CCACGAACAG
 25 CGGCTTCAAG AGGTGGAAGC CGAGGTGGCA GCCACAGGCA CCTACCAGCT TAGGGAGAGC GAGCTGGTGT
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 30 AGCCAACGTG GAGATCACCG AGCTCTGCAT TCAGCACGGC TGGACCCAG GAAACGGTCG CTTGCGAGTG
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 35 GCATGGACCT GGATACCCGG ACCACCTCGT CCCTGTGGAA AGACAAGGCA GCAGTGGAAA TCAACGTGGC
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 40 GTGGCCAAAC CCGTGAAGAT CTCCGAGACC GGCCGGGGCC AGAGCTACGC ACAGCAGCTG GGGAGACTCT TCCGGAAGGC
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 45 GCAGGGGGCC TGGGCACCCT CAGGTTCTGT GTGTTCTGGG TCGGCTCCCG GGCATACCCC CACTTCTGCG
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 50 GCCAGAGGTA CCGCTGAGC GCCCAGGCC AGGGCCTGCA GTTGAAAAC CTGCAAAGCA GCAAGTCCAC ATAGGTGTCT
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 60 GTGCCCTGCT TCATCCGGGG GGCTCCCTCC TTCCGGCTGC CACCCGATCC CAGCTTGCCC TGCATCCTGG
 TGGGTCCAGG CACTGGCATT GCGCCCTTCC GGGGATTCTG GCAGGAGCGG CTGCATGACA TTGAGAGCAA
 AGGGCTGCAG CCCACTCCA TGACTTTGGT GTTCGGCTGC CGATGCTCCC AACTTGACCA TCTTACC GC

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- GACGAGGTGC AGAACGCCCA GCAGCGCGGG GTGTTTGGCC GAGTCCTCAC CGCCTTCTCC CGGGAACCTG
 ACAACCCCAA GACCTACGTG CAGGACATCC TGAGGACGGA GCTGGCTGCG GAGGTGCACC GCGTGCTGTG
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 5 AGCAACGCTA CCAAGAAGAC ATTTTCGGGC TCACGCTGCG CACCCAGGAG GTGACAAGCC GCATACGCAC
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 GACACCAACA GCCCCTGAGA GCCGCTGGC TTTCCTTCC AGTTCGGGA GAGCGGCTGC CCGACTCAGG
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 10 GGGCCTGGGT CCGCCTTAAT CTGGAAGGCC CCTCCAGCA GCGGTACCCC AGGGCCTACT GCCACCCGCT
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 AGTGCCTACC CCAGCTC-3' (FRAG. NO:) (SEQ. ID NO: 2508)
 5'-CCCCGGGG-3' (FRAG. NO:1898) (SEQ. ID NO: 1911)
 15 5'-GGGGCCGCTGGG-3' (FRAG. NO:1899) (SEQ. ID NO:1912)
 5'-GGGGGTGTGG-3' (FRAG. NO:1900) (SEQ. ID NO: 1913)
 5'-CTGCCTCCCCGGGT-3' (FRAG. NO:1442)(SEQ. ID NO:1451)
 5'-TTCTGCTGCTTGC-3' (FRAG. NO:1443)(SEQ. ID NO:1452)
 5'-CTTCTTTCCCGTC-3' (FRAG. NO:1444)(SEQ. ID NO:1453)
 20 5'-CTTCTTTCCCGTC-3' (FRAG. NO:1445)(SEQ. ID NO:1454)
 5'-TTTTTGCTCTTT-3' (FRAG. NO:1446)(SEQ. ID NO:1455)
 5'-GGTTCCTGTTGTT-3' (FRAG. NO:1447)(SEQ. ID NO:1456)
 5'-GGCCTGCTTGGTGGCG-3' (FRAG. NO:1448)(SEQ. ID NO:1457)
 5'-GCTTGTGCGTTTC-3' (FRAG. NO:1449)(SEQ. ID NO:1458)
 25 5'-TCTCTCTTCTCTTGGTCTCCGCTTCTCGTCCGCC-3' (FRAG. NO:1450)(SEQ. ID NO:1459)
 5'-TTTTCTGTCTCTTCGCG-3' (FRAG. NO:1451)(SEQ. ID NO:1460)
 5'-GCCGTTCTCTCTCT-3' (FRAG. NO:1452)(SEQ. ID NO:1461)
 5'-GGCGTCCCTCTGCTCC-3' (FRAG. NO:1453)(SEQ. ID NO:1462)
 5'-TGTGCTGTTTGGC-3' (FRAG. NO:1454)(SEQ. ID NO:1463)
 30 5'-GTGGTGGGGTCCC-3' (FRAG. NO:1455)(SEQ. ID NO:1464)
 5'-GGTGTCTCCCCGGC-3' (FRAG. NO:1456)(SEQ. ID NO:1465)
 5'-GGGCCGGCTGTTGCCTGGGC-3' (FRAG. NO:1457)(SEQ. ID NO:1466)
 5'-CTGTCTGGTGGGGTGTGGGCG-3' (FRAG. NO:1458)(SEQ. ID NO:1467)
 5'-GCTGGGTGGGGGTGTGGTG-3' (FRAG. NO:1459)(SEQ. ID NO:1468)
 35 5'-GGCTCTCTGTGGGC-3' (FRAG. NO:1460)(SEQ. ID NO:1469)
 5'-TGTGGGGTGTGGTG-3' (FRAG. NO:1461)(SEQ. ID NO:1470)
 5'-TCTGTGGGGCTGTG-3' (FRAG. NO:1462)(SEQ. ID NO:1471)
 5'-CTGGGTCTGGGGCTTC-3' (FRAG. NO:1463)(SEQ. ID NO:1472)
 5'-CTCCCTGTGCTGGG-3' (FRAG. NO:1464)(SEQ. ID NO:1473)
 40 5'-TGCGGCTCCCCG-3' (FRAG. NO:1465)(SEQ. ID NO:1474)
 5'-CCCCCTCTGGGC-3' (FRAG. NO:1466)(SEQ. ID NO:1475)
 5'-GGTGGCCTGGCTCTGTGG-3' (FRAG. NO:1467)(SEQ. ID NO:1476)
 5'-GCGCTCTGGCTCTG-3' (FRAG. NO:1468)(SEQ. ID NO:1477)
 5'-CCCTGTCTCTCTGCTCGT-3' (FRAG. NO:1469)(SEQ. ID NO:1478)
 45 5'-GGCTGTGGGCTG-3' (FRAG. NO:1470)(SEQ. ID NO:1479)
 5'-CTGCCCCBGTGTTTGTGCTCTCBCTGCCGTGGGGGGBCBTGG-3' (FRAG. NO:1901) (SEQ. ID NO: 1914)

NF-kB Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCGGTG
 CCTCTCTTG GCTGTCCCT CGTTGTCCTT GGGCCCCG TCCCGCTGCT CGGCCTCCGT GTTCTTTGGC
 50 CTCTTGCTCC GCCGTCTGTC TTGTCCCGTC CCTCCTCGC TTGCGTTTCC CTCTTCCTTG TCTTCCAGGC
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 55 CCGCCGCTC TGTCGCTCC GGGGCTCCTC GTTTTCGCTG CTTCGGGTGT CCTTCTCGGC GTGTGGCCCC
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 GCTTGTCTCG GGTCTCTGGC CTCTGTGCTG GGCCTCTC TGCCTCTGC TCCGCCCTCC TGGTGGCTCG
 GCTGGGGGT CCCGTCGGG GGTGGGTGTG GGGTGTTC GGGTCTCTC CCTTCCC-3' (FRAG. NO:1902) (SEQ.
 ID NO:1915)
 60 5'-GGGCGGGGTCGC-3' (FRAG. NO:1903) (SEQ. ID NO:1916)
 5'-GCGCCGTCC-3' (FRAG. NO:1904) (SEQ. ID NO:1917)

- 5'-GGGCGTGGTGG-3' (FRAG. NO:1905) (SEQ. ID NO:1918)
 5'-GTTGGGCTTGGCCGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1480)
 5'-CTGCCCGGTGCCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1481)
 5'-TCTTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1482)
 5 5'-TGTCCTTGGGCCCC-3' (FRAG. NO:1474)(SEQ. ID NO:1483)
 5'-GCTCCCGTGTCTCGCCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1484)
 5'-GTTCTTGGCCTCTGTCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1485)
 5'-GCCTGCTGTCTTGCTCC-3' (FRAG. NO:1477)(SEQ. ID NO:1486)
 5'-CGTCCCCCTCTCGCTTGCGTTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1487)
 10 5'-CCTCTTCTTGTCTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1488)
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 5'-GGGGGCGCTCGGCTCCGCGGCTTCTCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1491)
 5'-CTGGGGGGTCTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1492)
 15 5'-TCTCCGGGGCCTGCGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1493)
 5'-GGGCTCGGGGCTGCGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1494)
 5'-GCGCGCGCGTCCGCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1495)
 5'-GGTGGCGCTGTCCCGCC-3' (FRAG. NO:1487)(SEQ. ID NO:1496)
 5'-GTGGTGTGTCTCCCTTCTCGTCTGCGCCGTC-3' (FRAG. NO:1488)(SEQ. ID NO:1497)
 20 5'-CTGGTCTGCCCGTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1498)
 5'-GGTCTTGGGCGTGGTGG-3' (FRAG. NO:1490)(SEQ. ID NO:1499)
 5'-GGGGCGTCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1500)
 5'-CTCGTCTGCCCGTGG-3' (FRAG. NO:1492)(SEQ. ID NO:1501)
 5'-GGGCTTGGGGCTC3G-3' (FRAG. NO:1493)(SEQ. ID NO:1502)
 25 5'-GGCTGTTCGTCCCTCCTGCGCTCTGTGGCCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1503)
 5'-GGGGCTCTCGTTTTC-3' (FRAG. NO:1495)(SEQ. ID NO:1504)
 5'-GCTGCTTCGGGTGCTCTCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1505)
 5'-GGCGTGTGGCCCC3G-3' (FRAG. NO:1497)(SEQ. ID NO:1506)
 5'-GTCCCCGCCCTGCTGGGCTGGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1507)
 30 5'-GCTGCCCTGGGCTCTGGGCCGCTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1508)
 5'-GGTTGTCTGTGCGT-3' (FRAG. NO:1500)(SEQ. ID NO:1509)
 5'-GCTTGTCTCGGTCTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1510)
 5'-CCTCTGTGCTGGGCT-3' (FRAG. NO:1502)(SEQ. ID NO:1511)
 5'-GCTTCTCTGCCCTCTGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1512)
 35 5'-GCCCTCCTGGTGGCTC-3' (FRAG. NO:1504)(SEQ. ID NO:1513)
 5'-GGCTGGGGGTGCCCGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1514)
 5'-GGGGTGGGTGTGGGTGTT-3' (FRAG. NO:1506)(SEQ. ID NO:1515)
 5'-TTCGGGCTCCTCCCTTCCC-3' (FRAG. NO:1507)(SEQ. ID NO:1516)
 5'-CGGCCCTTCTACCTGGAGGCACCGGCGAGTCTCCATGGGAGG-3' (FRAG. NO:1906)(SEQ. ID NO:1919)
- 40 **Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments**
 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC G¹G TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG
 TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT
 45 CCC TGC TGG GGG G²B GTT TCB TCT TGG-3' (FRAG. ID:1907) (SEQ. ID NO:1920)
 5'-GGG GGA GTT-3' (FRAG. ID:1908) (SEQ. ID NO:1921)
 5'-G CCC TGG GCC C-3' (FRAG. ID:1909) (SEQ. ID NO:1922)
 5'-GTT TCA TCT TGG CTT TAT CC-3' (FRAG. NO:1508) (SEQ. ID NO:1517)
 5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1509)(SEQ. ID NO:1518)
 50 5'-TCT CCT GCT CTG GRG TCT CCT C-3' (FRAG. NO:1510)(SEQ. ID NO:1519)
 5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1520)
 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1521)
 5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1513)(SEQ. ID NO:1522)
 5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1523)
 55 5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1524)
 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC G¹G TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TCG-3' (FRAG. ID:1910) (SEQ. ID NO:1923)
 5'-GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC
 60 TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB
 GTT TCB TCT TGG-3' (FRAG. ID:1911) (SEQ. ID NO:1924)

Human Eosinophi| Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1525)
 5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO: 1526)
 5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1527)
 5 5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO: 1528)
 5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO: 1529)
 5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO: 1530)
 5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO: 1531)
 5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO: 1532)
 10 5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO: 1533)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO: 1534)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1526)(SEQ. ID NO: 1535)
 5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO: 1536)
 5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO: 1537)
 15 5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO: 1538)
 5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO: 1539)
 5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO: 1540)
 5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO: 1541)
 5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO: 1542)
 20 5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1534)(SEQ. ID NO: 1543)
 5'-GG GGB GTT TCB TCT C-3' (FRAG. NO:1535)(SEQ. ID NO: 1544)
 5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1536)(SEQ. ID NO: 1545)
 5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO: 1546)
 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO: 1547)
 25 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO: 1548)
 5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO: 1549)
 5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO: 1550)
 5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO: 1551)
 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO: 1552)
 30 5'-G GGB GTT TCB TCT-3' (FRAG. NO:1544)(SEQ. ID NO: 1553)
 5'-G GGB GTT TCB TC-3' (FRAG. NO:1545)(SEQ. ID NO: 1554)
 5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO: 1555)
 5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO: 1556)
 5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO: 1557)
 35 5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO: 1558)
 5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO: 1559)
 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO: 1560)
 5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO: 1561)
 5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO: 1562)
 40 5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO: 1563)
 5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO: 1564)
 5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO: 1565)
 5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO: 1566)
 5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO: 1567)
 45 5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO: 1568)
 5'-GB GTT TCB TCT T-3' (FRAG. NO:1560)(SEQ. ID NO: 1569)
 5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO: 1570)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO: 1571)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1563)(SEQ. ID NO: 1572)
 50 5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO: 1573)
 5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO: 1574)
 5'-B GTT TCB TCT TGG-3' (FRAG. NO:1566)(SEQ. ID NO: 1575)
 5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO: 1576)
 5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO: 1577)
 55 5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO: 1578)
 5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO: 1579)
 5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO: 1580)
 5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO: 1581)
 5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO: 1582)
 60 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO: 1583)
 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO: 1584)

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- 5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO: 1585)
 5'-T TCB TCT TGG C-T T-3' (FRAG. NO:1577)(SEQ. ID NO: 1586)
 5'-T TCB TCT TGG C-T-3' (FRAG. NO:1578)(SEQ. ID NO: 1587)
 5'-T TCB TCT TGG C-T-3' (FRAG. NO:1579)(SEQ. ID NO: 1588)
 5 5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO: 1589)
 5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO: 1590)
 5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1591)
 5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO: 1592)
 5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO: 1593)
 10 5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO: 1594)
 5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO: 1595)
 5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1587)(SEQ. ID NO: 1596)
 5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO: 1597)
 5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO: 1598)
 15 5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1590)(SEQ. ID NO: 1599)
 5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO: 1600)
 5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO: 1601)
 5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO: 1602)
 5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO: 1603)
 20 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO: 1604)
 5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO: 1605)
 5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO: 1606)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO: 1607)
 5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO: 1608)
 25 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO: 1609)
 5'-T TCB TCT TGG CTT-3' (FRAG. NO:1601)(SEQ. ID NO: 1610)
 5'-TCB TCT TGG CTT 3' (FRAG. NO:1602)(SEQ. ID NO: 1611)
 5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO: 1612)
 5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO: 1613)
 30 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO: 1614)
 5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO: 1615)
 5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO: 1616)
 5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO: 1617)
 5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO: 1618)
 35 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO: 1619)
 5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO: 1620)
 5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO: 1621)
 5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO: 1622)
 5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO: 1623)
 40 5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO: 1624)
 5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO: 1625)
 5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1617)(SEQ. ID NO: 1626)
 5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO: 1627)
 5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO: 1628)
 45 5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO: 1629)
 5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO: 1630)
 5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO: 1631)
 5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO: 1632)
 5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO: 1633)
 50 5'-B GTT TCB TCT TGG-3' (FRAG. NO:1625)(SEQ. ID NO: 1634)
 5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO: 1635)
 5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO: 1636)
 5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO: 1637)
 5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO: 1638)
 55 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO: 1639)
 5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO: 1640)
 5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO: 1641)
 5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO: 1642)
 5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO: 1643)
 60 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO: 1644)
 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO: 1645)
 5'-GGB GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO: 1646)

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- 5'-GB GTT TCB TCT 1-3' (FRAG. NO:1638)(SEQ. ID NO: 1647)
 5'-GGG GGB GTT TCE TCT-3' (FRAG. NO:1639)(SEQ. ID NO: 1648)
 5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1640)(SEQ. ID NO: 1649)
 5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO: 1650)
 5 5'-GGG GTT TCB TCT 3' (FRAG. NO:1642)(SEQ. ID NO: 1651)
 5'-GGG GGB GTT TCE TC-3' (FRAG. NO:1643)(SEQ. ID NO: 1652)
 5'-GG GGB GTT TCB TC-3' (FRAG. NO:1644)(SEQ. ID NO: 1653)
 5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO: 1654)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO: 1655)
 10 5'-GG GGB GTT TCB T-3' (FRAG. NO:1647)(SEQ. ID NO: 1656)
 5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO: 1657)
 5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO: 1658)
 5'-TCT CCT GCT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO: 1659)
 5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO: 1660)
 15 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO: 1661)
 5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1653)(SEQ. ID NO: 1661)
 5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO: 1663)
 5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO: 1925)
 5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO: 1926)

20 BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-CCGTGTGTC BGIGGTGCTG CCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC TTGTTTTCCG
 TTTCTCTGC CGTCTGTGGT T-3' (FRAG. NO:1914) (SEQ. ID NO: 1927)
 5'-CCCGTTTGBGGTB1GGC-3'(FRAG. NO:1915) (SEQ. ID NO: 1928)
 5'-GCTCCBCCBBTTCCTTTTCTCC-3'(FRAG. NO:1916) (SEQ. ID NO: 1929)
 25 5'-TTGTTTTCCGTTTC TTTG-3'(FRAG. NO:1917) (SEQ. ID NO: 1930)
 5'-CCGTCTGTGGT-3'(FRAG. NO:1918) (SEQ. ID NO: 1931)
 5'-CCCGTTTGAGGTA1GGC-3'(FRAG. NO:1919) (SEQ. ID NO: 1932)
 5'-GCTCCBCCAATTCCCTTTTCTCC-3'(FRAG. NO:1920) (SEQ. ID NO: 1933)

C/EBPNucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments

- 30 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCC GGCC-3' (FRAG. NO:1921) (SEQ. ID NO: 1934)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCC GGC-3' (FRAG. NO:1922) (SEQ. ID NO: 1935)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCCGG-3' (FRAG. NO:1923) (SEQ. ID NO: 1936)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCCG-3' (FRAG. NO:1924) (SEQ. ID NO: 1937)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCC-3' (FRAG. NO:1925) (SEQ. ID NO: 1938)
 35 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCC-3' (FRAG. NO:1926) (SEQ. ID NO: 1939)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCC-3' (FRAG. NO:1927) (SEQ. ID NO: 1940)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGC-3' (FRAG. NO:1928) (SEQ. ID NO: 1941)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBG-3' (FRAG. NO:1929) (SEQ. ID NO: 1942)
 5'-GGGCCCCGCCCCGCGCCTTTTCTB-3' (FRAG. NO:1930) (SEQ. ID NO: 1943)
 40 5'-GGGCCCCGCCCCGCGCCTTTTCT-3' (FRAG. NO:1931) (SEQ. ID NO: 1942) 1944)
 5'-GGGCCCCGCCCCGCGCCTTTTC-3' (FRAG. NO:1932) (SEQ. ID NO: 1945)
 5'-GGGCCCCGCCCCGCGCCTTTT-3' (FRAG. NO:1933) (SEQ. ID NO: 1946)
 5'-GGGCCCCGCCCCGCGCCTTT-3' (FRAG. NO:1934) (SEQ. ID NO: 1947) [1945]
 5'-GGGCCCCGCCCCGCGCCTT-3' (FRAG. NO:1935) (SEQ. ID NO: 1948)
 45 5'-GGGCCCCGCCCCGCGCCT-3' (FRAG. NO:1936) (SEQ. ID NO: 1949)
 5'-GGGCCCCGCCCCGCGCC-3' (FRAG. NO:1937) (SEQ. ID NO: 1950)
 5'-GGGCCCCGCCCCGCGC-3' (FRAG. NO:1938) (SEQ. ID NO: 1951)
 5'-GGGCCCCGCCCCGCG-3' (FRAG. NO:1939) (SEQ. ID NO: 1952)
 5'-GGGCCCCGCCCCGCG-3' (FRAG. NO:1940) (SEQ. ID NO: 1953)
 50 5'-GGGCCCCGCCCCGCG-3' (FRAG. NO:1941) (SEQ. ID NO: 1954)
 5'-GGGCCCCGCCCCG-3' (FRAG. NO:1942) (SEQ. ID NO: 1955)
 5'-GGGCCCCGCCCC-3' (FRAG. NO:1943) (SEQ. ID NO: 1956)
 5'-GGGCCCCGCCCC-3' (FRAG. NO:1944) (SEQ. ID NO: 1957)
 5'-GGGCCCCGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1945) (SEQ. ID NO: 1958)
 55 5'-GCCCBGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1946) (SEQ. ID NO: 1959)
 5'-CCCBGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1947) (SEQ. ID NO: 1960)
 5'-CCBGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1961)
 5'-CBGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1962)
 5'-BGCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1950) (SEQ. ID NO: 1963)
 60 5'-GCCCCGCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1951) (SEQ. ID NO: 1964)

- 5'-CCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO: 1965)
 5'-CCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO: 1966)
 5'-CCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO: 1967)
 5'-CGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO: 1968)
 5'-GCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO: 1969)
 5'-CCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO: 1970)
 5'-CGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO: 1971)
 5'-GCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO: 1972)
 5'-CCTTTTCTBGCCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO: 1973)
 5'-CTTTTCTBGCCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO: 1974)
 5'-TTTCTBGCCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO: 1975)
 5'-TTTCTBGCCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO: 1976)
 5'-TTCTBGCCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO: 1977)
 5'-TCTBGCCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO: 1978)
 5'-CTBGCCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO: 1979)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1967) (SEQ. ID NO: 1980)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1968) (SEQ. ID NO: 1981)
 5'-GCGBGCTGTBCCTCGCTGGGC-3' (FRAG. NO:1969) (SEQ. ID NO: 1982)
 5'-GCGBGCTGTBCCTCGCTGGG-3' (FRAG. NO:1970) (SEQ. ID NO:1983)
 5'-GCGBGCTGTBCCTCGCTGG-3' (FRAG. NO:1971) (SEQ. ID NO:1984)
 5'-GCGBGCTGTBCCTCGCTG-3' (FRAG. NO:1972) (SEQ. ID NO:1985)
 5'-GCGBGCTGTBCCTCGCT-3' (FRAG. NO:1973) (SEQ. ID NO:1986)
 5'-GCGBGCTGTBCCTCGC-3' (FRAG. NO:1974) (SEQ. ID NO:1987)
 5'-GCGBGCTGTBCCTCG-3' (FRAG. NO:1975) (SEQ. ID NO:1988)
 5'-GCGBGCTGTBCCTC-3' (FRAG. NO:1976) (SEQ. ID NO:1989)
 5'-GCGBGCTGTBCCT-3' (FRAG. NO:1977) (SEQ. ID NO:1990)
 5'-GCGBGCTGTBCCT-3' (FRAG. NO:1978) (SEQ. ID NO:1991)
 5'-GCGBGCTGTBCCT-3' (FRAG. NO:1979) (SEQ. ID NO:1992)
 5'-GCGBGCTGTBC-3' (FRAG. NO:1980) (SEQ. ID NO:1993)
 5'-GCGBGCTGTCT-3' (FRAG. NO:1981) (SEQ. ID NO:1994)
 5'-GCGBGCTGT-3' (FRAG. NO:1982) (SEQ. ID NO:1995)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1983) (SEQ. ID NO:1996)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1984) (SEQ. ID NO:1997)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1985) (SEQ. ID NO:1998)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1986) (SEQ. ID NO:1999)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1987) (SEQ. ID NO:2000)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1988) (SEQ. ID NO:2001)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1989) (SEQ. ID NO:2002)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1990) (SEQ. ID NO:2003)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1991) (SEQ. ID NO:2004)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1992) (SEQ. ID NO:2005)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1993) (SEQ. ID NO:2006)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1994) (SEQ. ID NO:2007)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1995) (SEQ. ID NO:2008)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1996) (SEQ. ID NO:2009)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1997) (SEQ. ID NO:2010)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1998) (SEQ. ID NO:2011)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1999) (SEQ. ID NO:2012)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2000) (SEQ. ID NO:2013)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2001) (SEQ. ID NO:2014)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2002) (SEQ. ID NO:2015)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2003) (SEQ. ID NO:2016)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2004) (SEQ. ID NO:2017)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2005) (SEQ. ID NO:2018)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2006) (SEQ. ID NO:2019)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2007) (SEQ. ID NO:2020)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2008) (SEQ. ID NO:2021)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2009) (SEQ. ID NO:2022)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2010) (SEQ. ID NO:2023)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2011) (SEQ. ID NO:2024)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2012) (SEQ. ID NO:2025)
 5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:2013) (SEQ. ID NO:2026)

- 5'-GCGCGGCCGTCBT3G-3' (FRAG. NO:2014) (SEQ. ID NO:2027)
5'-GCGCGGCCGTCBT3-3' (FRAG. NO:2015) (SEQ. ID NO:2028)
5'-GCGCGGCCGTCBT-3' (FRAG. NO:2016) (SEQ. ID NO:2029)
5'-GCGCGGCCGTCB-3' (FRAG. NO:2017) (SEQ. ID NO:2030)
5 5'-GCGCGGCCGTC-3' (FRAG. NO:2018) (SEQ. ID NO:2031)
5'-GCGCGGCCGT-3' (FRAG. NO:2019) (SEQ. ID NO:2032)
5'-CGCGGCCGTCBTG3CGGCGTCGGGCCGGGC-3' (FRAG. NO:2020) (SEQ. ID NO:2033)
5'-GCGGCCGTCBTGG3GGCGTCGGGCCGGGC-3' (FRAG. NO:2021) (SEQ. ID NO:2034)
5'-CGGCCGTCBTGGC3GGCGTCGGGCCGGGC-3' (FRAG. NO:2022) (SEQ. ID NO:2035)
10 5'-GGCCGTCBTGGCG3CGTCGGGCCGGGC-3' (FRAG. NO:2023) (SEQ. ID NO:2036)
5'-GCCGTCBTGGCGG3GTCGGGCCGGGC-3' (FRAG. NO:2024) (SEQ. ID NO:2037)
5'-CCGTCBTGGCGGC3TCGGGCCGGGC-3' (FRAG. NO:2025) (SEQ. ID NO:2038)
5'-CGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2026) (SEQ. ID NO:2039)
5'-GTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2027) (SEQ. ID NO:2040)
15 5'-TCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2028) (SEQ. ID NO:2041)
5'-CBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2029) (SEQ. ID NO:2042)
5'-BTGGCGGCGTCGG3CCGGGC-3' (FRAG. NO:2030) (SEQ. ID NO:2043)
5'-TGGCGGCGTCGGG3CGGC-3' (FRAG. NO:2031) (SEQ. ID NO:2044)
5'-GGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2032) (SEQ. ID NO:2045)
20 5'-GCGGCGTCGGGCC3GGC-3' (FRAG. NO:2033) (SEQ. ID NO:2046)
5'-CGGCGTCGGGCC3GC-3' (FRAG. NO:2034) (SEQ. ID NO:2047)
5'-GGCGTCGGGCCGG3C-3' (FRAG. NO:2035) (SEQ. ID NO:2048)
5'-GCGTCGGGCCGGG3-3' (FRAG. NO:2036) (SEQ. ID NO:2049)
5'-CGTCGGGCCGGGC-3' (FRAG. NO:2037) (SEQ. ID NO:2050)
25 5'-GTCGGGCCGGGC-3' (FRAG. NO:2038) (SEQ. ID NO:2051)
5'-TCGGGCCGGGC-3' (FRAG. NO:2039) (SEQ. ID NO:2052)
5'-CGGCCGGGC-3' (FRAG. NO:2040) (SEQ. ID NO:2053)
5'-CCGCBGGCCBGGG3GCGCCGCCGGGCCGGCC-3' (FRAG. NO:2041) (SEQ. ID NO:2054)
5'-CCGCBGGCCBGGG3GCGCCGCCGGGCCGGCC-3' (FRAG. NO:2042) (SEQ. ID NO:2055)
30 5'-CCGCBGGCCBGGG3GCGCCGCCGGGCCGGCC-3' (FRAG. NO:2043) (SEQ. ID NO:2056)
5'-CCGCBGGCCBGGG3GCGCCGCCGGGCCGGG-3' (FRAG. NO:2044) (SEQ. ID NO:2057)
5'-CCGCBGGCCBGGG3GCGCCGCCGGGCCG-3' (FRAG. NO:2045) (SEQ. ID NO:2058)
5'-CCGCBGGCCBGGG3GCGCCGCCGGCCG-3' (FRAG. NO:2046) (SEQ. ID NO:2059)
5'-CCGCBGGCCBGGG3GCGCCGCCGCC-3' (FRAG. NO:2047) (SEQ. ID NO:2060)
35 5'-CCGCBGGCCBGGG3GCGCCGCCGGC-3' (FRAG. NO:2048) (SEQ. ID NO:2061)
5'-CCGCBGGCCBGGG3GCGCCGCCG-3' (FRAG. NO:2049) (SEQ. ID NO:2062)
5'-CCGCBGGCCBGGG3GCGCCGCC-3' (FRAG. NO:2050) (SEQ. ID NO:2063)
5'-CCGCBGGCCBGGG3GCGCCGC-3' (FRAG. NO:2051) (SEQ. ID NO:2064)
5'-CCGCBGGCCBGGG3GCGCCG-3' (FRAG. NO:2052) (SEQ. ID NO:2065)
40 5'-CCGCBGGCCBGGG3GCGCC-3' (FRAG. NO:2053) (SEQ. ID NO:2066)
5'-CCGCBGGCCBGGG3GCGC-3' (FRAG. NO:2054) (SEQ. ID NO:2067)
5'-CCGCBGGCCBGGG3GCG-3' (FRAG. NO:2055) (SEQ. ID NO:2068)
5'-CCGCBGGCCBGGG3GCG-3' (FRAG. NO:2056) (SEQ. ID NO:2069)
5'-CCGCBGGCCBGGG3GC-3' (FRAG. NO:2057) (SEQ. ID NO:2070)
45 5'-CCGCBGGCCBGGG3G-3' (FRAG. NO:2058) (SEQ. ID NO:2071)
5'-CCGCBGGCCBGGG3-3' (FRAG. NO:2059) (SEQ. ID NO:2072)
5'-CCGCBGGCCBGGG3' (FRAG. NO:2060) (SEQ. ID NO:2073)
5'-CCGCBGGCCBGG-3' (FRAG. NO:2061) (SEQ. ID NO:2074)
5'-CCGCBGGCCBG-3' (FRAG. NO:2062) (SEQ. ID NO:2075)
50 5'-CCGCBGGCCB-3' (FRAG. NO:2063) (SEQ. ID NO:2076)
5'-CCGCBGGCC-3' (FRAG. NO:2064) (SEQ. ID NO:2077)
5'-CGCBGGCCBGGGCGCGCCGCCGGGCCGGCCG-3' (FRAG. NO:2065) (SEQ. ID NO:2078)
5'-GCBGGCCBGGGCGCGCCGCCGGGCCGGCCG-3' (FRAG. NO:2066) (SEQ. ID NO:2079)
5'-CBGGCCBGGGCGCGCGCCGCCGGGCCG-3' (FRAG. NO:2067) (SEQ. ID NO:2080)
55 5'-BGGCCBGGGCGCGCGCCGCCGGGCCG-3' (FRAG. NO:2068) (SEQ. ID NO:2081)
5'-GGCCBGGGCGCGCGCGCCGCCGGGCCG-3' (FRAG. NO:2069) (SEQ. ID NO:2082)
5'-GCCBGGGCGCGCGCGCCGCCGGGCCG-3' (FRAG. NO:2070) (SEQ. ID NO:2083)
5'-CBGGGCGCGCGCGCGCCGCCGGGCCG-3' (FRAG. NO:2071) (SEQ. ID NO:2084)
5'-CBGGGCGCGCGCGCGCGCCGCCG-3' (FRAG. NO:2072) (SEQ. ID NO:2085)
60 5'-BGGGCGCGCGCGCGCGCCGCCG-3' (FRAG. NO:2073) (SEQ. ID NO:2086)
5'-GGGCGCGCGCGCGCGCGCCG-3' (FRAG. NO:2074) (SEQ. ID NO:2087)
5'-GGGCGCGCGCGCGCGCGCC-3' (FRAG. NO:2075) (SEQ. ID NO:2088)

5'-GCGCGCCGCGCCGGCCGCGCCG-3' (FRAG. NO:2076) (SEQ. ID NO:2089)
5'-CGCGCCGCGCCGGCCGCGCCG-3' (FRAG. NO:2077) (SEQ. ID NO:2090)
5'-GCGCGCCGCGCCGGCCGCGCCG-3' (FRAG. NO:2078) (SEQ. ID NO:2091)
5'-CGCGCCGCGCCGGCCGCGCCG-3' (FRAG. NO:2079) (SEQ. ID NO:2092)
5'-GCCGCGCGCCGGGCGCCG-3' (FRAG. NO:2080) (SEQ. ID NO:2093)
5'-CCGCGCGCCGGGCGCCG-3' (FRAG. NO:2081) (SEQ. ID NO:2094)
5'-CGCGCGCCGGGCGCC-3' (FRAG. NO:2082) (SEQ. ID NO:2095)
5'-GCGCGCCGGGCGCCG-3' (FRAG. NO:2083) (SEQ. ID NO:2096)
5'-CCGCGCGGGCGCC-3' (FRAG. NO:2084) (SEQ. ID NO:2097)
5'-CGCGCGGGCGCC-3' (FRAG. NO:2085) (SEQ. ID NO:2098)
5'-GGCGCGGCGCCG-3' (FRAG. NO:2086) (SEQ. ID NO:2099)
5'-GGGCGCBGGCTCC3CB-3' (FRAG. NO:2087) (SEQ. ID NO:2100)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2088) (SEQ. ID NO:2101)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2089) (SEQ. ID NO:2102)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGGCC-3' (FRAG. NO:2090) (SEQ. ID NO:2103)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGGCC-3' (FRAG. NO:2091) (SEQ. ID NO:2104)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGGC-3' (FRAG. NO:2092) (SEQ. ID NO:2105)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCGG-3' (FRAG. NO:2093) (SEQ. ID NO:2106)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCCCG-3' (FRAG. NO:2094) (SEQ. ID NO:2107)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGCC-3' (FRAG. NO:2095) (SEQ. ID NO:2108)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCGC-3' (FRAG. NO:2096) (SEQ. ID NO:2109)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCCG-3' (FRAG. NO:2097) (SEQ. ID NO:2110)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCCC-3' (FRAG. NO:2098) (SEQ. ID NO:2111)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCCC-3' (FRAG. NO:2099) (SEQ. ID NO:2112)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCC-3' (FRAG. NO:2100) (SEQ. ID NO:2113)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTGCC-3' (FRAG. NO:2101) (SEQ. ID NO:2114)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTTG-3' (FRAG. NO:2102) (SEQ. ID NO:2115)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCTT-3' (FRAG. NO:2103) (SEQ. ID NO:2116)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGCT-3' (FRAG. NO:2104) (SEQ. ID NO:2117)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGGC-3' (FRAG. NO:2105) (SEQ. ID NO:2118)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCGG-3' (FRAG. NO:2106) (SEQ. ID NO:2119)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCCCG-3' (FRAG. NO:2107) (SEQ. ID NO:2120)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCC-3' (FRAG. NO:2108) (SEQ. ID NO:2121)
5'-GGGCCCCCTGGCTC3GCCCCGCGGCC-3' (FRAG. NO:2109) (SEQ. ID NO:2122)
5'-GGGCCCCCTGGCTC3GCCCCGCGGC-3' (FRAG. NO:2110) (SEQ. ID NO:2123)
5'-GGGCCCCCTGGCTC3GCCCCCGG-3' (FRAG. NO:2111) (SEQ. ID NO:2124)
5'-GGGCCCCCTGGCTC3GCCCCG-3' (FRAG. NO:2112) (SEQ. ID NO:2125)
5'-GGGCCCCCTGGCTC3GCCCCC-3' (FRAG. NO:2113) (SEQ. ID NO:2126)
5'-GGGCCCCCTGGCTC3GCCCC-3' (FRAG. NO:2114) (SEQ. ID NO:2127)
5'-GGGCCCCCTGGCTC3GCCCC-3' (FRAG. NO:2115) (SEQ. ID NO:2128)
5'-GGGCCCCCTGGCTC3GCCC-3' (FRAG. NO:2116) (SEQ. ID NO:2129)
5'-GGGCCCCCTGGCTC3GCC-3' (FRAG. NO:2117) (SEQ. ID NO:2130)
5'-GGGCCCCCTGGCTC3GC-3' (FRAG. NO:2118) (SEQ. ID NO:2131)
5'-GGGCCCCCTGGCTC3G-3' (FRAG. NO:2119) (SEQ. ID NO:2132)
5'-GGGCCCCCTGGCTC3-3' (FRAG. NO:2120) (SEQ. ID NO:2133)
5'-GGGCCCCCTGGCTC-3' (FRAG. NO:2121) (SEQ. ID NO:2134)
5'-GGGCCCCCTGGCT-3' (FRAG. NO:2122) (SEQ. ID NO:2135)
5'-GGCCCCCTGGCTCG3CCCCGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2123) (SEQ. ID NO:2136)
5'-GCCCCCTGGCTCGGC3CCCGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2124) (SEQ. ID NO:2137)
5'-CCCTGGCTCGGCC3CGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2125) (SEQ. ID NO:2138)
5'-CCCTGGCTCGGCC3CGCGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2126) (SEQ. ID NO:2139)
5'-CTTGCTCGGCC3CGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2127) (SEQ. ID NO:2140)
5'-CTTGCTCGGCC3CGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2128) (SEQ. ID NO:2141)
5'-TGGCTCGGCC3CGGCCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2129) (SEQ. ID NO:2142)
5'-GGCTCGGCC3CGGC3GCCCCGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2130) (SEQ. ID NO:2143)
5'-GCTCGGCC3CGGC3CCCGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2131) (SEQ. ID NO:2144)
5'-CTCGGCC3CGGC3CGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2132) (SEQ. ID NO:2145)
5'-TCGGCCCCGCGGC3CGGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2133) (SEQ. ID NO:2146)
5'-CGGCCCCGCGGCC3GGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2134) (SEQ. ID NO:2147)
5'-GGCCCCGCGGCC3GCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2135) (SEQ. ID NO:2148)
5'-GCCCCGCGGCC3GGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2136) (SEQ. ID NO:2149)
5'-CCCCGCGGCC3GGCTTGCCCCGCCCGGCCG-3' (FRAG. NO:2137) (SEQ. ID NO:2150)

- 5'-CCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2138) (SEQ. ID NO:2151)
5'-CCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2139) (SEQ. ID NO:2152)
5'-CGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2140) (SEQ. ID NO:2153)
5'-GCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2141) (SEQ. ID NO:2154)
5'-CGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2142) (SEQ. ID NO:2155)
5'-GGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2143) (SEQ. ID NO:2156)
5'-GCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2144) (SEQ. ID NO:2157)
5'-CCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2145) (SEQ. ID NO:2158)
5'-CCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2146) (SEQ. ID NO:2159)
5'-CGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2147) (SEQ. ID NO:2160)
5'-GGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2148) (SEQ. ID NO:2161)
5'-GCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2149) (SEQ. ID NO:2162)
5'-CTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2150) (SEQ. ID NO:2163)
5'-TTGCCCGCCCGGCCCGG-3' (FRAG. NO:2151) (SEQ. ID NO:2164)
5'-TGCCCGCCCGGCCCGG-3' (FRAG. NO:2152) (SEQ. ID NO:2165)
5'-GCCCCCGGCCCGG-3' (FRAG. NO:2153) (SEQ. ID NO:2166)
5'-CCCGCCCGGCCCGG-3' (FRAG. NO:2154) (SEQ. ID NO:2167)
5'-CCGCCCGGCCCGG 3' (FRAG. NO:2155) (SEQ. ID NO:2168)
5'-CGCCCGGCCCGG-3' (FRAG. NO:2156) (SEQ. ID NO:2169)
5'-GCCCCCGGCCCGG-3' (FRAG. NO:2157) (SEQ. ID NO:2170)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2158) (SEQ. ID NO:2171)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2159) (SEQ. ID NO:2172)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGGGCC-3' (FRAG. NO:2160) (SEQ. ID NO:2173)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGGGC-3' (FRAG. NO:2161) (SEQ. ID NO:2174)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGGG-3' (FRAG. NO:2162) (SEQ. ID NO:2175)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBGG-3' (FRAG. NO:2163) (SEQ. ID NO:2176)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTBG-3' (FRAG. NO:2164) (SEQ. ID NO:2177)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCTB-3' (FRAG. NO:2165) (SEQ. ID NO:2178)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCCT-3' (FRAG. NO:2166) (SEQ. ID NO:2179)
5'-GGCGGGGGCGGCGCGCCTGGCTCGCC-3' (FRAG. NO:2167) (SEQ. ID NO:2180)
5'-GGCGGGGGCGGCGCGCCTGGCTCGC-3' (FRAG. NO:2168) (SEQ. ID NO:2181)
5'-GGCGGGGGCGGCGCGCCTGGCTCG-3' (FRAG. NO:2169) (SEQ. ID NO:2182)
5'-GGCGGGGGCGGCGCGCCTGGCTC-3' (FRAG. NO:2170) (SEQ. ID NO:2183)
5'-GGCGGGGGCGGCGCGCCTGGCT-3' (FRAG. NO:2171) (SEQ. ID NO:2184)
5'-GGCGGGGGCGGCGCGCCTGGC-3' (FRAG. NO:2172) (SEQ. ID NO:2185)
5'-GGCGGGGGCGGCGCGCCTGG-3' (FRAG. NO:2173) (SEQ. ID NO:2186)
5'-GGCGGGGGCGGCGCGCCTG-3' (FRAG. NO:2174) (SEQ. ID NO:2187)
5'-GGCGGGGGCGGCGCGCCT-3' (FRAG. NO:2175) (SEQ. ID NO:2188)
5'-GGCGGGGGCGGCGCGCC-3' (FRAG. NO:2176) (SEQ. ID NO:2189)
5'-GGCGGGGGCGGCGCGC-3' (FRAG. NO:2177) (SEQ. ID NO:2190)
5'-GGCGGGGGCGGCGCG-3' (FRAG. NO:2178) (SEQ. ID NO:2191)
5'-GGCGGGGGCGGCGG-3' (FRAG. NO:2179) (SEQ. ID NO:2192)
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2180) (SEQ. ID NO:2193)
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2181) (SEQ. ID NO:2194)
5'-GGCGGGGGCGGC-3' (FRAG. NO:2182) (SEQ. ID NO:2195)
5'-GGCGGGGGCGG-3' (FRAG. NO:2183) (SEQ. ID NO:2196)
5'-GCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2184) (SEQ. ID NO:2197)
5'-CGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2185) (SEQ. ID NO:2198)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2186) (SEQ. ID NO:2199)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2187) (SEQ. ID NO:2200)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2188) (SEQ. ID NO:2201)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2189) (SEQ. ID NO:2202)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2190) (SEQ. ID NO:2203)
5'-CGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2191) (SEQ. ID NO:2204)
5'-GGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2192) (SEQ. ID NO:2205)
5'-GCGGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2193) (SEQ. ID NO:2206)
5'-CGGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2194) (SEQ. ID NO:2207)
5'-GGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2195) (SEQ. ID NO:2208)
5'-GCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2196) (SEQ. ID NO:2209)
5'-CGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2197) (SEQ. ID NO:2210)
5'-GCCTGGCTCGCCTGGGCCCC-3' (FRAG. NO:2198) (SEQ. ID NO:2211)
5'-CCTGGCTCGCCTBCGGCCCC-3' (FRAG. NO:2199) (SEQ. ID NO:2212)

- 5'-CTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2200) (SEQ. ID NO:2213)
 5'-TGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2201) (SEQ. ID NO:2214)
 5'-GGCTCGCCTBGGGCCCC-3' (FRAG. NO:2202) (SEQ. ID NO:2215)
 5'-GCTCGCCTBGGGCCCC-3' (FRAG. NO:2203) (SEQ. ID NO:2216)
 5'-CTCGCCTBGGGCCCC-3' (FRAG. NO:2204) (SEQ. ID NO:2217)
 5'-TCGCCTBGGGCCCC-3' (FRAG. NO:2205) (SEQ. ID NO:2218)
 5'-CGCCTBGGGCCCC-3' (FRAG. NO:2206) (SEQ. ID NO:2219)
 5'-GCCTBGGGCCCC-3' (FRAG. NO:2207) (SEQ. ID NO:2220)
 5'-CCTBGGGCCCC-3' (FRAG. NO:2208) (SEQ. ID NO:2221)
 5'-CTBGGGCCCC-3' (FRAG. NO:2209) (SEQ. ID NO:2222)
 5'-GGGTGGCBCGGCAGCC-3' (FRAG. NO:2210) (SEQ. ID NO:2223)
 5'-GGTCGGCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2211) (SEQ. ID NO:2224)
 5'-GGTCGGCGBBGBGTCGTCTGTGG-3' (FRAG. NO:2212) (SEQ. ID NO:2225)
 5'-GGTCGGCGBBGBGTCGTCTGTG-3' (FRAG. NO:2213) (SEQ. ID NO:2226)
 5'-GGTCGGCGBBGBGTCGTCTGT-3' (FRAG. NO:2214) (SEQ. ID NO:2227)
 5'-GGTCGGCGBBGBGTCGTCTG-3' (FRAG. NO:2215) (SEQ. ID NO:2228)
 5'-GGTCGGCGBBGBGTCGTCTC-3' (FRAG. NO:2216) (SEQ. ID NO:2229)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2217) (SEQ. ID NO:2230)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2218) (SEQ. ID NO:2231)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2219) (SEQ. ID NO:2232)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2220) (SEQ. ID NO:2233)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2221) (SEQ. ID NO:2234)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2222) (SEQ. ID NO:2235)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2223) (SEQ. ID NO:2236)
 5'-GGTCGGCGBBGBGTCGTCT-3' (FRAG. NO:2224) (SEQ. ID NO:2237)
 5'-GTCGGCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2225) (SEQ. ID NO:2238)
 5'-TCGGCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2226) (SEQ. ID NO:2239)
 5'-CGGCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2227) (SEQ. ID NO:2240)
 5'-GGCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2228) (SEQ. ID NO:2241)
 5'-GCGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2229) (SEQ. ID NO:2242)
 5'-CGBBGBGTCGTCTGTGGC-3' (FRAG. NO:2230) (SEQ. ID NO:2243)
 5'-GBBGBGTCGTCTGTGGC-3' (FRAG. NO:2231) (SEQ. ID NO:2244)
 5'-BBBGBGTCGTCTGTGGC-3' (FRAG. NO:2232) (SEQ. ID NO:2245)
 5'-BGBGTCGTCTGTGGC-3' (FRAG. NO:2233) (SEQ. ID NO:2246)
 5'-GBGTCGTCTGTGGC-3' (FRAG. NO:2234) (SEQ. ID NO:2247)
 5'-BGTCGTCTGTGGC-3' (FRAG. NO:2235) (SEQ. ID NO:2248)
 5'-GTCGTCTGTGGC-3' (FRAG. NO:2236) (SEQ. ID NO:2249)
 5'-CTCGTCGTGGC-3' (FRAG. NO:2237) (SEQ. ID NO:2250)
 5'-TCGTCGTGGC-3' (FRAG. NO:2238) (SEQ. ID NO:2251)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2239) (SEQ. ID NO:2252)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2240) (SEQ. ID NO:2253)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2241) (SEQ. ID NO:2254)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2242) (SEQ. ID NO:2255)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2243) (SEQ. ID NO:2256)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2244) (SEQ. ID NO:2257)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2245) (SEQ. ID NO:2258)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2246) (SEQ. ID NO:2259)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2247) (SEQ. ID NO:2260)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2248) (SEQ. ID NO:2261)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2249) (SEQ. ID NO:2262)
 5'-GGGGCCCCGCGCCGCCCC-3' (FRAG. NO:2250) (SEQ. ID NO:2263)
 5'-CCCCGCGCCGCCCCGCCCC-3' (FRAG. NO:2251) (SEQ. ID NO:2264)
 5'-CCCCGCGCCGCCCCGCCCC-3' (FRAG. NO:2252) (SEQ. ID NO:2265)
 5'-CCGCGCCGCCCCGCCCC-3' (FRAG. NO:2253) (SEQ. ID NO:2266)
 5'-CGCGCCGCCCCGCCCC-3' (FRAG. NO:2254) (SEQ. ID NO:2267)
 5'-GCGCGCCGCCCCGCCCC-3' (FRAG. NO:2255) (SEQ. ID NO:2268)
 5'-CGCGCCGCCCCGCCCC-3' (FRAG. NO:2256) (SEQ. ID NO:2269)
 5'-GCGCGCCGCCCCGCCCC-3' (FRAG. NO:2257) (SEQ. ID NO:2270)
 5'-GGGGCGCGCGGGGCGCGGGG-3' (FRAG. NO:2258) (SEQ. ID NO:2271)
 5'-GGCGGGGCGCGGGGCGCGGGG-3' (FRAG. NO:2259) (SEQ. ID NO:2272)
 5'-GGCGGTCGCGCGTCGCCCCGCGCG-3' (FRAG. NO:2260) (SEQ. ID NO:2273)
 5'-GCGCGGCGCGCGTCGCGCGCG-3' (FRAG. NO:2261) (SEQ. ID NO:2274)

5'-GCGCBCGGGCCCCBCTGCGCGGGC-3' (FRAG. NO:2262) (SEQ. ID NO:2275)
 5'-GGGCGGGTGGGCTGCCCTGCGGCGGCC-3' (FRAG. NO:2263) (SEQ. ID NO:2276)
 5'-GGGCTGCTGCGCG3CGGCTCCGGCGA-3' (FRAG. NO:2264) (SEQ. ID NO:2277)
 5'-CTCCCGGGCGGGG3CGGGCGCGGG-3' (FRAG. NO:2265) (SEQ. ID NO:2278)
 5'-GGGCTGCCGCGGT3CGGGCCCCCTCTGCGGCG-3' (FRAG. NO:2266) (SEQ. ID NO:2279)
 5'-GCGCTCGCGCCGCTGCCG-3' (FRAG. NO:2267) (SEQ. ID NO:2280)
 5'-GCGCCGCTTGCC TGTGCGGCG-3' (FRAG. NO:2268) (SEQ. ID NO:2281)
 5'-GCTGCTCCBCGCGCTGG-3' (FRAG. NO:2269) (SEQ. ID NO:2282)
 5'-GCCGGBGGCCGGC3BGGTCCCGCG-3' (FRAG. NO:2270) (SEQ. ID NO:2283)
 5'-CCCGGCGGCCGGC3GGBBGGGCGGGCTGGG-3' (FRAG. NO:2271) (SEQ. ID NO:2284)
 5'-GTCTCTCCCGCCCCGGCCGCG-3' (FRAG. NO:2272) (SEQ. ID NO:2285)
 5'-GGGCGTCCGCTCCGGGCGGCTCGGG-3' (FRAG. NO:2273) (SEQ. ID NO:2286)
 5'-GCGGGCACGCGGC3GCTCTGGCGTCGCG-3' (FRAG. NO:2274) (SEQ. ID NO:2287)

Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

15	5'-GGTGBCBTTG	BGCBTGTCGG	CGCGTCCCG	TBBGBGTGG	GCCCGCCAGC	CCAGCCACTC	CACTTGGGGG
	CGGGTGGCCA	GCACGAACAG	CACCCAGAGG	AAGGGGGGCG	GCCGAGAAGG	GCAGCCCGCA	GGCCAGGATC
	AGGTCTGCTG	CGGC CGGAGA	TAATGGCATT	CACCACGCGG	CGGCCAGCG	CACGCCGCGC	ATCCGGCCCC
	GGTTCTGACC	TGCA GCCCCC	GTCTCCTTGG	CATTCTTGGG	CCCCAGTCAC	TCCTCTCCCT	GCCCCCCTTG
	CTGGGGCAGG	GAC3GGGTG	BCBTGTGBGC	TGTGCGGCGG	GTCCCGTTBB	GBGTGGGCC	GCCAGCCACG
20	CCACTCCACT	TGGG3GCGGG	TGGCCAGCAC	GAACAGCACC	CAGAGGAAGG	GGGGCGGCC	AGAAGGCGAG
	CCCGCAGGCC	AGGATCAGGT	CTGCTGCGGC	CGGAGATAAT	GGCATTACAC	ACGCGGCGGC	CCAGCGCACG
	CCGCGCATCC	GGCCCGGGTT	CTGACCTGCA	GCCCCCGTCT	CCTTGGCATT	CCTGGGCCCC	AGTCACTCCT
	CTCCCTGCCC	CCCTTGCTGG	GGCAGGGACG	GCCGTGTTGT	CBGTGGTGCT	GCCCCGTTGB	GGTBTGGCGC
	TCCBCCBBTT	CCCTTTTCTC	CTTGTITTC	GTTTCTCTTG	CCGTCTGTGG	TT CAGATTCACA	AACTGCAGGA
25	CTGGGCAGGG	AGCA GACAGT	GAGCAAACGC	CAGCAGGGCT	GCTGTGAATT	TGTGTAAGGA	TTGAGGGACA
	GTTGCTTTTC	AGCA TGGGCC	CAGGAATGCC	AAGGAGACAT	CTATGCACGA	CCTTGGGAAA	TGAGTTGATG
	TCTCCGGTAA	AACA CCGGAG	ACTAATTCCT	GCCCTGCCCA	ATTTTGCAGG	GAGCATGGCT	GTGAGGATGG
	GGTGAACCTA	CGCA CAGCCA	AGGACTCCAA	AATCACAACA	GCATTACTGT	TCTTATTTGC	TGCCACACCT
	GAGCCAGCCT	GCTCCTTCCC	AGGAGTGGAG	GAGGCCTGGG	GGGAGGGAGA	GGAGTGACTG	AGCTTCCCTC
30	CCGTGTGTTC	TCCGTCCTTG	CCCCAGCAAG	ACAACCTAGA	TCTCCAGGAG	AACTGCCATC	CAGCTTGGGT
	GCAATGGCTG	AGTCACAAAG	TGAGTTGTTG	CCCTGGGTTT	CTTTAATCTA	TTCAGCTAGA	ACTTTGAAGG
	ACAATTTCTT	GCATTAATAA	AGGTAAAGCC	CTGAGGGGTC	CCTGATAACA	ACCTGGAGAC	CAGGATTTTA
	TGGTCCCTCT	CACT3ATGGA	CAGGAGGTC	TGTGCCAAAG	AAGAATCCAA	TAAGCACATA	TTGAGCACTT
	GCTGTATATG	CAGTATTGAG	CACTGTAGGC	AAGACCCAAAG	AAAGAGAAGG	AGCCATCTCC	ATCTTGAAGG
35	AACTCAAAGA	CTCAAGTGGG	AACGACTGGG	CACTGCCACC	ACCAGAAAGC	TGTTGACGGA	GACGGTCGAG
	CAGGGTGCTG	TGGGTGATAT	GGACAGCAGA	AGGGGGAGAC	CAAGGTTCCA	GCTCAACCAA	TAAGTATTGC
	ACAACCACCT	GTCCCTGCCT	CAGTTCCTCT	TTATGTAACA	TGAAGTCGTT	GTGAGGGTTA	AAGGCAGTAA
	CAGGTATAAA	GTACTTAGAA	AAGCAAAGGG	TGCTACGTAC	ATGTGAGGCA	TCATTACGCA	GACGTAACTG
	GGATATGTTT	ACTATAAGGA	AAAGACACTG	AGGTCTAGAA	ATAGTCCCGT	GGAGCAGAAT	CAGTATTGGG
40	AGCCGGTGGC	GGTC TGAAGC	ACCACTGTCT	GGCACACAGT	AGGTGCTCAT	TGGCTCCCTT	CCACCTGTCA
	TTCCCAACCAC	CCTG AGGCC	CAACCGCAC	ACACAGCAGA	GCATTGAGAG	AGAAAGCCAT	GTCTTCAAAG
	TCTGATTTGT	GATG AGGCAG	AGGAAGATAT	TTCTAATCGG	TCTTGCCAG	AGGATCAGAG	TGCTGAGACC
	CCCCACCACC	AGCCGGTACC	TGGGAAGGGG	GAGAGTGCAG	GCCTGCTCAG	GGACTGTTCC	TGTCTCAGCA
	ACCAAGGGAT	TGTTCCTGTC	AATCAATGGT	TTATTGGAAG	GTGGCCAGT	ATGAGCCCTA	GAAGAGTGTG
45	AAAAGGAATG	GCA TGGGTG	TCACCATCGG	CAGTGCCAGG	GCAGCACTCA	TTCACTTGAT	AAATGAATAT
	TTATTAGCTG	GTTGGAGAGC	TAGAACCTGG	AGAGCTAGAA	CCTGGAGAAC	TAGAACCTGG	AGGGCTAGAA
	CCTGGAGAGG	CTAGAACCAA	GAAGGGCTAG	AACCTGGAGG	GGCTAGAACC	TAGAGAAGCT	AAAACCTGAG
	CTAGAAGCTG	GAGGACTAGA	ACCTGGAGGG	TGGAATCTG	AAGGGCTAGA	ACCTGGAGGG	CTGGAATCTG
	GAGAGCTAGA	ACCTGGAGGG	CTAGAACCTG	GAGGGCTAGA	ACCTAGAAGG	GCTAGAACCT	GGAGGGCTGG
50	AATCTGGAGA	GCTAGAACCT	GGAGGGCTAG	AACCTGGAGG	GCTAGAACCT	AGAAGGGCTA	GAACCTGGAG
	GGCTAGAACC	TGGCAGGTTA	GAACCTAGAA	GGGCTAGAAC	CTGGAGAGCC	AGAACCTGGA	GGGCTAGAAC
	CTGGAAGGGC	TAGAACCTGT	AGAGCTAGAA	CATGGAGAGC	TAGAACCCGG	CAGGCTAGAA	CCTGGCAAGC
	TAGAACCTGG	AGGGAATGAA	CCTGGAGGGC	TAGAACCTGG	AGAATGAGAA	AAATTTACAT	GGCAAAGAGC
	CCATAAATCC	TGACCAATCC	AACTCTGAAT	TTTAAAGCAA	AAGCGTGAAA	AAAAAGATTC	CCTCCTTACC
55	CCCAACCCAC	TCTTTTTC	CACCACCCAC	TCTCTCTG	CTCAGTAAGT	ATCTGGAGGA	AGAAAACAGG
	TGAAAGAAAG	AGT AAAACC	ATTAGTATT	AGTATTAGAA	TGAAGTCAAA	CTGTGCCACA	CATGGTGAAT
	GAAAAAAGAA	AAAAGAGGGC	TGTGTTTGT	CACACAGGGC	AGTCATTGAG	CACGAGAGCA	CGTATGGTGC
	TGAGACTCTC	TTAGGAGCAG	AGCTCTGCCG	CAATGGCCAT	GTGGGGATCC	ACACCTGGTC	TGAGGGGCAA
	CTGAGTCTGC	GGGAGAAGAG	CGGCCCTATG	CATGGTGTAG	ATGCCCTGAT	AAAGAACATC	TGTCTGTGA
60	AAGACTCAAT	GAGCTGTTAT	GTTGTAAACA	GGAAGCATTT	CACATCCAAA	CGAGAAAATC	ATGTAACAT
	GTGTCTTTTC	TGTAGAGCAT	AATAAATGGA	TGAGGTTTTT	GCAAAAAAAA	AAAAAAGAAA	AAATGATAGA

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 10 CTGAACTGAC CGTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT
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 15 TTACCTCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG GGAGTGATGT GAAACTTGAA
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 25 TGAGATATCC TCTGACCA TCATCCCTCC ACCCTGTTA GTTCTGCTCA CCCTCAGTGT TCTCATCAAT
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 25 GAGAGTGCAG GCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT
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 TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG
 GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA
 10 GGAAGGGTTT TAAAGCTTCA AAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGTCTCT ACCGTCTCAG
 CCCTGGGAGT GTAAGTGTCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC
 TTGACATGGG AGAAGCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAAAC
 CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA
 TCCCAGGACT CCGCTGCCC ACCTGGCCAC CCTCTGTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA
 15 TCCAAAATC AGACAAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG
 CAAATTTATT CACATGGGGC TTCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCAC
 GACTCCAACG GGCAGCCGG CCTACGCAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC
 AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT
 GGGCAGGAGT GCAGAGCTCA GCTGGAGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG
 20 CCCTTCAAAG ATGAGCTGTT CCCGCGGCCA TCCAGCTCT GGCTTCTGG CTCCGAGGAG GGGTGGGAC
 GGTGGTGACG GTGCGGACAT CAGGCTGCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC
 TCCGGAGAAG GTGCGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC
 CAGCACAGAG GGACGGAGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTCTGGGG AGTTGGGAAA
 AGTTCCCTTCTTCCGGAGG GAGG-3' (FRAG. NO:2275) (SEQ. ID NO:3018)
 25 5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT
 CAGAGGGCTT GTGCACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAACTCC
 AGATTAAGGA GCCCAATGT GGTGGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG
 AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCATAAAC
 TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGTTT GTAGGCTTGT
 30 TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC
 CCAGATCCAC TGGC CCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAATG
 TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT
 AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC
 TCCGAAGAAA CGGCAGCGTG TCTCAGGGGA GCGCAAAAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC
 35 ACTGTCGCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCTGCC ACCTGGCCAC
 CCTCTGTTA CACCTTCCG GTAAACGCCC ACTGTTTACA TCCAAAATC AGACACAAAA TAACCACCTC
 AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCAGGCC
 ACTTTGTGGT CAGCGGGGAG GGACGTTTTT GCCGTCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA
 CATGGAAATC TTCCAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
 40 CCGCAGCCTT CCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG
 AGGGGGAAGT GCCCAGGAG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCA
 CTCCAGCTCT GGCTCTGGG CTCCGAGGAG GGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC
 CGCAGTACCA GGGAGCGACT GAAGTGCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCC GGCAGGGGCT
 GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGG AGGCAGGCA
 45 GCGGGGAGAA GTTTCCTGT GGTCTGGGG AGTTGGGAAA AGTTCCCTTCTTCCGGAGG GAGG-3'
 (FRAG. NO:2275) (SEQ. ID NO:2461)
 5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
 CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG
 50 CTCCGGAGAA GGTCGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAAGTCTC
 CCAGCACAGA GGAAGGAGG GAGGGCAGGC AGCGGGGAGA AGTTCCCTG TGGTCGTGGG GAGTT-3' (FRAG.
 NO:2275) (SEQ. ID NO:2460)
 5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
 CGGTGGGGAC ATCAGGCTGC CCCGAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGAGA
 AGGTGGGTGC CCGCAGGGG CTGCTCCAGC CGCTCACCT CTGCTGGGAG GACAACTGT CCCAGCACAG
 55 AGGGAGGGAG GGAGGCGAGG CAGCGGGGAG AAGTTCCCT GTGGTCGTGG GAGATT-3' (FRAG. NO:2275) (SEQ. ID
 NO:2459)
 5'- ATGTTCTCTC CTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCAAC ACGGCCTCTT
 TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
 CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCTGTCTG
 60 GCCACCCTAG AGAAGCATCTT TGTCTCAGC GTCTTCTGCC TGACAAAGAG CAGCTGCACG GTGGCAGAGA
 TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCTGGC CTGCGGGCTG CCCTTCTGGG CCATACCAT
 CTCCAACAAC TTCGACTGCG TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC

CTGTACAGCA GCA¹CTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
 CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
 CCTGAGCTCA CCC²CTGCTGG TGTTCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTACCCGCT
 TGTGTCATCA GCT³CCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
 5 TGCTGCCCCT GAGTGTCTATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
 GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTTCATC
 ATCTGCTGGC TGCC⁴CTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
 GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
 CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
 10 TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTACAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
 TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
 GGCTGCTGTG AATTGTGTA AGGATTGAGG GACAGTTGCT T-3' (FRAG. NO:2275) (SEQ. ID NO:2458)
 5'- ATGTTCTCTC CTTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCACC ACGCCTCTT
 TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG ACCTTTGCC AGAGCAAATG
 15 CCCCCAAGTG GAG⁵GGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
 GCCACCCTAG AGA⁶CATCTT TGTCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
 TCTACCTGGG GAA⁷CTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT
 CTCCAACAAC TTCCACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
 CTGTACAGCA GCA⁸CTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
 20 CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
 CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTACCCGCT
 TGTGTCATCA GCT⁹CCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
 TGCTGCCCCT GAGTGTCTATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
 GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTTCATC
 25 ATCTGCTGGC TGCC¹⁰CTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
 GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT
 CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
 TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTACAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
 TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
 30 GGCTGCTGTG AATTGTGTA AGGATTGAGG GACAGTTGCT T-3' (FRAG. NO:2275) (SEQ. ID NO:2457)
 5'- TGATCCTATC AC¹¹AACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
 AAGTAACTTC CCCAGCTCAC ACGCTTATA AGTAAAGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG
 CTGCAAAGTC CCC¹²CCCTCC CTCGCCATCT GTATCTTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT
 ACGGAAATAC GATC CCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA
 35 CCGAGATGG AAT¹³CTCAGG TCTGGAATGA TATCATTTTT CTCTTTTAAT AAATTAACCT ACCCACCACA
 CGGCTTTGAG AGGT¹⁴TCAAAG GTGACCAACT CCTTGGGAG GGGCCCGGTT GATAAGGAAAG GATAGTGAAT
 CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGTCCAAC ACTTGAGATT GTTAGTGCTG TTGGTGGATA
 CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
 CTCTGTAAAG CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG
 40 GCTTCTCCTT GCCCTGGCTG GTTGCTCTTA ACCCCTGTCT CTTTCTGGAC CAGTTTTTGT CTTTCCCTTG
 TGACCTGAGG GGT¹⁵ACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTAATGTCA CCTTGCAAGG
 GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
 ATCCAGCCCC CTT¹⁶CTCTG GGTGCTGTTT GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT
 TCTGCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CTTGGGGAAC CTGGCCGAG CAGACCTGAT
 45 CCTGGCCTGC GGG¹⁷CTGCCCT TCTGGGCCAT CACCATCTCC AACAACCTCG ACTGGCTCTT TGGGGAGACG
 CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCTG ATGCTGGTGA
 GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA
 GCTCTACAGC TTGGTGATCT GGGGGTGATC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG
 AAGGAGTACA GCG¹⁸ATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG
 50 GTTTCACCA CATGCTCCTG AATGTCGTGG GCTTCTGTCT GCCCCTGAGT GTCATCACCT TCTGCACGAT
 GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC
 ACGGTGCTAG TCC¹⁹GGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTCCAGATC AGCACCTTCC
 TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
 GATCGCCTCC TTCA²⁰IGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
 55 TTCCGAAAGA AGTC²¹TTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC
 AGATGGAGAA CTCC²²ATGGGC AACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA
 CTGGGCAGGG AGC²³GACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA
 GTTGCTTTTC AGCA²⁴TGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGA
 TGTCTCCGGT AAAA²⁵ACCCGG AGACTAATTC TGCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT
 60 GGGGTGAAC CACC²⁶CACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT GCTGCCACAC
 CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT GAGCTTCCCT
 CCCGTGTGTT CTCC²⁷CTCCCT GCCCCAGCAA GACAACCTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG

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TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG
 ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT
 ATGGCTCCCC TCACGTATGG ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC
 TGTATATCAG TATTGAGCAC TGTAGGCA -3' (FRAG. NO:2275) (SEQ. ID NO:2456)

5 5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC
 CTTCTGGACC AGTTTGTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG
 CGCCGACATG CTCATGTCA CCTTGCAAGG GCCACTCTT AACGGGACCT TGCCCAGAG CAAATGCCCC
 CAAGTGGAGT GGC'GGGCTG GCTCAACACC ATCCAGCCCC CCTCCTCTG GGTGCTGTTC GTGCTGGCCA
 CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA
 10 ACTGGGGAAC CTG'CCGCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC
 CCAACTTTCG ACT'GCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT
 ACAGCAGCAT CTG'TTCTCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT
 GGGCCGGATG CGC'GCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGATC GCTGCTCTG
 AGCTCACCCA TGCTGGTGT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTC
 15 TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT
 GCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
 TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT
 GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA
 GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG TTGCCTCAAC
 20 CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GTGATGTGCC
 AGAAAGGGGG CTG'AGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC
 CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAAACGC CAGCAGGGCT
 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT
 CTATGCACGA CTTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCA
 25 ATTTTCAGG GAGCATGGCT GTGAGGATGG GGTGAATCA CGCACAGCCA AGGACTCAA AATCACAACA
 GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG
 GGCAGGGAGA GGA'GTGACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA
 TCTCCAGGAG AAC'GCCATC CAGCTTTGGT GCAATGGCTG AGTGACAAG TGAGTTGTTG CCCTGGGTTT
 CTTTAATCTA TTCACTAGTA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC
 30 CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA
 GAAGAATCCA ATA'GCACAT ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA
 GAAAGAGAAG GAG'CATCTC CATCTGAAG GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC
 ACCAGAAAGC TGTTGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC
 CAAGGTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTC TTCTGTAACA
 35 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC
 ATGTGAGGCA TCAT'ACGCA GACGTAACCTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'
 (FRAG. NO:2275) (SEQ. ID NO:2455)

5'- AAATGATAGA CAGTCAATAA TTTGTTAAAT GCTTTTAAAA ATGAATGCTT TAAGCCGGGT GCAGTGCTCTC
 ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT
 40 GGCCAACATG GCA'AACTC ACTCTCTACC AAAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG
 TGATCCAGC TACT'AGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC
 AAGATTACGC CATT'CTACT CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAATAA AAAAAAATAA
 AAAAAATTAC GCT'CAACA CAATGATCTCT CACCAGTGT GAATTTTCTT TCTATGAGCC CAGGAGGGCC
 TCTCAGAGAG GAA'GCTCCT AGGTCTTCTT TTCCCTCTGC AAACCTCCTG CCTTGAAGGT TCAGAAAGGAC
 45 TGTGCTGTCT CGTT'CATCC TTTGCAAGTG TCCAAACCT GATCCCAGCT GTGCTTAGGG GTTCTGCAA
 ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCTCT TTTACCAACT CAGCTTTTTG TTTTAGTGTG
 TTTGAATTCC CTGA'CTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG
 AAACCCAGGT GCCC'GGTGT GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC
 ACACACACAC ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC
 50 ATAGACCACA GCTITCCACA CCTTCTCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT GTGAAGTCCT
 GGAATGGAAA GAG'GGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA CAAGTCACCA CCAACCCATC
 TGCGCCTTGT TTAC'CTCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG GGAGTGATGT
 GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA
 GGGGCACAGA GGAG'GCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA
 55 CTGGAAATAC TCACATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCCTGT CTCCATCACA
 GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT GGGGTGCGAT
 CCCACCTGC CTGGAATTCT CCAAAGAACC TCCCTTTTAA CAGTTCCAGC CTTTAAACAGT TCCAGTCTAA
 ACACATGACC TTTC'ICCTCT AAATCAGCCC CCAATCTCTG CCTTGCAGG AGATGGAAGC CATGACACCT
 GCCTCGCCCC TGTC'CTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG TCAGTTTAC CCTCTAAACT
 60 CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG TCCTTGCTTC
 CACTTACCC CCAC'GCACT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
 CCAACCTGAC TGACATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT

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[illegible]

AAGTTCAAGG AGA¹CCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCATCA
 TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG
 CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGTGCCCTC
 AACCCTACTG TGT¹CGTGAT CGTGGGCAAG CGCTTCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT
 5 GCCAGAAAGG GGG¹TCGAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT
 CTCCGTGGAA CGCCAGATTC ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG
 GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA
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 CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA
 10 ACAGCATTAC TGTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT
 GGGGGCAGGG AGA³GAGTGA CTGAGCTTCC TCCCGTGTG TTCTCCGTCC CTGCCCCCAG AAGACAACCT
 AGATCTCCAG GAGA¹ACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG
 TTTCTTTAAT CTAT¹TCAGCT AGAACTTTGA AGGACAATTT CTTGCAATTA TAAAGGTTAA GCCCTGAGGG
 GTCCCTGATA ACA¹CCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA
 15 AAGAAGAATC CAA¹AAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG
 AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC
 ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA
 GCCAGGTTC AGTCAACAA TACTATTGCA CACCACCTGT CCTGCCCTC -3' (FRAG. NO:2275) (SEQ. ID NO:2454)
 5'- CAGATTTCACA A¹CTGCAGGA CTGGGCGAGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT
 20 TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA
 CCTTGGGAAA TGAC¹TTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGACAG
 GAGCATGGCT GTGA¹GGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT
 TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA
 GGAGTGACTG AGC¹TCCCTC CCGTGTGTTT TCCGTCCCTG CCCCAGCAAG ACACTTAGA TCTCCAGGAG
 25 AACTGCCATC CAG¹TTTGGT GCAATGGCTG AGTGACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA
 TTCAGTAGA ACT¹TGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA
 ACCTGGAGAC CAG¹ATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA
 TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG
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 30 TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA
 GCTCAACCAA TAA¹TATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT
 GTGAGGGTTA AAGC CAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA
 TCATTACGCA GACGTAAC¹TG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT
 GGAGCAGAAT CAG¹ATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT
 35 TGGTCCCTT CCAC¹TGTC TCCACCAC CCTGAGGCC CAACCGCCAC ACACACAGGA GCATTTGGAG
 AGAAGGCCAT GTC¹TCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCAG
 AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG
 GGA¹CTTCC TGTC¹CAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCAGT
 40 ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA
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 AAAGAACATC TGTCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAACA GGAAGCATTT CACATCCAAA
 55 CGAGAAAATC ATG¹AAACAT GTGCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAA
 AAAAAA -3' (FRAG. NO:2275) (SEQ. ID NO:2453)
 5'- GAGCTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT
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 60 AGATTAAGGA GCCCAATGT GGTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG
 AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC
 TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT
 TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC

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 20 TGTTACCAA CATCCTCCTG AATGTCTGG GCTTCTGTCT GCTTCTGAGT GCCCTGAGT GTCATCAGT TCTGCAGAT
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 TGTATATCAG TATTGAGCAC TGTAGGCA -3' (FRAG. NO:2275) (SEQ. ID NO:2447)
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 CCTGATAACA ACCTGAGAC CAGGATTTTA TGCTCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA

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(FRAG. NO:2275) (SEQ. ID NO:2446)							
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20	TGCGCCTTGT GAAACTTGAA GGGCACAGA CTGGAATAC GTGCTCCAGT CCCCACCTGC ACACATGACC	TTACTTCCTC GGGCGGTGAG GGAAGCCCTG TCAAGTGTGT CCAGACCCCT CTGGAATTCT TTCTTCCTCT	TGTGAGGCAA AGCAAGGGTG GGGTGAGAAC CTGTCTCCCT CCTCTGAGCT CCAAAGAAC AAATCAGCCC	GCACAGAGCC GGGAATGGAA TTGACAGCAC TATTAGGTTT CCAGACCCCTG TCCCCTTTAA CCCATCTCTG	CATGCCTGCG GGCCCTTGGG CTGTGAATTG AAAGTCCCTC CTGGACCCAA CAGTTCACAG CCTTTGCAGG	CCCCTGGATG AAAAAAGGCC AAGAGCCAA AAGACCCCTG CCAGCCCTAT CTTTAACAGT AGATGGAAGC	GGAGTGATGT CTTTCAACTA CCCGAAGGGA TCCAGTCTAA CATGACACCT CCTCTAAACT TCCTTGCTTC
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30	CCAACTGTTT TCTTTCAGGT CCCTGGAAG AAAACCTCTC AGAGGGGCTC GAAGTGAAGG CTTGGA	TCTCCCTGGA GAGTCAAGG CTCAACTCTC AGGTGTCCAA AGGGAGGAGA GAAAGAGAGT AAATATCTCC	AGATATCAAT GATTCTCTAG ATGCCCCGGA GTCCCTGTTG AGGGCACATT AAACATTAAA AACCATGGC	TTTCTGTCT TTCACTAGTT CAACAGTTGA GAATCTTGGG CCTGGTTGTT GTAAATACCC TGACATTTGG	AGGGGAGGTG GGCAGACACC AGGAACCATG AGCAGAGGGA ATATGTTTCT AGTGGATCAG TGGGAGATCA	GGCAGTCCG GGCAGACACC GTGATGTTAA ATGTTCTGTG ATCTATCCCA ACAGCAATGT GAACACCCTA	CACCAAGGCG CTGGAGAACT GCCCCAAGAC GTCTAGAGGA GATGAACTTG GCCAGATTGC AAGAGAGAAT
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45	CGCTTACTCC AACATACCAA CCTTCTTGTC CACCAGCCCC GCAATGCAAA TGCCACCATT GAATATCAAG	CTCACTCAAC CAGCTTCCCC CGGTAAAAAT CTCTCCAAGT CTCTGCTGTC GAGTTCTGTC CGCTTCTGTC	CTCTTGCTAC AGTTCTGTGC GCTTCTTATC CTTGCTCCCA CAACCCCCCT GCTCCCTCCA GGGCACCCCTC	TTCCCACCTC CTCTGCTCAG CTTCAAGAGC CAAGTGTGCT GCTGCTCCCA CAGCTCTAGA GCTCCCTCCA	TCTGTGCTCA GCTGTTCCCT GCTGCTGGTC GTCACCTCCA GGGCACCCCTC GGGCACCCCTC GGGCACCCCTC	CATCTAGTGT CTGCTGGTCT GTCACCTCCA GGGCACCCCTC GGGCACCCCTC GGGCACCCCTC GGGCACCCCTC	CACCTTCCAG CACTTGTCTC ACCCCTTACC CACCTCTGTC CACCTCTGTC CACCTCTGTC CACCTCTGTC
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 GGACTGTTC TGTCICAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCAGT
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 10 TTCACTTGAT AAATTAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC
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 25 CGAGAAAATC ATGTAACAT GTGCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAAA
 AAAAAAAAA-3' (FRAG. NO:2275) (SEQ. ID NO:2444)
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 30 AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC
 TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT
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 CCAGATCCAC TGGC CCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAATG
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 35 AGTAAGTCT TGAGCAAAAC TGAGAAAGCC AGCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC
 TCCGAAGAAA CGGC CGCGTG TCTCAGGGGA GCGCAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC
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 AAGAAGATAA ATAA TGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCAGGCC
 40 ACTTTGTGGT CAGC GGGGAG GGACGTTTTT GCCGTCCAC GACTCCAACG GGCAGCCGGG CTTACGCAAA
 CATGGAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
 CCGCAGCCTT CCCGCCCCA CAGCCAGCCT GGCTCCAGT GGGCAGGAGT GCAGAGCTCA CTTGGAGGCG
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 45 CTCCAGCTCT GGCTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC
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 GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA
 GCGGGGAGAA GTTCCCTGT GGTCGTGGG AGTTGGGAAA AGTTCCCTC CTCCGGAGG GAGG-3'
 (FRAG.NO:2275) (SEQ. ID NO:2443)
 5'- GCCCTTCAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGTGGGGA
 50 CGGTGGTGAC GGTGCGGACA TCAGGCTGCC CCGCAGTACC AGGGAGGAC TGAAGTGCCC ATGCCGCTTG
 CTCCGGAGAA GTTCGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACGTGTC
 CCAGCACAGA GGGA GGGAGG GAGGGCAGGC AGCGGGGAGA AGTTCCCTG TGGTCGTGGG GAGTT -3' (FRAG.
 NO:2275) (SEQ. ID NO:2442)
 5'- AAATGATAGA CCGTCAATAA TTGTAAAT GCTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCTC
 55 ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT
 GGCCAACATG GCAAAACCTC ACTCTTACC AAAAAACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG
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 60 TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TTCCCTCTGC AAACCTCCTG CCTTGAAGGT TCAGAAGGAC
 TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCT GATCCAGCT GTGCTTAGGG GTTCTGCAA
 ACCTTTTCCA GTTC TTAATT ACCTCCCACT TCATTCTCTG TTTACCAACT CAGCTTTTGG TTTTAGTGTG

[illegible]

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	GTTGATAAGG	AAGCAACGTG	AATCCTCCCA	TCACGGAAGC	TTCAAGGAGG	TCAAGGGTCC	AACACTTGAG
	ATTGTTAGTG	CTGTGGGTGG	ATACTGCCCA	AGGAAATATC	CCAGTGGAGC	CTCGAGATGA	AGAACATGAG
	GCCCCGTTT	AGAACCAAGG	ATCAGAGGGG	GCTCTGTAAG	ACCCAGGGGA	GTCAGGTGCA	CTGGAGCGCG
5	GGCATGCAGA	AAA ⁺ CAGCCTG	AGCTCCACCT	CGGCTTCTCC	TTGTCTTGGC	TGTTTGTCTT	TAACCCCTGT
	CTCCTTCTGG	ACCA ⁺ GTTTT	GTCTTTCCT	TGTGACCGCT	GAGGGGTAAC	AGCCTCTTTC	CACCTTCTTT
	CAGCGCCGAC	ATGC ⁺ TCAATG	TCACCTTGCA	AGGGCCCACT	CTTAAACGGGA	CCTTTGCCCA	GAGCAAAATGC
	CCCCAAGTGG	AGTGGCTGGG	CTGGCTCAAC	ACCATCCAGC	CCCCCTTCTT	CTGGGTGCTG	TTCTGTCTGG
	CCACCCTAGA	GAACATCTTT	GTCTCTAGCG	TCTTCTGCCT	GCACAAGAGC	AGCTGCACGG	TGGCAGAGAT
10	CTACCTGGGG	AAC ⁺ TGGCCG	CAGCAGACCT	GATCCTGGCC	TGCGGGCTGC	CCTTCTGGGC	CATCACCATC
	TCCAACAAC	TCA ⁺ CTGGCT	CTTTGGGGAG	ACGCTCTGCC	GCGTGGTGAA	TGCCATTATC	TCCATGAAC
	TGTACAGCAG	CAT ⁺ TGTTTC	CTGATGCTGG	TGAGCATCGA	CCGCTACCTG	GCCCTGGTGA	AAACCATGTC
	CATGGGCGCG	ATG ⁺ GCGGCG	TGCGCTGGGC	CAAGCTCTAC	AGCTTGGTGA	TCTGGGGGTG	TACGCTGCTC
	CTGAGCTCAC	CCATGCTGGT	GTTCCGGACC	ATGAAGGAGT	ACAGCGATGA	GGGCCACAAC	GTCAACCGCT
15	GTGTCTATC	CTAC ⁺ CCATCC	CTCATCTGGG	AAGTGTTCAC	CAACATGCTC	CTGAATGTCT	TGGGCTTCTT
	GCTGCCCTG	AGTG ⁺ TCATCA	CCTTCTGCAC	GATGCAGATC	ATGCAGGTGC	TGCGGAACAA	CGAGATGCAG
	AAGTTCAAGG	AGA ⁺ TCAGAC	GGAGAGGAGG	GCCACGGTGC	TAGTCTGGT	TGTGCTGCTG	CTATTTCATCA
	TCTGCTGGCT	GCCCTTCCAG	ATCAGCACCT	TCTGGATAC	GCTGCATCGC	CTCGGCATCC	TCTCCAGCTG
	CCAGGACGAG	CGC ⁺ ATCATCG	ATGTAATCAC	ACAGATCGCC	TCCTTCATGG	CCTACAGCAA	CAGCTGCCTC
20	AACCCACTGG	TGTACGTGAT	CGTGGGCAAG	CGCTTCCGAA	AGAAGTCTTG	GGAGGTGTAC	CAGGGAGTGT
	GCCAGAAAGG	GGG ⁺ CTGCAGG	TCAGAACCCA	TTCAGATGGA	GAACCTCCATG	GGCACACTGC	GGACCTCCAT
	CTCCGTGGAA	CGCCAGATTC	ACAAACTGCA	GGACTGGGCA	GGGAGCAGAC	AGTGAGCAAA	CGCCAGCAGG
	GCTGTGTGA	ATT ⁺ TGTAA	GGATTGAGGG	ACAGTTGCTT	TTGAGCATGG	GCCCAAGAA	GCCCAAGGAGA
	CATCTATGCA	CGAC ⁺ CTTGGG	AAATGAGTTG	ATGTCTCCGG	TAAACACCCG	GAGACTAATT	CTCGCCTGCT
25	CCAATTTTGC	AGGGAGCATG	GCTGTGAGGA	TGGGGTGAAC	TCACGCACAG	CCAAGGACTC	CAAAATCACA
	ACAGCATTAC	TGT ⁺ CTTATT	TGCTGCCACA	CCTGAGCCAG	CCTGCTCCTT	CCCAGGAGTG	GAGGAGGCCT
	GGGGGCAGGG	AGA ⁺ AGAGTGA	CTGAGCTTCC	CTCCCGTGTG	TTCTCCGTCC	CTGCCCCAGC	AAGACAACCT
	AGATCTCCAG	GAG ⁺ ACTGCC	ATCCAGCTTT	GGTGCAATGG	CTGAGTGCAC	AAGTGAGTTG	TTGCCCTGGG
	TTTCTTTAAT	CTAT ⁺ TCAGCT	AGAACTTTGA	AGGACAATTT	CTTGCAATTA	TAAAGGTTAA	GCCCTGAGGG
30	GTCCCTGATA	ACA ⁺ CTTGGG	GACCAAGGAT	TTATGGCTCC	CCTCATGAT	GGACAAGGAG	GTCTGTGCCA
	AAGAAAGAA	CAAT ⁺ AAGCAC	ATATTGAGCA	CTTGCTGTAT	ATGCAGTATT	GAGCACTGTA	GGCAAGAGGG
	AAGAAAAGAGA	AGG ⁺ AGCCATC	TCCATCTTGA	AGGAACTCAA	AGACTCAAAGT	GGGAACGACT	GGGCACTGCC
	ACCACCAGAA	AGCT ⁺ GTTCTGA	TGAGACGGTC	GAGCAGGGTG	CTGTGGGTGA	TATGGACAGC	AGAAGGGGGA
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	TGTGTAAGGA	TTGAGGGACA	GTTGCTTTTC	AGCATGGGCC	CAGGAATGCC	AAGGAGACAT	CTATGCACGA
	CCTTGGGAAA	TGAC ⁺ TTGATG	TCTCCGGTAA	AACACCGGAG	ACTAATTCTT	GCCCTGCCCA	ATTTTGCAGG
	GAGCATGGCT	GTG ⁺ AGATGG	GGTGAACCTA	CGCACAGCCA	AGGACTCCAA	AATCACAACA	GCATTACTGT
	TCTTATTTGC	TGCCAACCTT	GAGCGACCTT	GCTCCTTCCC	AGGAGTGGAG	GAGGCTTGGG	GGGAGGGAGA
40	GGAGTGACTG	AGC ⁺ CTCCCTC	CCGTGTGTTT	TCCGTCCCTG	CCCCAGCAAG	ACAACCTAGA	TCTCCAGGAG
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	TTCAGCTAGA	ACT ⁺ TGAAGG	ACAATTTCTT	GCATTAATAA	AGGTAAAGCC	CTGAGGGGTC	CCTGATAACA
	ACCTGGAGAC	CAG ⁺ ATTTTA	TGGCTCCCTT	CACTGATGGA	CAAGGAGGTC	TGTGCCAAAG	AAGAATCCAA
	TAAGCATATA	TTGAGCACTT	GCTGTATATG	CAGTATTGAG	CACTGTAGGC	AAGACCCAA	AAAGAGAAGG
45	AGCCACTCTC	ATCT ⁺ TGAAGG	AACTCAAAAG	CTCAAGTGGG	AACGACTGGG	CAGTCCCAAC	ACCAAGAAAG
	TGTTTCGACGA	GACG ⁺ GTCGAG	CAGGGTGTCT	TGGGTGATAT	GGACAGCAGA	AGGGGGAGAC	CAAGGTTCCA
	GCTCAACCAA	TAACTATTGC	ACAACCACCT	GTCCTGCTCT	CAGTTCCTTT	TTATGTAACA	TGAAGTCGTT
	GTGAGGGTTA	AAG ⁺ CAAGTAA	CAGGTATAAA	GTACTTAGAA	AAGCAAAGGG	TGCTACGTAC	ATGTGAGGCA
	TCATTACGCA	GACC ⁺ TAA					

CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA
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 10 AAAAAAAAA -3' (FRAG. NO:) (SEQ. ID NO:2431)
 5'-GGTGBCBTTGBGCBTGTGCGGCGC-3' (FRAG. NO:2276) (SEQ. ID NO:2289)
 5'-GGTCCCGTTBBGBGTGGGCC-3' (FRAG. NO:2277) (SEQ. ID NO:2290)
 5'-GCCAGCCAGCCA(TCCACTTGGGGC-3' (FRAG. NO:2278) (SEQ. ID NO:2291)
 5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGC-3' (FRAG. NO:2279) (SEQ. ID NO:2292)
 15 5'-GGCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3'(FRAG.NO:2280)(SEQ.ID NO:2293)
 5'-GGAGATAATGGCA(TCACACGCGGC-3' (FRAG. NO:2281) (SEQ. ID NO:2294)
 5'-GGCCAGCGCACG(CGCGCATCCGGCC-3' (FRAG. NO:2282) (SEQ. ID NO:2295)
 5'-GGTTCTGACCTG(AGCCCC-3' (FRAG. NO:2283) (SEQ. ID NO:2296)
 5'-GTCTCCTTGGCATTCTGGGGCC-3' (FRAG. NO:2284) (SEQ. ID NO:2297)
 20 5'-CAGTCACTCCTCTCCCTGCCCC-3' (FRAG. NO:2285) (SEQ. ID NO:2298)
 5'-CTTGCTGGGGCAGGACGG-3' (FRAG. NO:2286) (SEQ. ID NO:2299)
 5'-GGTGBCBTTGBGCE TGTGCGGC-3' (FRAG. NO:2287) (SEQ. ID NO:2300)
 5'-GGTCCCGTTBBGBC TGGGCC-3' (FRAG. NO:2288) (SEQ. ID NO:2301)
 5'-GCCAGCCAGCCA(TCCACTTGGGGC-3' (FRAG. NO:2289) (SEQ. ID NO:2302)
 25 5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGC-3' (FRAG. NO:2290) (SEQ. ID NO:2303)
 5'-GGCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3'(FRAG.NO:2291)(SEQ.ID NO:2304)
 5'-GGAGATAATGGCA(TCACACGCGGC-3' (FRAG. NO:2292) (SEQ. ID NO:2305)
 5'-GGCCAGCGCACG(CGCGCATCCGGCC-3' (FRAG. NO:2293) (SEQ. ID NO:2306)
 5'-GGTTCTGACCTG(AGCCCC-3' (FRAG. NO:2294) (SEQ. ID NO:2307)
 30 5'-GTCTCCTTGGCATTCTGGGGCC-3' (FRAG. NO:2295) (SEQ. ID NO:2308)
 5'-CAGTCACTCCTCTCCCTGCCCC-3' (FRAG. NO:2296) (SEQ. ID NO:2309)
 5'-CTTGCTGGGGCAGGACGG-3' (FRAG. NO:2297) (SEQ. ID NO:2310)
 5'-CCGTGTTGTGCBGTGGTGCTG-3' (FRAG. NO:2298) (SEQ. ID NO:2311)
 5'-CCCGTTGBGGBTGGC-3' (FRAG. NO:2299) (SEQ. ID NO:2312)
 35 5'-GCTCCBCCBTTCCTTTCTCC-3' (FRAG. NO:2300) (SEQ. ID NO:2313)
 5'-TTGTTTTCCGTTTCTTG-3' (FRAG. NO:2301) (SEQ. ID NO:2314)
 5'-CCGTCTGTGGTT-3' (FRAG. NO:2302) (SEQ. ID NO:2315)

β2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments

5'- GCCGCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
 40 AGAGCAAGGC CACGCGGCC GCGCGGCCA GCAAGAAGAT ACTGCTGCC GAGCCAGCA TCCGCACTGT
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 45 CTGGGGAAGA AGCAGGTGCC TCCGATCTC TTCCAGCCAT ACATCGAAGA GATTGTCAA AACCTCCGAG
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 55 ACAGCAGTGC CGACTGGTTC TCTCTGGGT GCATGCTCTT CAAGTTGCTG CGGGGGCACA GCCCCTCCG
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 CTTGCAGAAG TACCTCCCC CGTGATCCC CCCACAGGGG GAGGTGAACG CGGCCGACGC CTTGACATT
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[illegible]

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 5 CTGTGATCTG AGGTCATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG
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 10 CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCGCGAGTC TGGTTCGGGG TCAGATTCCG CGCGGCCCTCC
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 15 CCGGGCCGGG CCGAGCGGCC AGCGAGCAGG AGCGGCGGCC GCGGCGGGCG CGGCGGGAGG AGGCAGCGCC
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 NO:) (SEQ. ID NO:24:9)
 5'-GCCGCCGCGG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
 20 AGAGCAAGGC CACGCCGCCG GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC GAGCCCAGCA TCCGCAGTGT
 CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAAGATCT TTCCCAGAA GCTGGGGTAC
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 TCAAGAAGTA CGACAAAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA
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 30 ATTCATTGTC TGCAITGCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCTGGA CCTCATGAAC
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 35 ACAGCAGTGC CGACTGGTTC TCTTGGGTG TCTGCTCTT CAAGTTGCTG CGGGGGCACA GCTCCCTCCG
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 TCCTTCTCCC CTGAACACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT
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 40 GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT
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 GACAGCCGGT CTGCAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG
 GGCAAGGACT GCACTATGCA TGGTACATG TCCAAGTGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
 GGTACTTCTA CTTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCGCAGA GCCTGCTGAC
 45 CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC
 GGTGGGAAAC AGTTCATTTT GCAGTGCAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGTGCAGC
 ACGCCTACCG CGACGCCAG CAGCTGGTGC AGCGGTGCC CAAGATGAAG AACAGCCGC GCTCGCCCGT
 GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TGTGACCCGC CCACCCGCT-3'
 (FRAG. NO:) (SEQ. ID NO:2428)

50 CCR-2 CC Chemoline Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT
 GATGGATTAT ACCTTGACC TCAGTGTGAC AACAGTGACC GACTACTACT ACCCTGATAT CTTCTCAAGC
 CCCTGTGATG CGGAACCTTAT TCAGACAAAT GGCAAGTTGC TCCTTGCTGT CTTTATTGTC CTCCTGTTG
 TATTAGTCT TCTGAGAAAC AGCCTGGTCA TCCTGGTCTT TGTGGTCTGC AAGAAGCTGA GGAGCATCAC
 55 AGATGTATAC CTCCTGAACC TGGCCCTGTC TGACCTGCTT TTTGTCTTCT CTTCCCTTAT TCAGACCTAC
 TATCTGCTGG ACCAGTGGGT GTTGGGAGT GTAATGTGCA AAGTGGTGTG TGGCTTTTAT TACATTGGCT
 TCTACAGCAG CATCTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG GCTGTGTGCC ATGCCGTGTA
 TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCCTGGCAG TATGGCTAAC CGCCATTATG
 GCTACCATCC CATGCTAGT GTTTTACCAA GTGGCCTCTG AAGATGGTGT TCTACAGTGT TATTATTTT
 60 ACAATCAACA GACTTGAAG TGGAAGATCT TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTGATCCC
 ATTCACCATC TTATGTTCT GCTACATTAA AATCCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG

ACCAAGGCCA TCAAGTTGGT GCTCATTGTG GTCATTGCAT CTTTACTTTT CTGGGTCCCA TTCAACGTGG
 TTCTTTTCCT CACT`CCTTG CACAGTATGC ACATCTTGGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA
 TGCCACCCAT GTC`CAGAAA TCATTTCCTT TACTCACTGC TGTGTGAACC CTGTTATCTA TGCTTTTGTT
 GGGGAGAAGT TCA`GAAACA CCTCTCAGAA ATATTTTCAGA AAAGTTGCAG CCAAATCTTC AACTACCTAG
 5 GAAGACAAAT GCC`AGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCTCCC GTTCTCCAG
 CGTAGACTAC ATTTTGTGAG GATCAATGAA GACTAAATAT AAAAAACATT TTCTGAATG GCATGCTAGT
 AGCAGTGAGC AAAGGTGTGG GTGTGAAAGG TTTCCAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT
 GTTGCCACA CTTGGAACAC AATGACTGGA GACATAGTTG TGCATGCCTG GCACAACATC AAGCCTGTGA
 TTGTGTTTAT TGATGATGTT GAACAAGTGG TGGCTTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAGA
 10 TGTCTCCGGA ATTCGACAGG TTATCA-3' (FRAG. NO:_) (SEQ. ID NO:2462)

CCR-4 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-TTTCATCTCT CCCGGCTTAT TTGCTGGTTT CTCCGAATGC GGGCCTTGTC TGGTTCACGC TGGATCCCCA
 ACGCCTAGAA CAGT`GCGTGG CACGCAGTTC GTCCTTCTAT AAATATCGGA CTAAATGCAT CTCTGTGATG
 GTAATACCCA CACCGTGTG TGAGAATGAA TGAGTGATTC TGTGCAAGTT CTAGTGATC TGTTACAAAA
 15 AGTACTGGTC GCTAAATTAC TCTATAATA AAGCATACTT TTAGGATAAT AAAGCACTAT TCGCGAATTG
 GTTACCCTA TTATGAAATT ACTGAGCAAT ACATATCTAC ATCTGATCAG TCTCCAGAAT TATGCCAAAT
 CCTACCTCT TCTG`AAAGTA TCTCCTAATT ATCTGCACCT GACCCTAGTG ATGCTGTGAA TGTGCAAGTA
 TAGCTACATC CTCCGAAGGA AGGATCTTTA CTCCTTTTAC CTCCTGAATG GGCTGCGTCT GAGGGAAGCG
 CGGGGGAATG GGC`GTTGGA AGCTTGGCCC TACTTCCAGC ATTGCCGCCT ACTGGTTGGG TTACTCCAGC
 20 AAGTCACTCC CCTTCCCTGG GCCTCAGTGT CTCTACTGTA GCATTCCCAG GTCTGGAATT CCATCCACTT
 TAGCAAGGAT GGAC`GCGCCA CAGAGAGACG CGTTCCTAGC CCGCGCTTCC CACCTGTCTT CAGGCGCATC
 CCGCTTCCT CAAACTTAGG AAATGCCTCT GGGAGGTCTT GTCCGGCTCC GGACTCACTA CCGACCACCC
 GCAAACAGCA GGG`CCCCTG GGCTTCCCAA GCCGCGCACC TCTCCGCCCC GCCCCTGCGC CCTCCTTCT
 CGCGTCTGCC CCTTCCCCC ACCCGCCTT CTCCTCCCC GCCCCAGCGG CGCATGCGCC GCGCTCGGAG
 25 CGTGTTTTAA TAAAGTCCG GCCGCGGCA GAAACTTCAG TTTGTTGGCT GCGGCAGCAG GTAGCAAAGT
 GACGCCGAGG GGC`GAGTGC TCCAGTAGCC ACCGCATCTG GAGAACCAGC GGTACCATG GAGGGGATCA
 GTGTAAGTCC AGTITCAACC TGCTTTGTCA TAAATGTACA AACGTTTGAA CTTAGAGCGC AGCCCCCTC
 CGAGCGGGCA GAA`GCGCCA GGACATTGGA GGTACCCGTA CTCCAAAAA GGGTCACCGA AAGGAGTTTT
 CTTGACCATG CCTATATAGT GCGGGTGGGT GGGGGGGGAG CAGGATTGGA ATCTTTTCT CTGTGAGTCG
 30 AGGAGAAACG ACTG`GAAAGA GCGTTCCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC CGCGCGCGGC
 GGCTTGACG CTGTITGCAA ACGTAAGAAC ATTCTGTGCA CAAGTGCAAG GAAGGCGTGC GCGCTGCCTC
 GGGACTCAGA CCAC`CGGTCT CTCTCTTGGG GAAGCGGGGA TGTCTTGGAG CGAGTTACAT TGTCTGAATT
 TAGAGCGGGA GGC`GCGGTG CCTGGGCTGA TCTCCAGGA GGAGATTGCG CCCGCTTAA CTTCGGGGTT
 AAGCGCCTGG TGAC`TGTCTT TGACACTGGG TGCGTGTGTT TTAAGCTCTG TGCGGCCGAC GGAGCTGTGC
 35 CAGTCTCCCA GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA
 TCGAGTGGTG GCAC`CAGCTA GGAGTTGATC CGCCCGCGCG CTTTGGGTTT GAGGGGAAA CCTTCCCGCC
 GTCCGAAGCG CGC`TCTTCC CCACGGCCGC GAGTGGGTCC TGCAGTTCGA GAGTTTGGGG TCGTGACAGAG
 GTCAGCGGAG TGG`TTGACC TCCCTTTTGA CACCGCGCAG CTGCCAGCCC TGAGATTGTC GTCCGGGGGA
 TAGGAGCGGG TACC`GGGTGA GGGGCGGGGG CGGTTAAGAC CGCACCTGGG CTGCCAGGTC GCCGCCGCGA
 40 AGACTCCGAG GTG`CAAGTGG GGAACCCGTT TGGCTCTCTC CGAGTCCAGT TGTGATGTT AACCGTCGGT
 GGTTTCCAGA AAC`TTTTGA AACCTCTTG CTAGGAGATT TTTGGTTTCC TGCAGCGCGC GCACCTTCAA
 AGACGCTCGC GGCC`GAGCCG CCCAGTCGCT CCCCAGACC CTGTGGGACA GAGCCTGGCG TGTGCCCCAG
 CGGAGCCCT GCAC`CGCTGC TTGCGGGCGG TTGGCGTGGG TGTAAGTGGG AGCCGCGCGG GCCCGGGGCT
 GGACGACCCG GCC`CCCAGC TGCCACCGC CTGGAGGCTT CCAGCTGCCC ACCTCCGGCC GGGTTAACTG
 45 GATCAGTGGC GGGG`TAATGG GAAGCCACCC GGGAGAGTGA GGAAATGAAA CTGGGGCGA GGACCACGGG
 TGCAGACCCC GTTACCTTCT CCACCCAGGA AAATGCCCG CTCCTAACG TCCCAAACGC GCCAAGTGAT
 AAACACGAGG ATG`CAAGAG ACCCACACAC CGGAGGAGCG CCCGCTTGGG GGAGGAGGTG CCGTTTGTTC
 ATTTCTGAC ACT`CCGCC AATATACCC AAGCACCGAA GGGCCTTCGT TTAAAGACCG CATTCTCTTT
 ACCCACTACA AGTIGCTTGA AGCCCAAGAT GGTTTGTATT TAGGCAGGCG TGGGAAAATT AAGTTTTTGC
 50 GCTTTAGGAG AATG`AGTCTT TGCAACGCCC CCGCCCTCCC CCGTGATCC TCCCTTCTCC CCTCTTCCCT
 CCCTGGGCGA AAA`CTTCTT AAAAAAGTT AATCACTGCC CCTCCTAGCA GCACCCACCC CACCCCCAC
 GCCGCCTGGG AGT`GGCTCT TTGTGTGTAT TTTTTTTTCT CTCCTAAGGA AGGTTTTTTT TCTTCCCTCT
 AGTGGGCGGG GCAG`AGGAGT TAGCCAAGAT GTGACTTTGA AACCTCAGC GTCTCAGTGC CCTTTTGTTC
 TAAACAAAGA ATTITGTAAT TGGTTCTACC AAAGAAGGAT ATAATGAAGT CACTATGGGA AAAGATGGGG
 55 AGGAGAGTTG TAGGATTCTA CATTAAATCT CTGTGCCCCT TAGCCCACTA CTTCAGAAAT TCCTGAAGAA
 AGCAAGCCTG AAT`GGTTTT TTAAATTGCT TTTAAACTG TTTTAACTG GGTAAATGCT TGTGAATTG
 GAAGTGAATG TCC`TTCTT TGCTCTTTT GCAGATATAC ACTTCAGATA ACTACACCGA GGAATGGGC
 TCAGGGGACT ATG`CTCCAT GAAGGAACCC TGTTTCCGTG AAGAAAATGC TAATTTCAAT AAAATCTTCC
 TGCCACCAT CTACTCCATC ATCTTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGGG
 60 TTACCAGAAG AA`CTGAGAA GCATGACGGA CAAGTACAGG CTGCACCTGT CAGTGGCCGA CCTCCTCTTT
 GTCATCACGC TTCC`TCTG GGCAGTTGAT GCCGTGGCAA ACTGGTACTT TGGGAACCTC CTATGCAAGG

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CAGTCCATGT CATCTACACA GTCAACCTCT ACAGCAGTGT CCTCATCCTG GCCTTCATCA GTCTGGACCG
 CTACCTGGCC ATCGTCCACG CCACCAACAG TCAGAGGCCA AGGAAGCTGT TGGCTGAAAA GGTGGTCTAT
 GTTGGCGTCT GGAATCCCTGC CCTCCTGCTG ACTATTCCCG ACTTCATCTT TGCCAACGTC AGTGAGGCAG
 5 ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGTT GTGTTCCAGT TTCAGCACAT
 CATGGTTGGC CTTATCTCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC CAAGCTGTCA
 CACTCCAAGG GCCACAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCCT CATCCTGGCT TTCTTCGCTT
 GTTGGCTGCC TTACTACATT GGGATCAGCA TCGACTCCTT CATCCTCCTG GAAATCATCA AGCAAGGGTG
 TGAGTTTGAG AACACTGTGC ACAAGTGGAT TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTTGTCTG
 10 AACCCCATCC TCTATGCTTT CCTTGGAGCC AAATTTAAAA CCTCTGCCCA GCACGCACTC ACCTCTGTGA
 GCAGAGGGTC CAGCTCAAG ATCCTCTCCA AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC
 TGAGTCTTCA AGTITTCCT CCAGCTAACA CAGATGTAAA AGACTTTTTT TTATACGATA AATAACTTTT
 TTTTAAGTTA CACA TTTTTC AGATATAAAA GACTGACCAA TATTGTACAG TTTTATTGCT TTGTTGGATT
 TTTGTCTTGT GTTTCTTAG TTTTGTGAA GTTTAATTGA CTATTTTATA TAAATTTTTT TTGTTTCATA
 TTGATGTGTG TCTAGGCAGG ACCTGTGGCC AAGTCTTAG TTGCTGTATG TCTCGTGGTA GGACTGTAGA
 15 AAAGGGAAGT GAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG
 CATAGATAAT CTCCTCATTC CCGTGAACG TTTTCTCTGT TCTTAAGACG TGATTTTGCT GTAGAAGATG
 GCACTTATAA CCAAGGCCA AAGTGGTATA GAAATGCTGG TTTTTCAGTT TTCAGGAGTG GGTTGATTTC
 AGCACCTACA GTGTACAGTC TTGTATTAAG TTGTTAATAA AAGTACATGT TAAACTTACT TAGTGTATG
 TTCTGATTTT TGTTTACATT CTTTGGCTA GTAGAAGACA AAAGTAATAC ATTTATGGTA TGCAAAGCAC
 20 TATCCTAGGT ATTICATTGT AATATTTTAC TTACCCCTTA TCACAACCTC GATAGATTCT GCTTCTGTTA
 CTAATTACAT TTTATAGAA AGGAAACGGA GGACAGAAA GCCTAAGTAA CTTGGTTAAA GGCATGTAGT
 AAGTATCAAA TCCGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT
 TCAATGGA GTTAGAAAT GGCCAGCCAG CACCTATTG TATGAAAGGT CATCTTTCAG AGGATAAGCA
 TGTATAAAGA AGAAAGGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT C-3' (FRAG. NO.:) (SEQ. ID NO: 2463)

25 **CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTACAGGA AAAGTTAACA CAAGTTAGCA
 AAAGTTAAC ATAACAAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA
 AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA
 30 CACACAGCAC AGGATCTGGT GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAAC
 GAAATGTCTA CACTCTATAA CTGAGGTCTT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA
 CTTAAAAATA AAGCAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCGTGCCCT
 GGCCACCGGC AAGCTGCGCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG
 GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC
 35 GGCAACCCAG CCTCCTCTCT AACGCCCTCC GCCTTTGGGA CCAACCAAGG GAGCTCAAGT TAGTAGCAGC
 CCAAGGAGAG GCTGCGCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC
 ACCCTCTCC CGGCGCGAGG GGGCGGGGAG AGCGCTCTCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
 GCGTCTCTCT AGGAACCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG
 CGGGGCTGGA CCGCGCTTTG CTGCTGAGT TGCTGCTCCTTTTGG CCTCGACGGC GGCAACCCAG
 40 CCTCCCTCTT AACGCCCTCC GCCTTTGGGA CCAACCAAGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG
 CGTGCCTTGC CCAAACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC ACCCTCTCTC
 CGGGCGGAGG GGGCGGGGAG AGCGCTCTCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT
 AGGAGCCGCG CGGCAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC
 CGCGCTTTGC TTGCTGAGT TGCTGCCTTC TGGGTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA
 45 GAGTTACCTA CCAAGGGAAC ATTTTCAAA GTTTCTACAA ATGTATCCTA CCAAGAACTA ACAACACCTA
 GTACCCTTGG AAGTACCAGC CTGCACCTGT TGCTCTACAA TGGCAATGAG GCCACAACA GCCACAGA
 AACGACAGTC AAAATCACAT CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAACTC TTCTGTCCAG
 TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCAG CCAACGTTTC AACTCCAGAG ACAACCTTGA
 AGCCTAGCCT GTCACTTGA AATGTTTCAG ACCTTCAAC CACTAGCACT AGCCTTGCAA CATCTCCAC
 50 TAAACCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTT AGGCATCAGA
 GAAAGTAAAT TGACTCAGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG
 ACAGGGGAGA GGGCTGGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT
 ATGCTCCCTG CTCTTGGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA
 GAAATTTCCA GCAAACTCCA ACTTATGAAA AAGCACCAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT
 55 TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG
 AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTCTCTG ATGAATCGCC GCAGCTGGAG CCCACAGGA
 GAAAGGCTGG GCGAAGACCC TTATTACACG GAAAACGGTG GAGGCCAGGG CTATAGCTCA GGACCTGGGA
 CCTCCCTTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC
 CTCCAGAAAC GGCCATTGAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG
 CAAGGCTGGG CAGTGTCCGA GAGAGCAACC CTCTCTGCAT CTGACCAGT GCTACCCCA TGCTGGAGGT
 60 GACATCTCTT ACGCCCAACC CTTCCTTCTT GCACACACCT CAGAGGCTGT TCTTGGGCC CTACACCTTG
 AGGAGGGGGC AGGTAAACTC CTGTCTTTTA CACATTCGGC TCCCTGGAGC CAGACTCTGG TCTTCTTTGG
 GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT
 CACACAGGAC CCCCCTCCCC TACCCCTTCC TCTCTGCCG AATACAGGAA CCCCAGGGG AAAGATGAGC
 TTTTCTAGGC TACAATTTTC TCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT

ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTGTC
 CTTGAACCAC TTCCCTCATC TCTCCTCCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT
 AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTGCA GAGTCTGCA CAGTTTCTG GCTGGAGCCT
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 5 TTTGGGCTCC TTTTCTCCC TCTGGATCAA AGTAGGCAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT
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 GGCTTCTCTC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT TGCCTCAGTC CCCCACAGA TGCTTTTCTG
 TCTCTGCCTC CCTCACCTCG AGCCCTTCC TTGCTCTGCA CCCCATATG GTCATAGCCC AGATCAGCTC
 CTAACCCTTA TCACAGCTG CCTCTCTGT GGGTGACCCA GGTCTTGTG TGCTGTGAT TTCTTTCCAG
 10 AGGGGTTGAG CAGGGATCCT GGTTCATG ACGGTTGGAA ATAGAAATT CCAGAGAAGA GAGTATTGGG
 TAGATATTTT TTCTGAATAC AAAGTGATGT GTTAAATAC TGCAATTAAG GTGATACTGA AACAC-3' (FRAG.No:)
 (SEQ. ID NO:2466)
 5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA
 AAAAGTTAAC ATAAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAAGA AAAGTCTCCA
 15 AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA
 CACACAGCAC AGGATCTGGT GAGGCTATCA CTAAATGTGC CACATTGTGG TTAAGTTTAA CCTGATTAAAC
 GAAATGCTCA CACTCTATAA CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA
 CTTAAAAATA AAGCAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT
 GGCCACCGGC AAGCTGCGCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTGAAGAA GTGGGATGGG
 20 GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTGGG CCTCGACGGC
 GGCAACCCAG CCTCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC
 CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC
 ACCCTCTCC CGGGCGGAGG GGGCGGGAAG GCTCGCTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
 GCGTCTCTCT AGGAGCCGCG CGGAAGGAT AGCGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG
 25 CGGGGCTGGA CCGCGCTTTC CTTGCTGAGT TTGCTGC-3' (FRAG. NO:) (SEQ. ID NO:2464)
 5'-CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG
 GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG
 GAAAAAGCA AGAATCCCCC ACCCTCTCCT CGGGCGGAGG GGGCGGGAAG AGCGCGTCTT GGCCAAGCCG
 30 AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC
 GCGAGGGCCC AGGATGCCGC GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTTCATG
 AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAA GTTTCTACAA
 ATGTATCCTA CCAAGAAACT ACAACACCTA GTACCCTTGG AAGTACCAGC CTGCACCCTG TGTCTCAACA
 TGGCAATGAG GCCACAACAA ACATCAGAGA AAGCAGAGTC AAATTACAT CTACCTCTGT CACAGTCTCA
 35 GTTTATGGAA ACACAAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCAG
 CCAACGTTTC AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTCAAC
 CACTAGCACT AGCTTTGCAA CATCTCCAC TAAACCCTAT ACATCATCTT CTCCTATCCT AAGTGACATC
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 TGCTCTACTG TGGTCTTGGC CAACAGAAACA GAACCTTCCA GAAACTTCCA ACTTATGAAA AGTACCAAT
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 AAAGACCCTG ATTGCACTGG TCACCTCGGG AGCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCTCTG
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 45 GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCTGA GGCTCAGGA AAGGCCAGTG TGAACCGAGG
 GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTTCAG CAAGACAACA CGTGGTGGCT
 GATACCGAAT TGTCCTCGG CTAGGTGGGG CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT
 CTGACCAGT GCTACCCCA TGCTGGAGGT GACATCTCTT ACGCCCAACC CTTCCTCAT ACCACACCT
 CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAAACTC CTGTCTTTTA CACATTCCGGC
 50 TCCCTGGAGC CAGCTCTGG TCTTCTTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT
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 AATACAGGAA CCCCTAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTT TCCAGGAAG CTTTGATTTT
 TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGA CCTGCTCTCT
 TGTAATGATA TAGCCAGAAA AACGTGTTGC CTTGAACCAC TTCCCTCATC TCTCCTCAA GACACTGTGG
 55 ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTGCA
 GAGTCTGCA CAGTCTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC
 TAGTCTCTCT GGGCCACAC AGAAACTCTT TTTGGGCTCC TTTTCTCCC TCTGGATCAA AGTAGGCAGG
 ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTCCGAA AAATCCTCTT CCTCTGAGGC
 TGGATCCTAG CCTTATCCTC TGATCTCCAT GGCTTCTCTC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT
 60 TGCTCAGTC CCCCACAGA TGCTTTCTG TCTCTGCTC CCTCACCTG AGCCCTTCC TTGCTCTGCA
 CCCCATATG GTCATAGCCC AGATCAGCTC CTAACCCTTA TCACCAGCTG CCTCTTCTGT GGGTGACCCA
 GGTCTTGTG TGCTTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTCATATG ACGGTTGGAA
 ATAGAAATTT CCACAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT GTTAAATAC

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 004040 " 5294560

1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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5'-GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAAATAAAC

	5'-GCATTTTTC	AAGTTTATG	ATTTATTTAA	CTGTGGAAC	AAAAATAAAC	CAGAAACCAC	CACCTCTCAC
5	GCCAAAGCTC	ACACCTTCAG	CCTCCAACAT	GAAGGTCTCC	GCAGCACTTC	TGTGGCTGCT	GCTCATAGCA
	GCTGCCTTCA	GCCCCAGGG	GCTCGCTGGG	CCAGCTTCTG	TCCCAACCAC	CTGCTGCTTT	AACCTGGCCA
	ATAGGAAGAT	ACCCCTTCAG	CGACTAGAGA	GCTACAGGAG	AATCACCAGT	GGCAAATGTC	CCCAGAAAGC
	TGTGATCTTC	AAGACCAAA	TGGCCAAGGA	TATCTGTGCC	GACCCCAAGA	AGAAGTGGGT	GCAGGATTCC
	ATGAAGTATC	TGGAACAAAA	ATCTCCAAC	CCAAAGCCAT	AAATAATCAC	CATTTTTGAA	ACCAAGTCCAA
10	AGCTGCATG	TTGCTAAAT	TGTTTTCCCT	TCTTACAATG	CATTCTGAGG	TAACCTCATT	ATCAGATCCAA
	AGGGCATGGG	TTTATTATA	TATATATATA	TTTTTTTTTT	AAAAAAAAC	GTATTGCATT	TAATTTATTG
	AGGCTTTAAA	ACTTATCCTC	CATGAATATC	AGTTATTTTT	AAACTGTAAA	GCCTTGTGCA	GATTCTTTAC
	CCCTGGGAG	CCCCAATTCG	ATCCCCTGTC	ACGTGTGGGC	AATGTTCCCC	CTCTCCTCTC	TTCTCCCTG
	GAATCTTGTA	AAGCTCCTGG	CAAAGATGAT	CAGTATGAAA	ATGTCATTGT	TCTTGTGAAC	CCAAAGTGTG
15	ACTCATTA	TGGAAGTAAA	TGTTGTTTTA	GGAATAC	ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG
	CTGCTCATAG	CAGTCGCTT	CAGCCCCCAG	GGGCTCGCTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT
	TTAACCTGGC	CAATAGGAAG	ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	GTGGCAAATG
	TCCCCAGAAA	GCTCTGATCT	TCAAGACCAA	ACTGGCCAA	GATATCTGTG	CCGACCCCAA	GAAGAAAGTG
	GTGCAGGATT	CCATGAAGTA	TCTGAGCCAA	AAATCTCCAA	CTCAAGGCC	ATAA	CCACATATTC
20	CCAAGGCAAG	ATCCAGATGG	ATTAAAAAAT	GTACCAAGTC	CCTCCTACTA	GCTTGCCTCT	CTTCTGTTCT
	GCTTGACTTC	CTAGGATCTG	GAATCTGGTC	AGCAATCAGG	AATCCCTTCA	TCGTGACCCC	CGCATGGGCA
	AAGGCTTCCC	TGGAATCTCC	CACACTGTCT	GCTCCCTATA	AAAGGCAGGC	AGATGGGCCA	GAGGAGCAGA
	GAGGCTGAGA	CCAACCCAGA	AACCACCACC	TCTACGCCA	AAGCTCACAC	CTTCAGCCTC	CAACATGAAG
	GTCTCCGAG	CACITCTGTG	GCTGCTGCTC	ATAGCAGCTG	CCTTCAGCCC	CCAGGGGCTC	GCTGGGCCAG
25	GTAAGCCCC	CAACTCCTTA	CAGGAAAGGT	AAGGTAACCA	CCTCCAGGCT	ACTAGGTCAG	CAAGAACTCT
	TACAGACTCA	CTGCAAAATC	TCCATTGGA	AAATAGGGAA	ACAGGTTTTG	TGGGTGGACA	AGAAATGCCT
	CAACCGTCAC	ATCCAGTCAC	TGGAAGAGCC	AGAACTAGAA	AGAGTCCGAG	TCTTTTCCCC	ACATTAAGA
	GGGCCGCTGG	GTGCATCCTT	ACCCAGCTAT	CCTTACAGTG	TTTGGGAATG	GGGAATGGCT	CTGTCTTACT
	GTGGGCATGG	TGGGCATTTT	TGGCAGTGGG	AGAGAAGGAA	AATCTGTTGA	TTAGAAGCTC	AGTATGTTAA
30	TTCGACTCCA	GGACAGCTTT	CAGAGACAGT	GGCTAAGAGA	AGAACGAGGT	CCCAGGGGAT	CTCTTGAGGT
	GACTTATTTT	GACACTCTTT	GGGAAAGTTA	TCTAGGAGAT	TGTTCCATA	ACTATTTTTC	CCATACTCTG
	GTGACAAATT	TACIGAGTGT	ATCGGTCCCA	CTGAGCCAGT	GCATAGCATG	GTAACAAACA	GTTCTAAATT
	ATCAATGACT	TAACAGAATT	AACTAAATTA	ACAAAAGTTA	CTTTCTCACT	TGTACTAAAT	ATCTATAATG
	TATGGGCTCA	GGCTCTGCA	TTTTATACTC	AGGATTCTAG	ACTGATGGAG	AAGTTGCCAT	GTGGGGGAAC
35	ATTGATGGAT	ACTGTGATAA	AGCAGAGAA	AGCTCTCAGG	AGCTTTGCAT	AGGCAATGCA	CTGTGGCTCA
	AAAATGACAC	CCAACACTTT	GTCTCCTTCT	TTATTGATCA	AAACTAATTA	ATGCCTCCAA	CCAAACAAAA
	GTGGCCAAGA	AATGCAAGTC	TACCTTGTGT	CTCAAAACAG	AGGATGGAGA	ATATTTGGTG	AAAATTACCA
	TGACCATCAC	ATGCCACAGT	AGGTCTTTAT	AATGACAGAG	CTAGCATTGT	TCACATTGAC	CAAGCTTTGT
	CCATACACTC	TACAGTAATG	ATGAGTCCTC	AGTGCACAGG	GGAGGATGCT	GAAGACACAG	GACAGCATCC
40	TCCAGACACA	TAAGACTTCA	GAGCAGAGGG	ATTCTCCCTC	CACCTCTCGC	AATTCCTTGC	TTTCTCCTAA
	CTTCCTTTAC	AAACTCATGC	TGGAATATGT	CTATGTATCA	TCATGTGGCT	CATTTTTTTT	TCTGTTTATT
	TTTTTTTCCC	AAAATTCAGC	TTCTTGCCCA	ACCACCTGCT	GCTTTAACTT	GGCCAAATAGG	AAGATAACCC
	TTCAGCGACT	AGAGAGCTAC	AGGAGAATCA	CCAGTGCCAA	ATGTCCCCAG	AAAGCTGTGA	TGTAAGTAAA
	TAAAGTTCAC	CCTCCCTAG	ACAAAAAAT	AATGTCTAGG	GCACAGAGTC	AAGAACTGTG	GGAGTCATAG
45	ACTCTGATAG	TTTGACCTCT	ATGGTCCAAT	TCATTAATTT	TCACAAGTGA	GTGTTCACTC	CCAGCTCCCT
	GCCTGGGAGA	TTGCTGTAGT	CATATCAATT	TCTTCAAGTC	AAGAGCAAAG	ATGGTTTTAC	TGGGCCTTTA
	AGAGCAGCAA	CTAACCCAAG	AGTCTCATCC	TTCTCTCTCT	CCGTAGCAAC	CCTTGTGTTA	GGGGCAGATG
	GTCCTTAAAT	ATTTAGGGTC	AAATGGGCAG	AATTTTCAAA	AACAATCCTT	CCAATTGCAT	CCTGATTCTC
	CCCACAGCTT	CAAGACCAA	CTGGCCAAAG	ATATCTGTGC	CGACCCCAAG	AAGAAGTGGG	TGCAGGATTCT
50	CATGAAGTAT	CTGCACAAA	AATCTCCAAC	TCCAAGCCA	TAAATAATCA	CCATTTTTGA	AACCAACCA
	GAGCCTGAGT	GTTGCCTAAT	TGTTTTTCCC	TCTTACAATG	GCATTCTGAG	GTAACCTCAT	TATCAGTCCA
	AAGGGCATGG	GTTTATTAT	ATATATATAT	ATATATTTTT	TTTTAAAAAA	AAACGTATTG	CATTTAATTT
	ATTGAGGCTT	TAAACTTAT	CCTCCATGAA	TATCAGTTAT	TTTTAAACTG	TAAAGCTTTG	TGCAGATTCT
	TTACCCCTCTG	GGAGCCCCAA	TTCGATCCCC	TGTCACGTGT	GGGCAATGTT	CCCCCTCTCC	TCTCTTCTCT
55	CCTGGAATCT	TGTAAAGGTC	CTGGCAAAGA	TGATCAGTAT	GAAAATGTCA	TGTTCTTGT	GAACCCAAAG
	TGTGACTCAT	TAAATGGAAG	TAATGTTGTT	TTAGGAATAC	ATAAAGTATG	TGC	

ATAGGAAGAT ACCCTTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC
 TGTGATCTTC AAGA CCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC
 ATGAAGTATC TGGACCAAAA ATCTCCAAT CCAAAGCCAT AAATAATCAC CATTTTGGAA ACCAAACCAG
 AGCCTGAGTG TGGCTAATT TGTTCCTT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA
 5 AGGGCATGGG TTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAC GTATTGCATT TAATTTATTG
 AGGCTTTAAA ACTATCCTC CATGAATATC AGTTATTTTT AAAGTGAAA GCTTTGTGCA GATTCTTTAC
 CCCCTGGGAG CCCCAATTCTG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG
 GAATCTTGTA AAGCTCTGG CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG
 ACTCATTTAA TGGAA GTAAA TGTGTGTTTA GGAATAC-3' (FRAG.NO:) (SEQ. ID NO:2491)
 10 5'-ATGAAGGTCT CCACAGCACT TCTGTGGCTG CTGCTCATAG CAGTGCCTT CAGCCCCCAG GGGCTCGCTG
 GGCCAGCTTC TGTC CCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA
 GAGCTACAGG AGAATCACCA GTGGCAAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG
 GATATCTGTG CCGACCCCAA GAAGAAGTGG TGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA
 CTCCAAAGCC ATAA-3' (FRAG. NO:) (SEQ. ID NO:2492)
 15 5'-CCACATATTC CCTCTCTTTT CCAAGGCAAG ATCCAGATGG ATTAATAAAT GTACCAAGTC CCTCTACTA
 GCTTGCCCTC CTTCIGTTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA
 TCGTGACCCC CGCA TGGGCA AAGGCTTCCC TGGAAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC
 AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCACGCCA AAGCTCACAC
 CTTCAGCCTC CAACATGAAG GTCTCCGAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC
 20 CCAGGGGCTC GCTCGGCCAG GTAAGCCCCC CAATCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT
 ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAAATC TCCATTGAA AAATAGGGAA ACAGGTTTGT
 TGGGTGGACA AGAATATGCCT CAACCGTCAC ATCCAGTCAC TGAAGAGGCC AGAACTAGAA AGCTCCCGAG
 TCTTTTCCCC ACATCAAGA GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTTGGGAATG
 GGAATGGCT CTGCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA
 25 TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT
 CCCAGGGGAT CTCGTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA
 ACTCATTTTC CCATCTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG
 GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA ACAAAGTTA CTTTCTCACT
 TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG
 30 AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAT
 AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAATAATTA
 ATGCCTCAA CCAACAAAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA
 ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG
 TCACATTGAC CAACCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC AGTGACAGG GGAGGATGCT
 35 TAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC
 AATTCTTGC TTCTCTTAA TCTCTTTAC AAAGTCATGC TTGAAATGT CTATGTATCA TCATGTGGCT
 CATTTTTC TCTGTCATT TTTTTCCTT AAAATTACAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT
 GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGCCAA ATGTCCCCAG
 AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCTAG ACAAATAAAT AATGTCTAGG GCACAGAGTC
 40 AAGAAGTGTG GGAATCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA
 GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG
 ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCTCTCTCT CCGTAGCAAC
 CCTTTGTCCA GGGGCAGATG GTCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAACTCTT
 CCAATTGCAT CCTGATTCCT CCCACAGCTT CAAGACCAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG
 45 AAGAAGTGGG TGCA GGATTC CATGAAGTAT CTGGACCAA AATCTCCAAC TCCAAAGCCA TAAATAATCA
 CCATTTTGA AACCAACCA GAGCCTGAGT GTTGCTTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG
 GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA
 AAACGTATTG CATITAATT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG
 TAAAGCTTTG TGCAGATTCT TTACCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT
 50 CCCCTCTCC TCTCTCTCT CCTGGAATCT TGTAAGGTG CTGGCAAAGA TGATCAGTAT GAAAATGTCA
 TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG
 TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTGTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' (FRAG.NO:)
 (SEQ. ID NO:2493)

FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments

55 5'- GCCAGGTCGC TGITGGTCCA CGCCGCCCGT CGCGCCGCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA
 GGCCGGAGCC GAGCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCTGTGGG ACCGCTATGG
 GCGTGGAGAT CGAC ACCATC TCCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
 GCACTACACA GGAATGTCTC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
 TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGACGC CCAGATGAGC TTGGGGCAGA
 60 GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
 TGCCACCCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG

[illegible]

TGCCATAAAC CTCAGTTAT TCATTTTATT TTGTTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT
 GGATATAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG
 GAATTGGTGT TGGG:GGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTTT GGATGAAAT TTTATCTATT
 ATATATTAAA CATICTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT
 5 ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAATAAG CCCTACCTAA AACTGAGGTG GGGATGGGGA
 GAGCCTTTGC CTCCACCATT CCCACCCACC CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC
 ACTGCAATGC TGG/CACTAC AGGTATCTGT CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC
 TTTTTTTTTT TTCA`CCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTG TAATCTCATA ACTTTCCAAG
 CTCCACCACT TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA
 10 CACCCAGTGA AAGC:CCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG
 CAGCTTCAGC ATC/CCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTTCCTCC
 CTCAGCCCCCT TCTACCCCT TTGCTGTCCT GTGTAGTGAT TTGGTGAGAA ATCGTTGCTG CACCCTTCCC
 CCAGCACCAT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC-3' (FRAG.NO:_)
 (SEQ. ID NO:2497)
 15 5' GCCGCCGCCA TG3GAGTGCA GGTGGAAACC ATCTCCCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC
 AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCTCTCC GGGACAGAAA
 CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAAGGGT TGCCAGATG
 AGTGTGGGTC AGA:AGCCAA ACTGACTATA TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA
 TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC
 20 TCCCTTAGCT CCCTTTCCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC
 ATATGGAGCT TTCTCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGA:CTGAATG TGTTCTGTCA
 CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCTT TCTCCTCGTA TGTGTGTTTA CCTAAACTAT
 ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO:_) (SEQ. ID NO:2498)

wherein B is adenosine, or, more preferably, replaces adenosine and is an "equivale\lent" or a
 25 "universal" base, and adenosine A_{2a} receptor agonist or only minimally antagonist, an adenosine A_{2b}
 receptor antagonist, an adenosine A₃ receptor antagonist, or an adenosine A₁ receptor antagonist.
 Similarly, adenosine (A) may always be replaced by an "alternative", "equivalent" and/or "universal"
 base having a small fraction, preferably less than 0.3 of the activity of adenosine at the adenosine
 receptor(s), as described above.
 30 In one preferred embodiment, the links between neighboring mononucleotides are phosphodiester
 links. In another preferred, at least one mononucleotide phosphodiester residue of the anti-sense
 oligonucleotide(s) is substituted by a methylphosphonate, phosphotriester, phosphorothioate,
 phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate,
 35 sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, 2'-O-methyl,
 methylene(methylimino), methyleneoxy (methylimino), phosphoramidate residues, and combinations
 thereof. The oligos having one or more phosphodiester residues substituted by one or more of the other
 residues are generally longer lasting, given that these residues are more resistant to hydrolysis than the
 phosphodiester residue. In some cases up to about 10%, about 30%, about 50%, about 75%, and even all
 phosphodiester residues may be substituted (100%). Typically, the multiple target anti-sense
 40 oligonucleotide (oligo) of the invention comprises at least about 7 mononucleotides, in some instances up
 to 60 and more mononucleotides, preferably about 10 to about 36, and more preferably about 12 to about
 21 mononucleotides. However, other lengths are also suitable depending on the length of the target
 macromolecule. Examples of the MTA oligos of the invention are provided in Table 3 below, which
 includes ninety-four sequences (SEQ ID NOS.: 2316 through 2410).

45 **Table 3: MTA Oligos, Location Targeted & Target**

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
<u>HUMNFKBP65A AS</u>				
CCC GGC CCC GCC TCG TGC C	3019	5'=1	EPI 2192	
CGT CCB TGC CGC GGG CCC	3020	5'=28 (AUG)	EPI 2193	
GCC CCG CTG CTT GGG CTG CTC TGC CGG G	3021	5'=65	EPI 2194	
TCT GTG CTC CTC TCG CCT GGG	3022	5'=137	EPI 2195	
TGG TGG GGT GGG TCT TGG TGG	3023	5'=159	EPI 2196	
CTG TCC CTG GTC CTG TG	3024	5'=196	EPI 2197	

	GGT CCC GCT TCT TC	3025	5'=362	EPI 2198
	GGG GTT GTT GTT GGT CTG G	3026	5'=401	EPI 2199
	TGT CCT CTT TCT GC	3026	5'=656	EPI 2200
	GCC TCG GGC CTC CC	3027	5'=697	EPI 2201
5	GGC TGG GGT CTG CGT	3028	5'=769	EPI 2202
	GGC CGG GGG TCG GTG GGT CCG CTG	3029	5'=953	EPI 2203
	GGG CTG GGG TGC TGG CTT GGG G	3030	5'=1022	EPI 2204
	GGG GCT GGG GCC TGG GCC	3031	5'=1208	EPI 2205
	GCC TGG GTG GGC TTG GGG GC	3032	5'=1272	EPI 2206
10	GCT GGG TCT GTG CTG TTG CC	3033	5'=1362	EPI 2207
	GTT GTG TGG GGG GCC	3034	5'=1451	EPI 2208
	GCT GGG TCG GGG GGC CTC TGG GCT GTC	3035	5'=1511	EPI 2209
	GCC CCG GGG CCC CC	3036	5'=1550	EPI 2210
	TGG CTC CCC CCT CC	3037	5'=1772	EPI 2211
15	GCT CCC CCC TTT CC	3038	5'=1863	EPI 2212
	CGG ACG AAG ACA GAG A	3039	5'=1979	EPI 2213
	GGC TTT GTG GGC TC	3040	5'=2011	EPI 2214
	GCC TGC TCT CCC CC	3041	5'=2312	EPI 2215
	CCC GGC CCC GCC BCG BBC C	3042	intron	EPI 2192-01A HSU50136C4Synth
20	CCC GGC CCC GCC BCG	3043	intron	EPI 2192-01B
	CCC GGC CCC GCC BCG BBC C	3044	5'untr	EPI 2192-02A HUMLIPOX5LO
	CCC GGC CCC GCC BCG	3045	5'untr	EPI 2192-02B
	CCC GBC CCC GCC TCB BG	3046	trans	EPI 2192-03A HSNFKBS Subunit
	CCC GBC CCC GCC TC	3047	trans	EPI 2192-03B
25	CCG GCC CCG CCT C	3048	5'untr	EPI 2192-04 TGFβR1
	CCC GBB CCC GCB TBG TGC C	3049	5'trans	EPI 2192-05A HSU58198I1 enhan
	CCC GCB TBG TGC C	3050	5'untr	EPI 2192-05B
	CCC GGB CCC BCC BBG TGC C	3051	3'trans	EPI 2192-06 HSVECAD
	CBG BBC CCG CCT CGT GCC	3052	intron	EPI 2192-07A NFKB2
30	C CCG CCT CGT GGC	3053	intron	EPI 2192-07B NFKB2
	CCG GCB CCG CCT CBT GCC	3054	5'trans	EPI 2192-08 Carboxypep
	CCG GCC CCG CCB CBT GCC	3055	3'trans	EPI 2192-09 HumADRA2Cα2AdrKid
	CCC GBC CCC GBC TCG	3056	5'untrs	EPI 2192-10 HUMFK506B
	CCC GGC CBC GBC TCG	3057	5'untrs	EPI 2192-11 HSNBARKS1βAdrKin
35	CCC GGC CCB GCC TBG	3058	5'UTR	EPI 2192-12 HSNFXN1 (NFKB1)
	CCC GGC BCB GBC TCG TBC C	3059	3'UTR	EPI 2192-13 HSILF(transcrp. Factor ILF)
	CCC GGC CCC GCC BCG	3060		EPI-2192-14 NFKB/C4Syn/5-LO/TGFBrecl MTA
40	CCC GGC CCC GCC BCG	3061		EPI-2192-15NFKB/C4Syn/5-LOMTA
	TCC BTG CCG CGG GC	3062	3' trans	EPI-2193-01 METOncogene
	TCC BTG CCB CGG GCC	3063	3' trans	EPI-2193-02 HSFGR2 (IG)
	TCC BTG CCB CGG GCC	3064	mid cod	EPI-2193-03 5-LO
	TCC BTG CCB CBG GCC	3065	mid cod	EPI-2193-04 HUMTK14
45	GTC CBT GBC GCG G	3066	3'trans	EPI-2193-05 HUMTNFR
	TC CBT GBC GCG GG	3067	AUG	Probl.HUMPTCH cardiacK+channel
	TCT GBG CTC CTC TBB CCT GGG	3068	intr	EPI-2195-01 humCSPAcytotox. Ser. Protease
50	CTG TGC BCC TBB CBC CTG GG	3069	intr	EPI-2195-02 HSINOSX08induc.NOS
	TGT GBT CCB CTB GBC TGG G	3070		EPI-2195-03 HUMACHRM2musc.m2 acetylch.rec.
	TCT GTB CTC BBC TCB CCT G	3071		EPI-2195-04 s86371s1 Neurokinin3Recept
55	TGC TCC TCB CBB CTG GG	3072		EPI-2195-05 HUMMIP1 Amacro
	inflam.factor			

"GAGGAG" GAGGAG

Table 3: MTA Oligos, Location Targeted & Target (Cont'd)

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
CTC CTC TBG CCT GG	3073		EPI-2195-06	HSNBARKS4
5 GTG CTC CBB TCB BCT GGG	3074		EPI-2195-07	β -Adr Rec Kinase
GTG CBC CBB TCB CCT GGG	3075		EPI-2195-08	HSTNFR2SO6TNF R2
				humfkbk fk506 binding prot.
10 TCT GTG CBC CTC TBG BCT	3076	exon	EPI-2195-09	HSNBARKS1 β -Adr. Recept. Kinase
CTG TBB TCC TBB CBC CTG G	3077	intron	EPI-2195-10	HUMIL8
TGT GCT BBT CBC BCB TGG G	3078		EPI-2195-11	HSU50157 PDE4
GTG CBC CBC TCB CCT G	3079	intron/exon	EPI-2195-12	IL-2 R
CTG TGC BCC TCT C	3080	3'UTR	EPI-2203-05	IL-6 R HSIL6R
15 CBG TGC BCC BCT CBC CTG	3081	intr/ex	EPI-2203-06A	HSIL2rG6
G TGC BCC BCT CFC CTG	3082	intr/ex	EPI-2203-06B	HSIL2rG6
CBC CTC TCB CCT GGG	3083	coding	EPI-2203-07A	HUMIL71
C CTC TCB CCT GCG	3084	coding	EPI-2203-07B	IL-7 HUMIL71
GCT CCB CTC GCC T	3085	coding	EPI-2203-08	IL-6 R HSI6REC
20 TGC TCC TCB CGC C	3086	intron PDGF A	EPI-2303-09	Chain HUMPDGFAB
GTT GTT GBT CTG G	3087	3'utr	EPI-2199-01	GATA-4Transcrip. Factor for IL-5
GGT TGB BBT TGG TCT TGG	3088	Coding	EPI-2199-02	TNF α HUMTNFA
GGT TGT TGB TGB TCT G	3089	Far 5'UTR	EPI-2199-03	HSSUBP1G(Sub Pr)
25 GGG TTB BBG TTG BTC TGG	3090	Coding	EPI-2199-04	NeutrophilAdh. R HUMNARIA
GGG TTB BBG TTG BTC TGG	3091	HSHM2	EPI-2199-05	m2 Muscarinic R
TTG TTG TBG BTC TGG	3092	HUML1CAM	EPI-2199-06	L1 LeukAadhProt
GGG TBG BBG BGT CCG CTG	3093	coding	EPI-2203-01	HUMGATA2A
30 GGG TCB GBG GBT CBG CTG	3094	S71424S2	EPI-2203-02	IGE eps
GGG TBG GTG GGT C	3095	coding	EPI-2203-03	HSGCSFR2
GGG TCG GBG GGT CBG C	3096	HUMITGF	EPI-2203-04	TGF β 3
GGG TGG GCT T	3097	HUMNK65PRO	EPI-2206-01	NFKB/NK & TCell
35 GGG TGG GCT TGG G	3098	HUMPEREEB	EPI 2206-02	Activating Prot NFKB/Prostagl. EP3 Rec
CCTGGGTGGGBBTGGG	3099		EPI 2206-03	HSNF2B/GCSF NFKB/GranuLocCSF/Transcr. FactorNF2B
40 CCTGGBTGGGCBTGGG	3100		EPI-2206-04	HUMLAP/NFKB Leuk. Adhes. Prot
GCCTGBGTGBBCTTGCG	3101		EPI2206-05	NFKB/Endothel N2 S63833
45 CCCAVGVCCVCCCAGGC	3102		EPI 2206-06	NFKBAS13/B Lymph SerThrProt. Kinase
AGCCCACCCAGGC	3103		EPI2206-07	NFKBAS13/GCSF1 HSGCSFR1Rec
50 BCCTGGGTGGGCTB	3104		EPI2206-08	NFKBAS13/GCSF1/ NK7TCELLACT. Prot
GGTGGGCTTGGG	3105		EPI 2206-09	NFKBAS13/ HSTGFB1 TGFB
CCBBGGTGGGCTTGGG	3106		EPI 2206-10	NFKBAS13/ HSTGFB1 TGFB1
55 CTGGGTGGGBBTGGG	3107		EPI 2206-11	NFKBAS13/ HSGCSFR1 GCSFR1
CCBGGGTGGGCTTGG	3108		EPI 2206-12	NFKBAS13/HUMCD30A LymphActAntigCoding
GGGTGGGCTTGG	3109		EPI-2206-12B	NFKBAS13/HUMCD30A
60 CCTGBGTGBGCBTGGG	3110		EPI 2206-13	NFKBAS13/HUMCAM1V Vasc. Endoth. Cell Adh. Molec

B: Universal Base

The MTA oligos of Table 3 are suitable for use with two or more of the targets listed in Table 4 below.

09543670.040400

Table 4: Targets for the MTA Oligos of Table 3

Compound	Target
EPI 2010	Adenosine A1 receptor
EPI 2045	Adenosine A3 receptor
EPI 2873, EPI 2193	NFκB
EPI 1873	Interleukin-1
EPI 1857	Interleukin -5
EPI 2945	Interleukin -4
EPI 2977	Interleukin -8
EPI 2031	5-Lipoxygenase
EPI 1898	Leukotriene C-4 Synthase
EPI 1856	Eotaxin
EPI 1131	ICAM
EPI 1085	VCAM
EPI 2085	TNFα
EPI 1908	PAF
EPI 1925	IL-4 receptor
EPI 2643	β2 adrenergic receptor kinase
EPI 2934	Tryptase
EPI 2033	Major Basic Protein
EPI 2795	Eosinophil Peroxidase

NfκB: nuclear factor κB

ICAM: intracellular adhesion molecule

VCAM: vascular cell adhesion molecule

TNF: tumor necrosis factor

PAF: platelet activating factor

The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein, whether for existing targets or those to be found in the future. Sequences for many target genes of different systems are presently known. See, GenBank data base, NIH, the entire sequences of which are incorporated here by reference. The sequences of those genes, whose sequences are not yet available, may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, anti-sense oligonucleotides are produced as described above and utilized to validate the target by in vivo administration and testing for a reduction of the production of the targeted protein in accordance with standard techniques, and of specific functions. As already described above, the anti-sense oligonucleotides may be of any suitable length, e.g., from about 7 to about 60 nucleotides in length, depending on the particular target being bound and the mode of delivery thereof. The anti-sense oligonucleotide preferably is directed to an mRNA region containing a junction between intron and exon or to regions vicinal to the junction. Where the anti-sense oligonucleotide is directed to an intron/exon junction, it may either entirely overlie the junction or may be sufficiently close to the junction to inhibit splicing out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g., with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, 10, 5, 3, or 2 nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon and, more generally, those that target the coding region of the target mRNA. When practicing the present invention, the anti-sense oligonucleotides administered may be related in origin to the species to which it is administered. When treating humans, human anti-sense may be used if desired. Anti-sense oligos to endogenous sequences from other species,

however, are also encompassed.

Pharmaceutical compositions comprising an anti-sense oligonucleotide as given above effective to reduce expression of an A₁ or A₃ adenosine receptor by passing through a cell membrane and binding specifically with mRNA encoding an A₁ or A₃ adenosine receptor in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are provided in a suitable pharmaceutically acceptable carrier, e.g., sterile pyrogen-free saline solution. The anti-sense oligonucleotides may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g., in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may also be coupled to a substance which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject to inhibit the activation of a target, such as the adenosine receptors, which subject is in need of such treatment for any of the reasons discussed herein. Furthermore, the pharmaceutical formulation may also contain chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular uptake pathways to increase cellular concentrations of oligonucleotides. Examples of macromolecules used in this manner include transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin. In the pharmaceutical formulation, the anti-sense compound may be contained within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar, so long as the anti-sense oligonucleotide is contained therein. Positively charged lipids such as N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammoniummethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known. See, e.g., U.S. Patent Nos. 4,880,635 to Janoff et al.; 4,906,477 to Kurono et al.; 4,911,928 to Wallach; 4,917,951 to Wallach; 4,920,016 to Allen et al.; 4,921,757 to Wheatley et al.; etc.

Subjects may be administered the active composition by any means which transports the anti-sense nucleotide composition to the lung. The anti-sense compounds are particularly disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by generating an aerosol comprised of respirable particles, the respirable particles comprised of the anti-sense compound, which particles the subject inhales. The respirable particles may be liquid or solid. The particles may optionally contain other therapeutic ingredients. Particles comprised of anti-sense compound for practicing the present invention should include particles of respirable size: that is, particles of a size sufficiently small to pass through the mouth and larynx upon inhalation and into the bronchi and alveoli of the lungs. In general particles ranging from about .5 to about 10 microns in size are respirable. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is preferably minimized. For nasal administration, a particle size in the range of 10-500 nm is preferred to ensure retention in the nasal cavity. Thus, particles of about 4, about 10, about 25, about 50 to about 75, about 100, about 250, about 500, and other specific ranges therewithin, are preferred. Others, however, are also contemplated within the confines of this invention.

Liquid pharmaceutical compositions of active compound for producing an aerosol can be prepared by combining the anti-sense compound with a suitable vehicle, such as sterile pyrogen free water. Other therapeutic compounds may optionally be included. Solid particulate compositions containing respirable dry particles of micronized anti-sense compound may be prepared by grinding dry anti-sense compound with a mortar and pestle, and then passing the micronized composition through a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprised of the anti-sense compound may optionally contain a dispersant which serves to facilitate the formation of an aerosol. A suitable dispersant is lactose, which may be blended with the anti-sense compound in any suitable ratio (e.g., a 1 to 1 ratio by weight). Again, other therapeutic compounds may also be included.

The dosage of the anti-sense compound administered will depend upon the disease being treated, the condition of the subject, the particular formulation, the route of administration, the timing of administration to a subject, etc. In general, intracellular concentrations of the oligonucleotide of from about

0.01, about 0.05, about 0.1, about 0.2, about 1 to about 5 μM , about 50 μM , about 100 μM or more, and more particularly about 0.2 to about 0.5 μM , are desired. For administration to a subject such as a human, a dosage of from about 0.01, about 0.1 or about 1 mg/Kg up to about 50, about 100, or about 150 mg/Kg and even higher doses are typically employed depending on the route of administration as is known in the art.

5 Depending on the solubility of the particular formulation of active compound administered, the daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically (i.e., as a rescue treatment) or prophylactically. Aerosols of liquid particles comprising the anti-sense compound may be produced by any suitable means, such as with a nebulizer. See, e.g., U.S. Patent No. 4,501,729. Nebulizers are commercially available devices which

10 transform solutions or suspensions of the active ingredient into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in nebulizers consist of the active ingredient in a liquid carrier, the active ingredient comprising up to 40% w/w of the formulation, but preferably less than 20% w/w. The carrier is typically water or a dilute aqueous alcoholic solution, preferably made isotonic with body fluids by the addition of, for example, sodium chloride. Optional additives include preservatives

15 if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants.

In one preferred embodiment, the pharmaceutical composition comprises nucleic acid(s) which comprise the anti-sense oligo(s) described above and one or more surfactants. Suitable surfactants or

20 surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine,

25 dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycerol-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid,

30 polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as a single, or as part of a multiple component, surfactant in a formulation, or as covalently bound additions to the 5' and/or

35 3' ends of the anti-sense oligo(s). Aerosols of solid particles comprising the active compound may likewise be produced with any solid particulate medicament aerosol generator. Aerosol generators for administering solid particulate medicaments to a subject produce particles which are respirable, as explained above, and generate a volume of aerosol containing a predetermined metered dose of a medicament at a rate suitable for human administration. One illustrative type of solid particulate aerosol

40 generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder (e.g., a metered dose thereof effective to carry out the treatments described herein) is contained in capsules or cartridges, typically made of gelatin or plastic, which are either pierced or opened in situ and the powder delivered by air drawn through the device upon

45 inhalation or by means of a manually-operated pump. The powder employed in the insufflator consists either solely of the active ingredient or of a powder blend comprising the active ingredient, a suitable powder diluent, such as lactose, and an optional surfactant. The active ingredient typically comprises from 0.1 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically containing a suspension or

solution formulation of the active ingredient in a liquefied propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically from 10 to 150 μ l, to produce a fine particle spray containing the active ingredient. Suitable propellants include certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane and mixtures thereof. The formulation may additionally contain one or more co-solvents, for example, ethanol, surfactants, such as oleic acid or sorbitan trioleate, antioxidants and suitable flavoring agents. The aerosol, whether formed from solid or liquid particles, may be produced by the aerosol generator for example at a rate of from about 10, about 30, about 70 to about 100, about 150, about 150 liters per minute, more preferably from about 30 to 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater amounts of medicament, however, may be administered more rapidly as is known in the art.

The relevant disclosures of all scientific publications and patent references cited in this patent are specifically intended to be incorporated herein by reference, particularly in reference to preparatory methods and technologies which are enabling of the invention. The following examples are provided to illustrate the present invention, and should not be construed as limiting thereon.

EXAMPLES

In the following examples, μ M means micromolar, ml means milliliters, μ m means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius, μ g means micrograms, mg means milligrams, g means grams, kg means kilograms, M means molar, and h or hr. means hours.

Example 1: Design and Synthesis of Anti-sense Oligonucleotides

The design of anti-sense oligonucleotides against the A_1 and A_3 adenosine receptors may require the solution of the complex secondary structure of the target A_1 receptor mRNA and the target A_3 receptor mRNA. After generating this structure, anti-sense nucleotide are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments.

The mRNA secondary structure of the adenosine A_1 receptor was analyzed and used as described above to design a phosphorothioate anti-sense oligonucleotide. The anti-sense oligonucleotide which was synthesized was designated HAdA₁AS and had the following sequence: 5' -GAT GGA GGG CGG CAT GGC GGG-3' (SEQ ID NO:1). As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdA1MM1 was synthesized with the following sequence: 5' -GTA GCA GGC GGG GAT GGG GGC-3' (SEQ ID NO:2). Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine A_1 receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine A_3 receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA3AS1) synthesized had the following sequence: 5' -GTT GTT GGG CAT CTT GCC-3' (SEQ ID NO:3). As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA3MM1) was synthesized, having the following sequence: 5' -GTA CTT GCG GAT CTA GGC-3' (SEQ ID NO:4). A second phosphorothioate anti-sense oligonucleotide (HAdA3AS2) was also designed and synthesized, having the following sequence: 5' -GTG GGC CTA GCT CTC GCC-3' (SEQ ID NO:5). Its control oligonucleotide (HAdA3MM2) had the sequence: 5' -GTC GGG GTA CCT GTC GGC-3' (SEQ ID NO:6). Phosphorothioate oligonucleotides were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, MD).

Example 2: In Vivo Testing of Adenosine A_1

Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human A₁ receptor (SEQ ID NO:1) described above. was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the A₁ adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory.

HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0 μ M HAdA1AS or HAdAIMM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdA1AS-treated, HAdAIMM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdA1AS but not HAdAIMM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdA1AS is a good candidate for an anti-asthma drug since it depletes intracellular mRNA for the adenosine A₁ receptor, which is involved in asthma.

Example 3: In Vivo Efficacy of Adenosine A₁ Receptor Anti-sense Oligos

A fortuitous homology between the rabbit and human DNA sequences within the adenosine A₁ gene overlapping the initiation codon permitted the use of the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine A₁ receptor in a rabbit model. Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (C_{dyn}) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC50 were obtained for aerosolized adenosine. Anti-sense (HAdA1AS) or mismatched control (HAdAIMM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 μ g (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 μ g in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerset, PA), producing aerosol droplets 80% of which were smaller than 5 μ m in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC50 values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC50 values obtained for these animals prior to exposure to oligonucleotide. Following a 1 week interval, animals were crossed

over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC50 values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 5 below.

Table 5: Effect of Adenosine A₁ Receptor Anti-sense Oligo upon PC50 Values in Asthmatic Rabbits

Mismatch Control		A ₁ Receptor Anti-sense Oligo	
Pre Oligonucleotide	Post Oligonucleotide	Pre Oligonucleotide	Post Oligonucleotide
3.56 ± 1.02	5.16 ± 1.03	2.36 ± 0.68	>19.5 ± 0.34**

The results are presented as the mean (n=8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

**Significantly different from all other groups, p<0.01

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC50 values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A₁ receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresponsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

Example 4: Specificity of A₁-adenosine Receptor Anti-sense Oligonucleotide

At the conclusion of the cross-over experiment of Example 3 above, airway smooth muscle from all rabbits was quantitatively analyzed for adenosine A₁ receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine A₂ receptors, which should not have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmacol. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by reference, with slight modifications. Crude plasma membrane preparations were stored at 70°C until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37°C to remove endogenous adenosine. The binding of [³H] DPCPX (A₁ receptor-specific) or [³H] CGS-21680 (A₁ receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine A₁ anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in A₁ receptor number compared to controls, as assayed by specific binding of the A₁-specific antagonist DPCPX. There was no change in adenosine A₂ receptor number, as assayed by specific binding of the A₂ receptor-specific agonist 2- [p- (2-carboxyethyl)-phenethylamino] -5' - (N-ethylcarboxamido) adenosine (CGS-21630). This is illustrated in Table 6 below.

Table 6: Specificity of Action of Adenosine A₁ Receptor Oligonucleotide Anti-sense

Mismatch Control Oligonucleotide	A ₁ Anti-sense Oligonucleotide
----------------------------------	---

A₁-Specific Binding	1105 ± 48**	293 ± 18
A₂-Specific Binding	302 ± 22	442 ± 171

The results are presented as the mean (n = 8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test

**Significantly different from mismatch control, p<0.01.

The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

Example 5: Anti-sense Oligos directed to other Target Nucleic Acids

This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were prepared to adenosine receptor mRNAs exemplified by the adenosine A₁, A_{2b}, and A₃ receptor mRNAs. Anti-sense Oligo I was disclosed above (SEQ. ID NO:1). Five additional anti-sense phosphorothioate oligos were designed and synthesized as indicated above.

- 1- Oligo II (SEQ. ID NO: 7) also targeted to the adenosine A₁ receptor, but to a different region than Oligo I.
- 2- Oligo V (SEQ. ID NO: 10) targeted to the adenosine A_{2b} receptor.
- 3- Oligos III (SEQ. ID NO: 8) and IV (SEQ. ID NO: 9) targeted to different regions of the adenosine A₃ receptor.
- 4- Oligo I-PD (SEQ. ID NO: 1681) (a phosphodiester oligo of the same sequence as Oligo I).

These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific for that species, unless the segment of the target mRNA of other species happens to contain a similar sequence. All anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

Example 6: Design & Sequences of other Anti-sense Oligos

Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected for this study to complement the data on Oligo I (SEQ ID NO: 1) provided in Examples 1 to 4 above. This oligo is anti-sense to one region of the adenosine A₁ receptor mRNA. The oligos tested are identified as anti-sense Oligos I (SEQ ID NO: 1) and II (SEQ. ID No: 7) targeted to a different region of the adenosine A₁ receptor mRNA, Oligo V (SEQ. ID No:8) targeted to the adenosine A_{2b} receptor mRNA, and anti-sense Oligos III and IV (SEQ. ID NOS: 9 and 10) targeted to two different regions of the adenosine A₃ receptor mRNA. The sixth oligo (Oligo I-PD) is a phosphodiester version of Oligo I (SEQ. ID NO:1). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

(I) Anti-sense Oligo I

The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A₁ adenosine receptor mRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ. ID NO:1). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., Nature, 385:721 (1977), the relevant portions of which reference are incorporated in their entirety herein by reference.

(II) Anti-sense Oligo II

A phosphorothioate anti-sense oligo (SEQ. ID NO:7) was designed in accordance with the invention to target the rabbit adenosine A₁ receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: 5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7).

5 (III) Anti-sense Oligo III

A phosphorothioate anti-sense oligo other than that provided in Example 1 above (SEQ. ID NO:8) was designed in accordance with the invention to target the anti-sense A₃ receptor mRNA region +3 to +22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: 5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8).

10 (IV) Anti-sense Oligo IV

Yet another phosphorothioate anti-sense oligo (SEQ. ID NO:9) was designed in accordance with the invention to target the adenosine A₃ receptor mRNA region +386 to +401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: 5'-GGC CCA GGG CCA GCC-3' (SEQ. ID NO:9).

15 (V) Anti-sense Oligo V

A phosphorothioate anti-sense oligo (SEQ. ID NO:10) was designed in accordance with the invention to target the adenosine A_{2b} receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: 5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10).

20 (VI) A₁ Mismatch Oligos

Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (SEQ. ID NO: 1) described in Example 5 above: A₁ MM2:5'-GTA GGT GGC GGG CAA GGC GGG-3' (SEQ. ID NO:2421), and A₁ MM3:5'-GAT GGA GGC GGG CAT GGC GGG-3' (SEQ. ID NO:2422). Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A₁ receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

(VII) Anti-sense Oligo A₁-PD (Oligo VI)

30 A phosphodiester anti-sense oligo (Oligo VI; SEQ. ID NO:2420) having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGC CGG CAT GGC GGG-3' (SEQ. ID NO:2420).

III) Controls

35 Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

Example 7: Synthesis of Anti-sense Oligos

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucleotide II (SEQ. ID NO:7), anti-sense oligonucleotide III (SEQ. ID NO: 8) and anti-sense oligonucleotide IV (SEQ. ID NO: 9) were each synthesized and purified in this manner.

Example 8: Preparation of Allergic Rabbits

45 Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali,

S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant portions of which are incorporated in their entirety here by reference. Immunizations were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

10 **DOSE-RESPONSE STUDIES**

Example 9: Experimental Setup

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5µm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

Example 10: Crossover Experiments

For some experiments utilizing anti-sense oligo I (SEQ ID NO: 1) and a corresponding mismatch control oligonucleotide A1MM2, following a 2 week interval, the animals were crossed over, with those previously administered the mismatch control A1MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A1MM2 oligo. The number of animals per group was as follows. For mismatch A1MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A1MM3 n=4 (Control 2) and for A1AS anti-sense oligo I, n=8. The A1MM3 oligo-treated animals were analyzed separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (SEQ. ID NO: 1), no PC₅₀ value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC₅₀ values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo (SEQ ID NO: 1), or the A1MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

40 **Example 11: Anti-sense Oligo Formulation**

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (SEQ. ID No:1) in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in Example 19 below and in Table 1 of Nyce & Metzger, Nature 385: 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (SEQ. IS NOS; 7, 8 and 9).

Example 12: Specificity of Oligo I for Adenosine A₁ Receptor (Receptor Binding Studies)

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi from rabbits which had been administered 20 mg oligo I (SEQ ID NO: 1) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37°C to remove endogenous adenosine. See, Bradford, M. M. Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [³H]DPCPX, [³H]NFC17731, or [³H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., Pharmacol. Exptl. Ther. 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

Example 13: Pulmonary Function Measurements (Compliance C_{dyn} and Resistance)

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, Proc. Soc. Exp. Biol. Med. 144: 509-512 (1973), the relevant portion of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow (v) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH). An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure (P_{tp}). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance (R_t) and dynamic compliance (C_{dyn}) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and C_{dyn} was calculated using the total volume and the difference in P_{tp} at zero flow, and R_t was calculated as the ratio of P_{tp} and V at mid-tidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., Arch. Int. Pharmacodyn. Ther. 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness. Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The BHR was then determined by calculating the concentration of histamine (mg/ml) required to reduce the C_{dyn} 50% from baseline (PC_{50} Histamine).

Example 15: Cardiovascular Effect of Anti-sense Oligo I

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.5 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent disclosure being incorporated in its entirety here by reference. A thermocouple was then inserted into the left carotid artery of each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured. A thermodilution curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20EC to determine the correctness of positioning of the thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were isolated. The femoral vein was used as a portal for drug injections, and the femoral artery for blood pressure and heart rate measurements. Once constant baseline cardiovascular parameters were established, CardiomaxJ measurements of blood pressure, heart rate, cardiac output, total peripheral resistance, and cardiac contractility were made.

Example 16: Duration of Action of Oligo I (SEQ. ID NO: 1)

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% (PC_{50} Adenosine) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized doses of (SEQ. ID NO: 1) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the PC_{50} Adenosine values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

Example 17: Reduction of Adenosine A_{2b} Receptor Number by Anti-sense Oligo V

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (SEQ ID NO:10) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine A_{2b} receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at $p < 0.05$ using Student's paired t test, and are discussed in Example 28 below.

Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)

Oligo I (SEQ ID NO:1) countered the effects of adenosine and eliminated sensitivity to it for adenosine amounts up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (SEQ ID NO:1681), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (SEQ ID NO:1), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at $p < 0.001$, Student's paired t test. The results are discussed in Example 29 below.

RESULTS OBTAINED FOR ANTI-SENSE OLIGO I (SEQ. ID NO: 1)

Example 19: Results of Prior Work

The nucleotide sequence and other data for anti-sense oligo I (SEQ. ID NO: 1), which is specific for the adenosine A₁ receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (SEQ. ID NO: 1):

- (1) The anti-sense oligo I reduces the number of adenosine A₁ receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5 below.
- (2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.
- (3) The Oligo I attenuates bronchial hyperresponsiveness as measured by PC₅₀ histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5 above.
- (4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine A₁ receptor, and has no effect at all at any dose on either the very closely related adenosine A₂ receptor or the related bradykinin B₂ receptor. This is seen in Table 5 below.
- (5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (SEQ. ID NO:1682 and SEQ. ID NO:1683) which have identical base composition and molecular weight but differed from the anti-sense oligo I (SEQ ID NO: 1) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors (A₁, A₂ or B₂).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine A₁ receptor, are unexpected results. The showings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.

Example 20: Oligo I Significantly Reduces Response to Adenosine Challenge

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A₁-selective ligand [³H]DPCPX and the bradykinin B₂-selective ligand [³H]NPC 17731 in membranes isolated from airway smooth muscle of A₁ adenosine receptor and B₂ bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

Table 5: Binding Characteristics of Three Anti-Sense Oligos

Treatment ¹	A ₁ receptor		B ₂ receptor	
	Kd	B _{max}	Kd	Bmax
Adenosine A₁	Receptor			
20 mg	0.36±0.029 nM	19±1.52 fmoles*	0.39±0.031 nM	14.8±0.99fmoles
2 mg	0.38±0.030 nM	32±2.56 fmoles*	0.41±0.028 nM	15.5±1.08
0.2 mg	0.37±0.030 nM	49±3.43 fmoles	0.34±0.024 nM	15.0±1.06
A₁MM1	(Control)			
20 mg	0.34±0.027 nM	52.0±3.64 fmoles	0.35±0.024 nM	14.0±1.0 fmoles
2 mg	0.37±0.033 nM	51.8±3.88 fmoles	0.38±0.028 nM	14.6±1.02
B₂A (Bradykinin	Receptor)			
20 mg	0.36±0.028 nM	45.0±3.15 fmoles	0.38±0.027 nM	8.7±0.62

2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
B₂MM				
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

¹ Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected t test. n = 4-6 for all groups.

* Significantly different from mismatch control- and saline-treated groups, p<0.001;

**Significantly different from mismatch control- and saline-treated groups, p<0.05.

Example 21: Dose-response Effect of Oligo I

Anti-sense oligo I (SEQ ID NO:1) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

Table 6: Dose-Response Effect to Anti-sense Oligo I

Total Dose (mg)	PC ₅₀ Adenosine (mg Adenosine)
Anti-sense Oligo I	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
A₁MM2 oligo (control)	
0.2	2.51±0.46
2.0	3.13± 0.71
20	3.25± 0.34
The above results were studied with the Student's paired t test and found to be statistically different, p=0.05	

The oligo I (SEQ. ID NO:1), an anti-adenosine A₁ receptor oligo, acts specifically on the adenosine A₁ receptor, but not on the adenosine A₂ receptors. These results stem from the treatment of rabbits with anti-sense oligo I (SEQ. ID NO:1) or mismatch control oligo (SEQ. ID NO:1682; A₁MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A₁ and adenosine A₂ receptors determined as reported in Nyce & Metzger (1997), supra.

Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product

Oligo I (SEQ. ID No:1) is specific for the adenosine A₁ receptor whereas its mismatch controls had no activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (SEQ. ID NO:1682 and SEQ. ID NO:1683) evidenced no effect on the PC₅₀ Adenosine value. On the contrary, the administration of anti-sense oligo I (SEQ. ID NO:1) showed a seven-fold increase in the PC₅₀ Adenosine value. The results clearly indicate that the anti-sense oligo I (SEQ. ID NO: 1) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 6 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 5). The Oligo I was also shown to be totally specific for the adenosine A₁ receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A₂ receptor or the bradykinin B₂ receptor (see, lines 8-10 of Table 6 above). In addition, the results shown in Table 6 establish that the anti-sense oligo I (SEQ. ID NO:1) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an

anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A₁MM2; SEQ. ID NO:1682 and A₁MM3; SEQ. ID NO:1683) show any effect on PC₅₀ Adenosine values or on attenuating the number of adenosine A₁ receptors.

Example 23: Effect on Aeroallergen-induced Bronchoconstriction & Inflammation

The Oligo I (SEQ. ID NO:1) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID NO:1) and the mismatch oligos (A₁MM2, SEQ. ID NO:1682 and A₁MM3, SEQ. ID NO:1682) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%, p<0.05; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A₁MM2 (Control) on allergen-induced airway obstruction. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced BHR was determined as above. As calculated from the PC₅₀ Histamine value, the anti-sense oligo I (SEQ. ID NO:1) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched control (61%, p<0.05; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A₁MM mismatch control on allergen-induced BHR was observed. The results indicated that anti-sense oligo I (SEQ. ID NO:1) is effective to protect against aeroallergen-induced bronchoconstriction (house dust mite). In addition, the anti-sense oligo I (SEQ. ID NO:1) was also found to be a potent inhibitor of dust mite-induced bronchial hyperresponsiveness, as shown by its effects upon histamine sensitivity which indicates anti-inflammatory activity for anti-sense oligo I (SEQ. ID NO:1).

Example 24: Anti-sense Oligo I is Free of Deleterious Side Effects

The Oligo I (SEQ. ID NO:1) was shown to be free of side effects that might be toxic to the recipient. No changes in arterial blood pressure, cardiac output, stroke volume, heart rate, total peripheral resistance or heart contractility (dPdT) were observed following administration of 2.0 or 20 mg oligo I (SEQ. ID NO:1). The addition, the results of the measurement of cardiac output (CO), stroke volume (SV), mean arterial pressure (MAP), heart rate (HR), total peripheral resistance (TPR), and contractility (dPdT) with a CardiomaxJ apparatus (Columbus Instruments, Ohio) were assessed. These results evidenced that oligo I (SEQ. ID NO:1) has no detrimental effect upon critical cardiovascular parameters. More particularly, this oligo does not cause hypotension. This finding is of particular importance because other phosphorothioate anti-sense oligonucleotides have been shown in the past to induce hypotension in some model systems. Furthermore, the adenosine A₁ receptor plays an important role in sinoatrial conduction within the heart. Attenuation of the adenosine A₁ receptor by anti-sense oligo I (SEQ. ID NO:1) might be expected to result, therefore, in deleterious extrapulmonary activity in response to the downregulation of the receptor. This is not the case. The anti-sense oligo I (SEQ. ID NO:1) does not produce any deleterious intrapulmonary effects and renders the administration of the low doses of the present anti-sense oligo free of unexpected, undesirable side effects. This demonstrates that when oligo I (SEQ. ID NO:1) is administered directly to the lung, it does not reach the heart in significant quantities to cause deleterious effects. This is in contrast to traditional adenosine receptor antagonists like theophylline which do escape the lung and can cause deleterious, even life-threatening effects outside the lung.

Example 25: Long Lasting Effect of Oligo I

The Oligo I (SEQ. ID NO:1) evidenced a long lasting effect as evidenced by the PC₅₀ and Resistance values obtained upon its administration prior to adenosine challenge. The duration of the effect was measured for with respect to the PC₅₀ of adenosine anti-sense oligo I when administered in four equal doses of 5 mg each by means of a nebulizer via an endotracheal tube, as described above. The effect of the agent is significant over days 1 to 8 after administration. When the effect of the anti-sense oligo I (SEQ. ID

NO:1) had disappeared, the animals were administered saline aerosols (controls), and the PC₅₀ Adenosine values for all animals were measured again. Saline-treated animals showed base line PC₅₀ adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (SEQ. ID NO: 1) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC₅₀ adenosine (p<0.05) and resistance (p<0.05). These results show that anti-sense oligo I (SEQ. ID NO:1) has an extremely long duration of action, which is completely unexpected.

Example 26: Anti-sense Oligo II

Anti-sense oligo II, targeted to a different region of the adenosine A₁ receptor mRNA, was found to be highly active against the adenosine A₁-mediated effects. The experiment measured the effect of the administration of anti-sense oligo II (SEQ. ID NO:7) upon compliance and resistance values when 20 mg anti-sense oligo II or saline (control) were administered to two groups of allergic rabbits as described above. Compliance and resistance values were measured following an administration of adenosine or saline as described above in Example 13. The effect of the anti-sense oligo of the invention was different from the control in a statistically significant manner, p<0.05 using paired t-test, compliance; p<0.01 for resistance. The results showed that anti-sense oligo II (SEQ. ID NO:7), which targets the adenosine A₁ receptor, effectively maintains compliance and reduces resistance upon adenosine challenge.

Example 27: Antisense Oligos III and IV

Oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) were shown to be in fact specifically targeted to the adenosine A₃ receptor by their effect on reducing inflammation and the number of inflammatory cells present upon separate administration of 20 mg of the anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) to allergic rabbits as described above. The number of inflammatory cells was determined in their bronchial lavage fluid 3 hours later by counting at least 100 viable cells per lavage. The effect of anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) upon granulocytes, and upon total cells in bronchial lavage were assessed following exposure to dust mite allergen. The results showed that the anti-sense oligo IV (SEQ. ID NO:9) and anti-sense oligo III (SEQ. ID NO:8) are very potent anti-inflammatory agents in the asthmatic lung following exposure to dust mite allergen. As is known in the art, granulocytes, especially eosinophils, are the primary inflammatory cells of asthma, and the administration of an i-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) reduced their numbers by 40% and 66%, respectively. Furthermore, anti-sense oligos IV (SEQ. ID NO:9) and III (SEQ. ID NO:8) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A₃ agents of the invention. Inflammation is known to underlie bronchial hyperresponsiveness and allergen-induced bronchoconstriction in asthma. Both anti-sense oligonucleotides III (SEQ. ID NO:8) and IV (SEQ. ID NO:9), which are targeted to the adenosine A₃ receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

Example 28: Anti-sense Oligo V

The anti-sense oligo V (SEQ. ID NO:10), targeted to the adenosine A_{2b} adenosine receptor mRNA was shown to be highly effective at countering adenosine A_{2b}-mediated effects and at reducing the number of adenosine A_{2b} receptors present to less than half.

Example 29: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS (SEQ. ID NO:1681)

Oligos I (SEQ. ID NO:1) and I-DS (SEQ. ID NO:1681) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (SEQ. ID NO:1681) was statistically significantly less effective in countering the effect of adenosine whereas oligo I (SEQ. ID NO:1) showed high effectiveness, evidencing a PC₅₀ Adenosine of 20 mg.

Example 30: Anti-sense Oligo VI

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A₁ receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A₁ receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A₁ receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A₁ receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The Oligo VI is directed to the adenosine A₁ receptor gene, and has the following sequence: 5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO: 2). The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

Example 31: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

Example 32: Adenosine Aerosol Preparation

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5 μm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) below.

Example 33: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the A₁ receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter, PC₅₀ adenosine studies were performed on the morning of the third day and compared to pre-treatment PC₅₀ values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 7 below.

Table 7: PC₅₀ Adenosine before & after Aerosolized Adenosine Treatment

Treatment Time	PC ₅₀ Adenosine (mg)
Pre-treatment	3.0 ±2.1
Post-treatment	>20.0*
* maximum achievable dose due to adenosine insolubility in saline	

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 7 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

Example 34: Conclusions

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine A₁ receptor mRNA, 1 anti-sense oligo targeting an adenosine A_{2b} receptor mRNA, and the 2 anti-sense oligos targeting an A₃ receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to. The activity of the anti-sense oligos of this invention, moreover, is specific to the target and substitutively fails to inhibit another target. In addition, the results presented also show that the administration of the present agents results in extremely low or non-existent deleterious side effects or toxicity. This represents 100% success in providing agents that are highly effective and specific in the treatment of bronchoconstriction and/or inflammation. This invention is broadly applicable in the same manner to all gene(s) and corresponding mRNAs encoding proteins involved in or associated with airway diseases. A comparison of the phosphodiester and a version of the same oligonucleotide wherein the phosphodiester bonds are substituted with phosphorothioate bonds evidenced an unexpected superiority for the phosphorothioate oligonucleotide over the phosphodiester anti-sense oligo.

Example 35: In Vivo Response to Adenosine Challenge with & without Oligo I Pretreatment

Two hyper responsive monkeys (ascaris sensitive) were challenged with inhaled adenosine, with and without pre-treatment with anti-sense oligo I (SEQ.ID NO: 1). The PC₄₀ adenosine was calculated from the data collected as being equivalent to that amount of adenosine in mg that causes a 40% decrease in dynamic compliance in hyper-responsive airways. The Oligo I (SEQ. ID NO:1; EPI 2010) was subsequently administered at 10 mg/day for 2 days by inhalation. On the third day, the PC adenosine was again measured. The PC₄₀ adenosine value prior to treatment with Oligo I was compared side-by-side with



to the PC₄₀ adenosine taken after administration of Oligo I (Figure not shown). The results of the experiment conducted with two animals showed that any sensitivity to adenosine was completely eliminated by the administration of the oligo of this invention in one animal, and substantially reduced in the second.

5 Example 36: Extension of the experimental Results

The method of the present invention is also practiced with anti-sense oligonucleotides targeted to many genes, mRNAs and their corresponding proteins as described above, in essentially the same manner as given above, for the treatment of various conditions in the lungs. Examples of these are Human A2a adenosine receptor, Human A2b adenosine receptor, Human IgE receptor β , Human Fc-epsilon receptor

- 10 CD23 antigen (IgE receptor), Human IgE receptor, α subunit, Human IgE receptor, Fc epsilon R, Human histidine decarboxylase, Human beta tryptase, Human tryptase-I, Human prostaglandin D synthase, Human cyclooxygenase-2, Human eosinophil cationic protein, Human eosinophil derived neurotoxin, Human eosinophil peroxidase, Human intercellular adhesion molecule-1 (CAM-1), Human vascular cell adhesion molecule 1 (VCAM-1), Human endothelial leukocyte adhesion molecule (ELAM-1), Human P Selectin, 15 Human endothelial monocyte activating factor, Human IL3, Human IL4, Human IL5, Human IL6, Human monocyte-derived neutrophil chemotactic factor, Human neutrophil elastase (medullasin), Human neutrophil oxidase factor, Human cathepsin G, Human defensin 1, Human defensin 3, Human macrophage inflammatory protein-1-alpha, Human muscarinic acetylcholine receptor HM1, Human muscarinic acetylcholine receptor HM3, Human fibronectin, Human interleukin 8, Human GM-CSF, Human tumor 20 necrosis factor α , Human leukotriene C4 synthase, Human major basic protein, and many more.

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

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set.seed(1234)
N = 1000
n = 100
K = 10
M = 1000000
nMC = 10000
nMC2 = 10000
nMC3 = 10000
nMC4 = 10000
nMC5 = 10000
nMC6 = 10000
nMC7 = 10000
nMC8 = 10000
nMC9 = 10000
nMC10 = 10000
nMC11 = 10000
nMC12 = 10000
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nMC98 = 10000
nMC99 = 10000
nMC100 = 10000

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**WHAT IS CLAIMED AS NOVEL & UNOBVIOUS
IN UNITED STATES LETTERS PATENT IS:**

1. A pharmaceutical composition, comprising
an oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or
5 lung inflammation, allergy(ies), or surfactant depletion or hyposecretion, when administered to a mammal,
the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the
group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking
regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a
gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the
10 polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and
a pharmaceutically or veterinarily acceptable carrier or diluent.
2. The composition of claim 1, wherein the oligo is A-free.
3. The composition of claim 1, wherein the target is selected from the group consisting of
the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3'
15 intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a
gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the
oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; the
polypeptides being selected from the group consisting of peptide factors and transmitters, antibodies,
cytokines and chemokines, enzymes, binding proteins, adhesion molecules, their receptors, and malignancy
20 associated proteins.
4. The composition of claim 3, wherein the target is selected from the group consisting of
the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3'
intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a
gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the
25 oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos;
wherein the polypeptides are selected from the group consisting of transcription factors, stimulating and
activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine
receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes,
immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous
30 and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding
proteins, and malignancy associated proteins.
5. The agent of claim 4, wherein the encoded polypeptide(s) is(are) selected from the group
consisting of adenosine receptors A1, A2a, A2b and A3, bradykinin receptors B1 and B2, Nf6B
35 Transcription Factor, Interleukin-8 Receptor (IL-8 R), Interleukin 5 Receptor (IL-5 R), Interleukin 4
Receptor (IL-4 R), Interleukin 3 Receptor (IL-3 R), Interleukin-1 β (IL-1 β), Interleukin 1 β Receptor (IL-
1 β R), Eotaxin, Tryptase, Major Basic Protein, β 2-adrenergic Receptor Kinase, Endothelin Receptor A,
Endothelin Receptor B, Preproendothelin, Bradykinin B2 Receptor, IgE High Affinity Receptor,
Interleukin 1 (IL-1), Interleukin 1 Receptor (IL-1 R), Interleukin 9 (IL-9), Interleukin-9 Receptor (IL-9 R),
40 Interleukin 11 (IL-11), Interleukin-11 Receptor (IL-11 R), Inducible Nitric Oxide Synthase, Cyclo-
oxygenase-1 (COX 1), Cyclo-oxygenase-2 (COX-2), Intracellular Adhesion Molecule 1 (ICAM-1)
Vascular Cellular Adhesion Molecule (VCAM), Rantes, Endothelial Leukocyte Adhesion Molecule
(ELAM-1), Monocyte Activating Factor, Neutrophil Chemotactic Factor, Neutrophil Elastase, Defensin 1,
2 and 3, Muscarinic Acetylcholine Receptors, Platelet Activating Factor, Tumor Necrosis Factor α , 5-
45 lipooxygenase, Phosphodiesterase IV, Substance P, Substance P Receptor, Histamine Receptor, Chymase,
CCR-1 CC Chemokine Receptor, CCR-2 CC Chemokine Receptor, CCR-3 CC Chemokine Receptor,
CCR-4 CC Chemokine Receptor, CCR-5 CC Chemokine Receptor, Prostanoid Receptors, GATA-3
Transcription Factor, Neutrophil Adherence Receptor, MAP Kinase, Interleukin-9 (IL-9), NFAT
Transcription Factor, STAT 4, MIP-1 α , MCP-2, MCP-3, MCP-4, Cyclophilins, Phospholipase A2, Basic

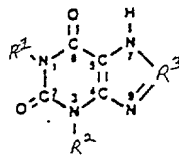
004040 004040 004040 004040 004040

Fibroblast Growth Factor, Metalloproteinase, CSBP/p38 MAP Kinase, Tryptose Receptor, PDG2, Interleukin-3 (IL-3), Interleukin-1 β (IL-1 β), Cyclosporin A-Binding Protein, FK5-Binding Protein, α 4 β 1 Selectin, Fibronectin, α 4 β 7 Selectin, Mad CAM-1, LFA-1 (CD11a/CD18), PECAM-1, LFA-1 Selectin, C3bi, PSGL-1, E-Selectin, P-Selectin, CD-34, L-Selectin, p150,95, Mac-1 (CD11b/CD18), Fucosyl transferase, VLA-4, CD-18/CD11a, CD11b/CD18, ICAM2 and ICAM3, C5a, CCR3 (Eotaxin Receptor), CCR1, CCR2, CCR4, CCR5, LTB-4, AP-1 Transcription Factor, Protein kinase C, Cysteinyl Leukotriene Receptor, Tachykinin Receptors (tach R), I κ B Kinase 1 & 2, STAT 6, c-mas and NF-Interleukin-6 (NF-IL-6).

6. The composition of claim 1, wherein one or more As is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors.

7. The composition of claim 6, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl.

8. The composition of claim 7, wherein the pyrimidines and purines are substituted at a position selected from the group consisting of positions 1, 2, 3, 4, 7, and 8, and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO₂ aryl.

9. The composition of claim 8, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

10. The composition of claim 1, where one or more methylated cytosine(s) (^mC) is(are) substituted for a C in one or more CpG dinucleotide(s), if present in the oligo(s).

11. The composition of claim 1, wherein one or more mononucleotide(s) of the oligo(s) is(are) linked or modified by one or more methylphosphonate, 5'-N-carbamate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMI), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

12. The composition of claim 11, wherein the mononucleotide residues are linked by phosphorothioate residues.

13. The composition of claim 1, wherein the anti-sense oligo comprises about 7 to about 60 mononucleotides.

14. The composition of claim 1, wherein the anti-sense oligo comprises fragments 1, 3, 5, 7 and 8 to 2313 (SEQ. ID NOS: 1 through 2419).

15. The composition of claim 1, wherein the anti-sense oligo is operatively linked to, or complexed with, an agent selected from the group consisting of cell internalized or up-taken agents and cell targeting agents.

16. The composition of claim 15, wherein the cell internalized or up-taken agent is selected from the group consisting of transferrin, asialoglycoprotein and streptavidin.

17. The composition of claim 1, wherein the oligo is operatively linked to a vector that is a prokaryotic or eukaryotic vector.

18. The composition of claim 1, wherein the oligo(s) is(are) hybridized to a ribonucleic acid.

19. A cell, carrying the oligo of claim 1.

20. The composition of claim 1, wherein the carrier or diluent is selected from the group consisting of gaseous, liquid, and solid carriers or diluents.

21. The composition of claim 20, further comprising an agent selected from the group consisting of other therapeutic agents, surfactants, flavoring and coloring agents, fillers, volatile oils, buffering agents, dispersants, RNA inactivating agents, anti-oxidants, flavoring agents, propellants and preservatives.

22. The composition of claim 21, comprising one or more oligo(s), a surfactant, and a carrier or diluent for the oligo and the surfactant.

23. The composition of claim 21, wherein the agent is an RNA inactivating agent which comprises an enzyme, optionally a ribozyme.

24. The composition of claim 1, wherein the anti-sense oligo is present in an amount of about 0.01 to about 99.99 w/w of the composition.

25. The composition of claim 1, which is a systemic or topical formulation.

26. The formulation of claim 25, selected from the group consisting of oral, intrabuccal, intrapulmonary, rectal, intrauterine, intratumor, intracranial, nasal, intramuscular, subcutaneous, intravascular, intrathecal, inhalable, transdermal, intradermal, intracavitary, implantable, iontophoretic, ocular, vaginal, intraarticular, otical, intravenous, intramuscular, intraglandular, intraorgan, intralymphatic, implantable, slow release and enteric coating formulations.

27. The formulation of claim 26, which is an oral formulation, wherein the carrier is selected from the group consisting of solid and liquid carriers.

28. The oral formulation of claim 27, which is selected from the group consisting of a powder, dragees, tablets, capsules, sprays, aerosols, solutions, suspensions and emulsions, optionally oil-in-water and water-in-oil emulsions.

29. The formulation of claim 25, which is a topical formulation, wherein the carrier is selected from the group consisting of creams, gels, ointments, sprays, aerosols, patches, solutions, suspensions and emulsions.

30. The formulation of claim 26, which is an injectable formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

31. The formulation of claim 26, which is a rectal formulation, optionally a suppository.

32. The formulation of claim 26, which is a transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

33. The transdermal formulation of claim 32, which is an iontophoretic transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions, and wherein the formulation further comprises a transdermal transport promoting agent.

34. The formulation of claim 26, which is provided in an implant, a capsule or a cartridge.

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53. The method of claim 51, wherein the composition is administered into the subject's respiratory system.

54. The method of claim 53, wherein the composition is administered directly into the subject's lung (s).

55. The method of claim 51, wherein the administered composition comprises an amount of the oligo(s) and is administered under conditions effective to reduce the production or availability, or to
5 increase the degradation, of the target mRNA or to reduce the amount of the target polypeptide present in the lungs.

56. The method of claim 51, wherein the agent is administered as a respirable aerosol.

57. The method of claim 51, wherein the pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction are associated with a disease or
10 condition selected from the group consisting of pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and cancer.

58. The method of claim 57, wherein the disease or condition is associated with an
15 allergy(ies), and the oligo is anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors or are anti-sense to the immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors mRNA; combinations of
20 the oligo(s); and mixtures of the oligos.

59. The method of claim 57, wherein the disease or condition is associated with a malignancy or cancer, and the oligo is anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and/or encodes a
25 malignancy associated protein, or is(are) anti-sense to the oncogene or malignancy associated protein mRNA; combinations of the oligo(s); and mixtures of the oligos and the oligo(s) is(are) administered in an amount effective to reduce either the level of the protein mRNA or of the malignancy associated protein, or to reduce the growth of or provide beneficial characteristics to malignant cells.

60. The method of claim 51, wherein the composition is administered transdermally or
30 systemically.

61. The method of claim 60, wherein the composition is administered orally, intracavitarily, intranasally, intraanally, intravaginally, intrauterally, intraarticularly, transdermally, intrabucally, intravenously, subcutaneously, intramuscularly, intravascularly, intratumorously, intraglandularly, intraocularly, intracranial, into an organ, intravascularly, intrathecally, intralymphatically, intraotically, by
35 implantation, by inhalation, intradermally, intrapulmonarily, intraotically, by slow release, by sustained release and by a pump.

62. The method of claim 51, wherein the subject is a non-human mammal.

63. The method of claim 51, wherein the mammal is a human.

64. The method of claim 51, wherein the oligo is administered in amount of about 0.005 to
40 about 150 mg/kg body weight.

65. The method of claim 51, wherein the oligo is obtained by

(a) selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C;

(b) obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected
45 fragment and has a C and G nucleic acid content of up to and including about 15%; and

(c) obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an A base content of up to and including about 15%.

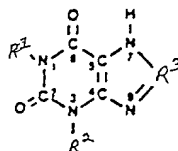
65. The method of claim 64, wherein the oligo is A-free.

66. The method of claim 51, wherein the target is selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene or a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide or oncogene mRNA; combinations of the oligo(s); and mixtures of the oligos; wherein the polypeptide is selected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules defensins, growth factors, vasoactive peptides, peptide receptors and binding proteins, and malignancy associated proteins.

67. The method of claim 51, wherein one or more As in the oligo(s) is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 0.3 of the adenosine base agonist or antagonist activity at an adenosine A₁, A_{2a}, A_{2b} and A₃ receptors.

68. The method of claim 67, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl.

69. The method of claim 67, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8 and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkoxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO₂ aryl.

70. The method of claim 69, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

71. The method of claim 51, further comprising substituting a methylated cytosine (mC) for a C in one or more CpG dinucleotide(s), if present in the oligo(s).

72. The method of claim 51, further comprising substituting by, or modifying one or more nucleotide residue(s) of the oligo(s) with, methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy

(methylimino) (MOMI), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

73 The method of claim 51, further comprising operatively linking to, or complexing the oligo(s) with, an agent selected from the group consisting of cell internalized and up-taken agent(s) and cell targeting agents.

74. The method of claim 73, wherein the cell internalized or up taken agent is selected from the group consisting of transferrin, asialoglycoprotein, and streptavidin.

75. The method of claim 73, wherein the cell targeting agent is a vector, optionally a prokaryotic or eukaryotic vector.

76. A method of treating a disease or condition associated with a target selected associated with a disease or condition afflicting lung airways, comprising conducting the method of claim 56.

77. The method of claim 76, wherein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to reduce the amount of the polypeptide present in the lungs.

78. The method of claim 77, wherein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to increase the amount of the surfactant present in the subject's lungs.

79. The composition of claim 4, wherein the oligo(s) is(are) anti-sense to the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an adenosine A1, A2a, A2b and/or A3 receptor, or anti-sense to the adenosine A1, A2a, A2b and/or A3 receptor mRNA.

80. The composition of claim 79, wherein all nucleotide linking residues are phosphorothioates.

81. The composition of claim 1, wherein the oligo is a DNA.

82. The composition of claim 1, wherein the oligo is an RNA.

83. The composition of claim 1, wherein the oligo comprises about 7 to up to about 60 mononucleotides.

84. The composition of claim 79, wherein the oligo(s) is selected from the group consisting of fragment(s) SEQ ID NOS: 1, 3, 5, 7, 8, and/or 11 through 2419, optionally wherein at least one mononucleotide residue is substituted or modified by methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino), (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMA), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate residues and/or combinations thereof.

85. The method of claim 51, wherein the oligo is administered topically to the airway, respiratory or pulmonary epithelium of the subject.

86. The composition of claim 1, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

87. The composition of claim 1, further comprising a propellant.

88. The method of claim 50, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

89. The method of claim 50, further comprising adding to the oligo a propellant.

90. The method of claim 51, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

91. The method of claim 51, further comprising adding to the oligo a propellant.

**LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT
& METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED
WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,
ALLERGY(IES) & SURFACTANT DEPLETION**

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ABSTRACT OF THE INVENTION

An in vivo method of selectively delivering a nucleic acid to a target gene or mRNA, comprises the topical administration, e. g. to the respiratory system, of a subject of a therapeutic amount of an oligonucleotide (oligo) that is anti-sense to the initiation codon region, the coding region, the 5' or 3' intron-exon junction; or regions within 2 to 10 nucleotides of the junctions of the gene, or antisense to a mRNA complementary to the gene in an amount effective to reach the target polynucleotide and reducing or inhibiting expression. In addition a method of treating an adenosine mediated effect, comprises topically administering to a subject an anti-sense oligo in an amount effective to treat the respiratory, pulmonary, or airway disease. In order to minimize triggering adenosine receptors by their metabolism, the administered oligos have a low content of or are essentially free of adenosine. A pharmaceutical composition and formulations comprise the oligo anti-sense to an adenosine receptor, genes and mRNAs encoding them, genomic and mRNA flanking regions, intron and exon borders and all regulatory and functionally related segments of the genes and mRNAs encoding the polypeptides, their salts and mixtures. Various formulations contain a requisite carrier, and optionally other additives and biologically active agents. The low adenosine or adenosine free (des-A) agent for practicing the method of the invention may be prepared by selecting a target gene(s), genomic flanking region(s), RNA(s) and/or polypeptide(s) associated with a disease(s) or condition(s) afflicting lung airways, obtaining the sequence of the mRNA(s) corresponding to the target gene(s) and/or genomic flanking region(s), and/or RNAs encoding the target polypeptide(s), selecting at least one segment of the mRNA which may be up to 60% free of thymidine (T) and synthesizing one or more anti-sense oligonucleotide(s) to the mRNA segments which are free of adenosine (A) by substituting a universal base for A when present in the oligonucleotide. The agent may be prepared by selection of target nucleic acid sequences with GC running stretches, which have low T content, and by optionally replacing A in the anti-sense oligonucleotides with a "Universal or alternative base". The agent, composition and formulations are used for prophylactic, preventive and therapeutic treatment of ailments associated with impaired respiration, lung allergy(ies) and/or inflammation and depletion lung surfactant or surfactant hypoproduction, such as pulmonary vasoconstriction, inflammation, allergies, allergic rhinitis, asthma, impeded respiration, lung pain, cystic fibrosis, bronchoconstriction. The present treatment is suitable for administration in combination with other treatments, e.g. before, during and after other treatments, including radiation, chemotherapy, antibody therapy and surgery, among others. Alternatively, the present agent is effectively administered prophylactically or therapeutically by itself for conditions without known therapies or as a substitute for therapies exhibiting undesirable side effects. The treatment of this invention may be administered directly into the respiratory system of a subject so that the agent has direct access to the lungs, or by other effective routes of administration, e. g. topically, transdermally, by implantation, etc., in an amount effective to reduce or inhibit the symptoms of the ailment.

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